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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 38.75 seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp19808:*\n2: Geneseqp19908:*\n3: Geneseqp20008:*\n4: Geneseqp20018:*\n5: Geneseqp20028:*\n6: Geneseqp20038:*\n7: Geneseqp20048:*\n8: Geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	5	3	AAV79068 Anti-fact
2	29	100.0	7	3	AAAB14789
3	29	100.0	12	3	AAAB14784
4	29	100.0	120	4	AAAG65570
5	29	100.0	121	5	ABG76537 HCV E1 an
6	29	100.0	128	5	ABG76559
7	29	100.0	206	6	ABU24807 Protein e
8	29	100.0	258	7	ABO77482 Pseudomon
9	29	100.0	278	8	ADN27332 Bacterial
10	29	100.0	307	4	AAAG72483
11	29	100.0	321	4	AAAG71475 Human OR-
12	29	100.0	531	8	ADRI10293 Human pro
13	29	100.0	690	3	AAAY50844 A. oryzae
14	29	100.0	690	3	AAAY50835 A. oryzae
15	29	100.0	703	3	AAAB14781
16	29	100.0	703	3	AAAB14782
17	29	89.7	46	4	AAAB82576
18	29	89.7	67	4	ABBA40299 Peptide #
19	29	89.7	67	4	AAAM33985
20	29	89.7	67	4	AAAW73798
21	29	89.7	67	4	AAAM61093
22	29	89.7	67	4	ABG55546
23	29	89.7	67	5	ABG433685
24	29	89.7	79	4	AAU18208
25	29	89.7	79	5	ABG92629

26	26	89.7	79	7	ADC25346	Adc25346 Human ext
27	26	89.7	89	5	ABG68752	Abg68752 Cytochrom
28	26	89.7	162	5	ABP01422	ABP01422 Human ORF
29	26	89.7	173	5	ABG68756	Abg68756 Cytochrom
30	26	89.7	194	7	ADBO8218	Adbo8218 Novel pro
31	26	89.7	205	7	ADBO8219	Adbo8219 Novel pro
32	26	89.7	213	5	ABBB91152	Abbb91152 Herdicia
33	26	89.7	221	6	ADAA55412	Adaa55412 Human pro
34	26	89.7	238	5	ABPA6042	Abpa6042 Human Bly
35	26	89.7	238	7	ADG96869	Adg96869 Single ch
36	26	89.7	242	5	ABBA49910	Abba49910 Listeria
37	26	89.7	304	6	ABU17641	Abu17641 Protein e
38	26	89.7	370	4	AAAG91423	AAg91423 C glutami
39	26	89.7	370	4	AAAG90014	AAg90014 C glutami
40	26	89.7	454	7	ABO63767	ABO63767 Klebsiell
41	26	89.7	455	7	ADFO8003	Adfo8003 Bacterial
42	26	89.7	501	8	ADOA47242	Adoa47242 Rabbit cy
43	26	89.7	502	5	AAE26192	AAe26192 Human cyt
44	26	89.7	502	7	ADE57186	Ades7186 Human pro
45	26	89.7	502	7	ADE57190	Ades7190 Human pro

ALIGNMENTS

RESULT 1
ID AAY79068 standard; peptide; 5 AA.
XX AAY79068;
AC AAY79068;
DT 12-JUN-2000 (first entry)

XX Anti-factor IX/IXa antibody H chain V domain CDRI amino acid sequence.

XX Complementarity determining region 1; CDRI; antibody; Gla domain;
XX factor IX/IXa; blood coagulation; deep venous thrombosis;
XX arterial thrombosis; unstable angina; post myocardial infarction;
XX coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
XX percutaneous transluminal coronary angioplasty; PTCA; inflammation;
XX septic shock; hypotension; adult respiratory distress syndrome; ARDS;
XX arterial fibrillation; disseminated intravascular coagulopathy; DIC.

OS Homo sapiens.

PN WO200012562-A1.

PD 09-MAR-2000.

XX 26-AUG-1999; 99WO-US019453.

XX 28-AUG-1998; 98US-0098233P.
XX 03-MAR-1999; 99US-012767P.

XX (GETH) GENENTECH INC.

XX Adams CW, Devaux B, Eaton DL, Hase PE, Judice JK, Kirchhofer D,
XX Suggett S;
XX WPI; 2000-256595/22.

XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
XX carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
XX stroke, and post myocardial infarction.

XX Claim 2; Fig 2; 84pp; English.

XX This sequence represents a complementarity determining region 1 (CDRI) of
XX the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
XX antibody. Factor IXa is a vitamin K dependent plasma serine protease that
XX participates in the blood coagulation pathways. The Gla domain of factor
XX IXa and its zymogen factor IX contains important structural determinants
XX for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)
CC
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 29; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 1 TYAMH 5

RESULT 2
AAB14789
ID AAB14789 standard; peptide; 7 AA.
XX
AC AAB14789;
XX
DT 06-DEC-2000 (first entry)
XX
DE Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.
XX
KW Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
KW fermentation; foodstuff production; miso; soy sauce; peptide fragment;
KW PCR primer design.
XX
OS Aspergillus oryzae.
XX
PN JP200016547-A.
XX
PD 20-JUN-2000.
XX
PF 07-DEC-1998; 98JP-00347127.
XX
PR 07-DEC-1998; 98JP-00347127.
XX
PA (AICH-) AICHI KEN PREFECTURE.
PA (ICHI-) ICHIBIKI KK.
XX
DR WPI; 2000-477931/42.
XX
PT A new glutaminase and its preparation.
XX
PS Example 2; Page 25; 27pp; Japanese.
XX
CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
CC have molecular weights of approximately 73 kD (as determined by gel
CC filtration). The enzymes have an optimum temperature of approximately 50
CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
CC used in the production of fermented foodstuffs such as soy sauce and
CC miso. Sequences AAB14781-814789 represent fragments of Aspergillus oryzae
CC KBN616 glutaminase which were used as the basis for the design of
CC degenerate PCR primers AAY2206, AAY2207 and AAY2209. These primers
CC were used in the isolation of genomic DNA encoding Aspergillus oryzae
CC KBN616 (AAY2204)
CC
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 29; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 3 TYAMH 7

RESULT 3
AAB14784
ID AAB14784 standard; peptide; 12 AA.
XX
AC AAB14784;
XX
DT 06-DEC-2000 (first entry)
XX
DE Aspergillus oryzae KBN616 glutaminase peptide fragment, SEQ ID NO:6.
XX
KW Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
KW fermentation; foodstuff production; miso; soy sauce;
KW V8 protease digestion.
XX
OS Aspergillus oryzae.
XX
PN JP200016547-A.
XX
PD 20-JUN-2000.
XX
PF 07-DEC-1998; 98JP-00347127.
XX
PR 07-DEC-1998; 98JP-00347127.
XX
PA (AICH-) AICHI KEN PREFECTURE.
PA (ICHI-) ICHIBIKI KK.
XX
DR WPI; 2000-477931/42.
XX
PT A new glutaminase and its preparation.
XX
PS Example 2; Page 9; 27pp; Japanese.
XX
CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
CC have molecular weights of approximately 73 kD (as determined by gel
CC filtration). The enzymes have an optimum temperature of approximately 50
CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
CC used in the production of fermented foodstuffs such as soy sauce and
CC miso. Sequences AAB14784-814786 represent the N-terminal sequences
CC determined for three V8 protease fragments (P1-P3) of Aspergillus oryzae
CC KBN616 glutaminase in an exemplification of the invention
CC
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 29; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 7 TYAMH 11

RESULT 4
AAG65570
ID AAG65570 standard; protein; 120 AA.
XX
AC AAG65570;
XX
DT 30-NOV-2001 (first entry)
XX
DE Amino acid sequence of protein seq Id No. 95.
XX
KW Gene library; immunoglobulin; antibody library; human.
XX


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OS Homo sapiens.
XX
XX WO200162907-A1.
XX
XX 30-AUG-2001.
XX
XX 22-FEB-2001; 2001WO-JP001298.
XX
XX 22-FEB-2000; 2000JP-00050543.
XX
XX (MEDICAL & BIOLOGICAL LAB CO LTD.
XX
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,
XX Okuno Y, Shiraki K;
XX
XX WPI; 2001-565420/63.
XX
XX N-PSDB; AAH47734.
XX
XX Producing gene libraries and antibody libraries, involves selecting a
XX light chain that binds to a heavy chain product to produce a functional
XX formation, and producing a gene library of the light chain variable
XX regions.
XX
XX Examples; p 171; 181pp; Japanese.
XX
XX The invention relates to producing gene libraries, comprising
XX immunoglobulin light and heavy variable region. The method involves
XX selecting light chain that binds with the heavy chain product to produce
XX a functional conformation, producing a gene library comprising a
XX collection of these light chain variable genes, and combining with gene
XX library of heavy chain variable genes. The method is used for production
XX of gene and antibody libraries
XX
XX Sequence 120 AA;
XX
XX Query Match 100.0%; Score 29; DB 4; Length 120;
XX Best Local Similarity 100.0%; Pred. No. 72;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TYAMH 5
XX |||||
XX Db 31 TYAMH 35
XX
XX RESULT 5
XX ABG76537
XX ID ABG76537 standard; protein; 121 AA.
XX
XX AC ABG76537;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE HCV E1 antigen monoclonal antibody #25.
XX
XX Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
XX hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
XX
XX Homo sapiens.
XX
XX WO200260954-A1.
XX
XX 08-AUG-2002.
XX
XX 14-JAN-2002; 2002MO-SE000044.
XX
XX 12-JAN-2001; 2001US-0260889P.
XX
XX (KARO-) KAROLINSKA INNOVATIONS AB.
XX
XX Drakenberg K, Persson MAA;
XX
XX WPI; 2002-608502/65.
XX

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PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
XX (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
XX
XX Disclosure; Page 36; 64pp; English.
XX
XX The invention relates to a human monoclonal antibody or its antigen
XX binding fragments, which exhibit immunological binding affinity for a
XX hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
XX homologous to the binding portion of a human antibody Fab molecule from a
XX combinatorial antibody library. The vaccine composition comprising the
XX antibodies or antigen binding fragments against HCV E1 or E2 antigen or
XX its hypervariable region is useful in treating or preventing HCV
XX infection in a subject. Sequences ABG76513-ABG76568 represent human
XX monoclonal antibodies against HCV E1 antigen
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 29; DB 5; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 73;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TYAMH 5
XX |||||
XX Db 33 TYAMH 37
XX
XX RESULT 6
XX ABG76559
XX ID ABG76559 standard; protein; 128 AA.
XX
XX AC ABG76559;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE HCV E1 antigen monoclonal antibody #47.
XX
XX Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
XX hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
XX
XX Homo sapiens.
XX
XX WO200260954-A1.
XX
XX 08-AUG-2002.
XX
XX 14-JAN-2002; 2002MO-SE000044.
XX
XX 12-JAN-2001; 2001US-0260889P.
XX
XX (KARO-) KAROLINSKA INNOVATIONS AB.
XX
XX Drakenberg K, Persson MAA;
XX
XX WPI; 2002-608502/65.
XX
XX Vaccine comprising a human monoclonal antibody against hepatitis C virus
XX (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
XX
XX Disclosure; Page 52-53; 64pp; English.
XX
XX The invention relates to a human monoclonal antibody or its antigen
XX binding fragments, which exhibit immunological binding affinity for a
XX hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
XX homologous to the binding portion of a human antibody Fab molecule from a
XX combinatorial antibody library. The vaccine composition comprising the
XX antibodies or antigen binding fragments against HCV E1 or E2 antigen or
XX its hypervariable region is useful in treating or preventing HCV
XX infection in a subject. Sequences ABG76513-ABG76568 represent human
XX monoclonal antibodies against HCV E1 antigen
XX
XX Sequence 128 AA;
XX
XX Query Match 100.0%; Score 29; DB 5; Length 128;
XX

```

Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||
32 TYAMH 36

RESULT 7

ABU24807
ID ABU24807 standard; protein; 206 AA.

XX
AC ABU24807;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #10334.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Clostridium botulinum.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA28677.

XX Claim 25; SEQ ID NO 52731; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 206 AA;

Query Match 100.0%; Score 29; DB 6; Length 206;

Best Local Similarity 100.0%; Pred. No. 1,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||
30 TYAMH 34

RESULT 8

ABO77482
ID ABO77482 standard; protein; 258 AA.

XX
AC ABO77482;

XX 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #9657.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD11053.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 26228; 455pp; English.

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using bioclip technology. Sequences ABO67826-
CC ABO84336 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC segdata.uspto.gov/sequence.html

XX Sequence 258 AA;

Query Match 100.0%; Score 29; DB 7; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||||
DB 201 TYAMH 205

RESULT 9
ADN27332
ID ADN27332 standard; protein; 278 AA.
XX AC ADN27332;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #9985.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KW pathogen tolerance; pest tolerance; plant disease resistance;
XX KW cell cycle pathway modification; plant growth regulator;
XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KW bacterial polypeptide.
XX OS Bacteria.
XX PN US200323675-A1.
XX PD 18-DEC-2003.
XX PP 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX DR WPI; 2004-061375/06.
XX PT New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 9985; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.

QY Sequence 278 AA;
|||||
DB 220 TYAMH 224

RESULT 10
AAG72483
ID AAG72483 standard; protein; 307 AA.
XX AC AAG72483;
XX DT 31-JUL-2001 (first entry)
XX DE Human OR-like polypeptide query sequence, SEQ ID NO: 2164.
XX KW Human; olfactory receptor; OR; primary scent determination;
XX KW secondary scent determination; polypeptide library; odour receptor;
XX KW scent profile; scent fingerprint; scent representation.
XX OS Homo sapiens.
XX PN WO200127158-A2.
XX PD 19-APR-2001.
XX PF 06-OCT-2000; 2000WO-US027582.
XX PR 08-OCT-1999; 99US-0158615P.
XX PR 24-FEB-2000; 2000US-0184809P.
XX PA (DIGI-) DIGISCENTS.
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX DR WPI; 2001-290713/30.
XX PT New polynucleotides which encode polypeptides involved in olfactory
XX PT sensation for identifying olfactory agonists and antagonists.
XX PS Example 6; Page 1455-1456; 1857pp; English.

CC The present sequence is a polypeptide encoded by one of 344 newly mined
XX human genes. It was used as a query sequence in a database search of
XX olfactory receptor (OR)-like sequences. The invention relates to isolated
XX polynucleotides encoding polypeptides involved in olfactory sensation.
XX The polynucleotides can be used in screening for olfactory agonists and
XX antagonists. The methods allow for the determination of primary scents
XX and the identification of the odour receptors used to detect these
XX primary scents. The methods also enable determination of secondary scents
XX and the identification of combinations of odour receptors that are
XX involved in detecting such secondary scents. This enables the
XX construction of a scent representation (also called a scent fingerprint
XX or scent profile), which may be used to re-create and edit scents.
XX Libraries of olfactory receptors are useful for determining the
XX interaction pattern of a composition with the receptors, and can be used
XX for determining differences in the olfactory faculties of different
XX individuals
XX Sequence 307 AA;
SQ Query Match 100.0%; Score 29; DB 4; Length 307;


```

AC  AA50844;
XX
XX  24-FEB-2000 (first entry)
XX
DE  A. oryzae glutaminase protein #2.
XX
XX  Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
XX  taste enhancer; seasoning; sauce; paste.
XX
OS  Aspergillus oryzae.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..20
XX  FT /label= signal_peptide
XX  FT Protein 21..690
XX
XX  WO9960104-A1.
XX
XX  25-NOV-1999.
XX
XX  12-MAY-1999; 99WO-JP002455.
XX
XX  15-MAY-1998; 98JP-00134080.
XX  11-SEP-1998; 98JP-00258974.
XX  14-OCT-1998; 98JP-00292443.
XX  30-MAR-1999; 99JP-00089157.
XX
XX  (AJIN ) AJINOMOTO CO INC.
XX
XX  Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
XX
XX  WPI; 2000-053292/04.
XX  N-PSDB; AAZ43684.
XX
XX  Aspergillus oryzae-originated glutaminase and partial amino-acid
XX  PT sequences for enhancing taste particularly in glutamic acid-converting
XX  food processing to make e.g. seasoning sauces and pastes.
XX
XX  Example 3; Page 52-55; 74pp; Japanese.
XX
XX  This invention describes a novel glutaminase enzyme isolated from
XX  CC Aspergillus oryzae which catalyses the decomposition of glutamine to
XX  CC glutamic acid and ammonia. The purified glutaminase and determined
XX  CC partial amino-acid sequence can be used for enhancing taste particularly
XX  CC in glutamic acid-converting food processing to give e.g. seasoning sauces
XX  CC and pastes as well as other seasoning materials. The gene thus obtained
XX  CC can be applied as probe for hybridization providing the gene-containing
XX  CC DNA fragments from genome and cDNA libraries of A. oryzae and A.
XX  CC nidulans, and subsequently modified glutaminase-producing breed. The
XX  CC novel strain of A. oryzae is a highly active because of its somatic
XX  CC secreting ability. This sequence represents the A. oryzae glutaminase
XX  CC enzyme described in the method of the invention
XX
XX  Sequence 690 AA;
XX
XX  Query Match 100.0%; Score 29; DB 3; Length 690;
XX  Best Local Similarity 100.0%; Pred. No. 4.5e+02;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 TYAMH 5
XX  |||||
XX  423 TYAMH 427
XX
XX  RESULT 14
XX  ID AA50835 standard; protein; 690 AA.
XX  AC AA50835;
XX  DT 24-FEB-2000 (first entry)
XX  DE A. oryzae glutaminase protein #1.
XX
XX

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XX  XX  Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
XX  KW taste enhancer; seasoning; sauce; paste.
XX  XX  Aspergillus oryzae.
XX
XX  XX  Key Location/Qualifiers
XX  XX  Peptide 1..20
XX  XX  FT /label= signal_peptide
XX  XX  FT Protein 21..690
XX
XX  XX  WO9960104-A1.
XX
XX  XX  25-NOV-1999.
XX
XX  XX  12-MAY-1999; 99WO-JP002455.
XX
XX  XX  15-MAY-1998; 98JP-00134080.
XX  XX  11-SEP-1998; 98JP-00258974.
XX  XX  14-OCT-1998; 98JP-00292443.
XX  XX  30-MAR-1999; 99JP-00089157.
XX
XX  XX  (AJIN ) AJINOMOTO CO INC.
XX
XX  XX  Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
XX
XX  XX  WPI; 2000-053292/04.
XX  XX  N-PSDB; AAZ43677.
XX
XX  XX  Aspergillus oryzae-originated glutaminase and partial amino-acid
XX  XX  PT sequences for enhancing taste particularly in glutamic acid-converting
XX  XX  food processing to make e.g. seasoning sauces and pastes.
XX
XX  XX  Claim 1a; Page 41-44; 74pp; Japanese.
XX
XX  XX  This invention describes a novel glutaminase enzyme isolated from
XX  CC Aspergillus oryzae which catalyses the decomposition of glutamine to
XX  CC glutamic acid and ammonia. The purified glutaminase and determined
XX  CC partial amino-acid sequence can be used for enhancing taste particularly
XX  CC in glutamic acid-converting food processing to give e.g. seasoning sauces
XX  CC and pastes as well as other seasoning materials. The gene thus obtained
XX  CC can be applied as probe for hybridization providing the gene-containing
XX  CC DNA fragments from genome and cDNA libraries of A. oryzae and A.
XX  CC nidulans, and subsequently modified glutaminase-producing breed. The
XX  CC novel strain of A. oryzae is a highly active because of its somatic
XX  CC secreting ability. This sequence represents the A. oryzae glutaminase
XX  CC enzyme described in the method of the invention
XX
XX  XX  Sequence 690 AA;
XX
XX  XX  Query Match 100.0%; Score 29; DB 3; Length 690;
XX  XX  Best Local Similarity 100.0%; Pred. No. 4.5e+02;
XX  XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  XX  1 TYAMH 5
XX  XX  |||||
XX  XX  423 TYAMH 427
XX
XX  XX  RESULT 15
XX  XX  ID AAB14781 standard; protein; 703 AA.
XX  XX  AC AAB14781;
XX  XX  DT 06-DEC-2000 (first entry)
XX  XX  DE Aspergillus oryzae KBN616 glutaminase.
XX  XX  KW Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
XX  XX  fermentation; foodstuff production; miso; soy sauce.
XX  XX  AS Aspergillus oryzae.
XX
XX

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```
XX FH Key Location/Qualifiers
FT Protein 34..703
XX /note="Mature glutaminase; specifically claimed"
XX JP2000166547-A.
XX PD 20-JUN-2000.
XX XX
XX 07-DEC-1998; 98JP-00347127.
XX PR 07-DEC-1998; 98JP-00347127.
XX XX
XX PA (AICH-) AICHI KEN PREFECTURE.
XX PA (ICHI-) ICHIBIKI KK.
XX DR WPI; 2000-477931/42.
XX DR N-PSDB; AAA72204.
XX PT A new glutaminase and its preparation.
XX PS Claim 2; Page 15-17; 27pp; Japanese.
XX XX
XX This sequence represents a novel glutaminase from Aspergillus oryzae
XX KBN616. The invention relates to two novel glutaminases (AAB14781,
XX AAB14782) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104
XX respectively which have molecular weights of approximately 73 kD (as
XX determined by gel filtration). The enzymes have an optimum temperature of
XX approximately 50 degrees Celsius, and an optimum pH of about 8.5. The
XX glutaminases catalyse the conversion of L-glutamine to L-glutamic acid,
XX and may be used in the production of fermented foodstuffs such as soy
XX sauce and miso
XX
XX SQ Sequence 703 AA;
OY
Db 1 TYAMH 5
436 TYAMH 440
Query Match 100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 16
AAB14782
ID AAB14782 standard; protein; 703 AA.
XX AC AAB14782;
XX DT 06-DEC-2000 (first entry)
XX XX
XX Aspergillus sojae BA-104 glutaminase.
XX DE
XX Aspergillus sojae BA-104; glutamic acid synthesis;
XX KM fermentation; foodstuff production; miso; soy sauce.
XX KW
XX Aspergillus sojae.
XX OS
XX Key Location/Qualifiers
XX FT Protein 34..703
XX /note="Mature glutaminase; specifically claimed"
XX JP2000166547-A.
XX PD 20-JUN-2000.
XX XX
XX 07-DEC-1998; 98JP-00347127.
XX PR 07-DEC-1998; 98JP-00347127.
XX XX
XX PA (AICH-) AICHI KEN PREFECTURE.
XX PA (ICHI-) ICHIBIKI KK.
```

```
XX DR WPI; 2000-477931/42.
XX DR N-PSDB; AAA72205.
XX PT A new glutaminase and its preparation.
XX PS Claim 6; Page 21-23; 27pp; Japanese.
XX XX
XX This sequence represents a novel glutaminase from Aspergillus sojae BA-
XX 104. The invention relates to two novel glutaminases (AAB14781, AAB14782)
XX from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively
XX which have molecular weights of approximately 73 kD (as determined by gel
XX filtration). The enzymes have an optimum temperature of approximately 50
XX degrees Celsius, and an optimum pH of about 8.5. The glutaminases
XX catalyse the conversion of L-glutamine to L-glutamic acid, and may be
XX used in the production of fermented foodstuffs such as soy sauce and miso
XX
XX SQ Sequence 703 AA;
OY
Db 1 TYAMH 5
436 TYAMH 440
Query Match 100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 17
AAM82576
ID AAM82576 standard; protein; 46 AA.
XX AC AAM82576;
XX DT 07-NOV-2001 (first entry)
XX XX
XX Human immune/haematopoietic antigen SEQ ID NO:10169.
XX DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KM cytostatic; gene therapy; vaccine; metastasis.
XX KW
XX Homo sapiens.
XX OS
XX WO200157182-A2.
XX FN
XX PD 09-AUG-2001.
XX XX
XX 17-JAN-2001; 2001WO-US001354.
XX PF
XX 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 11-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 14-JUL-2000; 2000US-0218290P.
XX PR 26-JUL-2000; 2000US-0220963P.
XX PR 26-JUL-2000; 2000US-0220964P.
XX PR 14-AUG-2000; 2000US-0224518P.
XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225213P.
XX PR 14-AUG-2000; 2000US-0225214P.
XX PR 14-AUG-2000; 2000US-0225266P.
XX PR 14-AUG-2000; 2000US-0225267P.
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PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226281P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231245P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0233397P.
PR 14-SEP-2000; 2000US-0233398P.
PR 14-SEP-2000; 2000US-0233399P.
PR 14-SEP-2000; 2000US-0234000P.
PR 14-SEP-2000; 2000US-0234013P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241222P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241825P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249267P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0251989P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251863P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCT INC.
FA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX MPI, 2001-483426/52.
XX N-PSDB; AAK53537.
DR
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Claim 11; SEQ ID NO 10169; 3071pp + Sequence Listing; English.
XX
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
XX
SQ Sequence 46 AA;
Query Match 89.7%; Score 26; DB 4; Length 46;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
35 TYALH 39

RESULT 18

ABBA0299
ID ABB40299 standard; peptide; 67 AA.

AC ABB40299;

DT 04-FEB-2002 (first entry)

DE Peptide #7805 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

XX MO200157277-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000669.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human foetal liver.

PS Claim 27; SEQ ID NO 32934; 639bp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human foetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at fcp.wipo.int/pub/published_pct_sequences

XX Sequence 67 AA;

XX Query Match 89.7%; Score 26; DB 4; Length 67;

XX Best Local Similarity 80.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;

XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 19

AAM33985

ID AAM33985 standard; protein; 67 AA.

XX AAM33985;

XX

DT 17-OCT-2001 (first entry)

DE Peptide #8022 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder.

XX Homo sapiens.

XX MO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 34254; 654bp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

CC see A13315-A157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX Sequence 67 AA;

XX Query Match 89.7%; Score 26; DB 4; Length 67;

XX Best Local Similarity 80.0%; Pred. No. 1.9e+02;

XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 20

AAM73798

ID AAM73798 standard; protein; 67 AA.

XX AAM73798;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 34104.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

XX microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX MO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX

PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 34104; 658bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention
XX
XX Sequence 67 AA;
XX

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
Db 48 TYALH 52

RESULT 21
AAM61093
ID AAM61093 standard; protein; 67 AA.
XX
XX AAM61093;
XX
XX 05-NOV-2001 (first entry)
XX

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33198.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX

XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX

PT Single exon nucleic acid probes for analyzing gene expression in human

PT brains.
XX
XX Example 4; SEQ ID NO 33198; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancer. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 67 AA;
XX

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
Db 48 TYALH 52

RESULT 22
ABG5546
ID ABG5546 standard; peptide; 67 AA.
XX
XX ABG5546;
XX
XX 25-FEB-2003 (first entry)
XX

DE Human liver peptide, SEQ ID No 34194.
XX
XX
XX

KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KM hypercholesterolaemia; coronary heart disease.
XX
XX Homo sapiens.
XX

XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX

XX 30-JAN-2001; 2001WO-US000664.
XX

XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 34194; 658bp; English.
XX

XX The invention relates to a single exon nucleic acid probe (SENP) (1) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (1) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human

CC 11mer single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Gy 1 TYAMH 5
Db 48 TYALH 52

RESULT 23
ABG43685
ID ABG43685 standard; peptide; 67 AA.

AC ABG43685;
XX
DT 19-AUG-2002 (first entry)

XX Human peptide encoded by genome-derived single exon probe SEQ ID 33350.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.

XX Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to

XX measure gene expression in human lung samples.

XX Claim 27; SEQ ID NO 33350; 634p; English.

XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung; comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 5; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Gy 1 TYAMH 5
Db 48 TYALH 52

RESULT 24
AAU18208
ID AAU18208 standard; protein; 79 AA.

XX AAU18208;

XX 21-NOV-2001 (first entry)

XX Novel human DNA-binding protein #55.

XX Human; DNA-binding protein; histone; chromo domain protein;
XX chromatin organisation modifier; Y-box binding protein; DNA organisation;
XX gene transcription; malignant disease; autoimmune disorder;
XX rheumatic disease; genetic abnormality; infectious disease;
XX neurologic disorder; gene therapy; immunomodulatory; anti-HIV;
XX anti rheumatic; anti microbial; cytostatic.

XX Homo sapiens.

XX WO200155162-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001305.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226272P.
PR 22-AUG-2000; 2000US-0226814P.
PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0228287P.
PR 01-SEP-2000; 2000US-0228343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251859P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI, 2001-465557/50.

N-Psdb; AAS29084.

Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases.

Claim 11; SEQ ID NO 193; 561bp; English.

The present invention relates to the isolation of novel DNA-binding proteins, and cDNA (AAS29080-AAS29157) and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and y-box binding proteins may

CC contribute to diseases resulting from aberrant DNA organisation and/or
 CC gene transcription. The sequences of the invention are useful in
 CC screening assays to identify antagonists and/or agonists that may enhance
 CC or block activities mediated by DNA-binding proteins. Blockers of DNA-
 CC binding proteins may be useful in treating disorders such as malignant
 CC diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus),
 CC rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities
 CC (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological
 CC disorders (e.g. Alzheimer's disease). The polynucleotide sequences of the
 CC invention may also be used in gene therapy. AA018154-AA018281 represent
 CC novel DNA-binding proteins. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences
 CC
 XX Sequence 79 AA;
 S0
 Qy 1 TYAMH 5
 Db 74 TYALH 78
 Query Match 89.7%; Score 26; DB 4; Length 79;
 Match Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 25
 ABG92629
 ID ABG92629 standard; protein; 79 AA.
 XX
 AC ABG92629;
 XX
 DT 18-NOV-2002 (first entry)
 XX
 DE Human DNA-binding protein #55.
 XX
 DE Human, DNA-binding protein; B cell immunodeficiency; autoimmune disorder;
 KW severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease;
 KW diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis;
 KW graft-versus-host disease; blood-related disorder; atherosclerosis;
 KW hyperproliferative disorder; cancer; renal disorder; arrhythmia;
 KW acute glomerulonephritis; cardiovascular disorder; respiratory disorder;
 KW Goodpasture's syndrome; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; endocrine disorder; Addison's disease;
 KW reproductive system disorder; endometriosis; infectious disease;
 KW viral infection; bacterial infection; fungal infection; vaccine;
 KW gastrointestinal disorder; multiple sclerosis; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX US2002102638-A1.
 FN
 XX
 PD 01-AUG-2002.
 XX
 PE 17-JAN-2001; 2001US-00764846.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224516P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
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 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBEN) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2002-690611/74.
 DR N-FSDB; ABS68224.
 XX
 XX Novel DNA-binding protein useful for diagnosis, prognosis, prevention and
 PT treatment of immune, hyperproliferative, respiratory, cardiovascular,
 PT reproductive, endocrine, gastrointestinal and neurological disorders.
 XX
 PS Claim 11; SEQ ID NO 193; 225bp; English.
 XX
 XX The present invention relates to a new DNA-binding protein. The invention
 CC is useful in treating, preventing, diagnosing and/or prognosing
 CC immunodeficiencies (e.g. B cell immunodeficiencies, severe combined
 CC immunodeficiencies), autoimmune disorders (rheumatoid arthritis, multiple
 CC sclerosis, diabetes mellitus), allergic reactions and conditions (e.g.
 CC asthma), inflammatory conditions, graft-versus-host disease, blood-
 CC related disorders (thrombosis, atherosclerosis), hyperproliferative
 CC disorders (e.g. cancer), renal disorders (e.g. acute glomerulonephritis),
 CC cardiovascular disorders (e.g. arrhythmia), respiratory disorders
 CC (Goodpasture's syndrome), neurological disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease), endocrine disorders (e.g. Addison's
 CC disease), reproductive system disorders (e.g. endometriosis), infectious
 CC gastrointestinal disorders (e.g. Crohn's disease) and
 CC neuronal damage which occurs in certain neuronal disorders or neuro-
 CC degenerative conditions. The present amino acid sequence represents a
 CC human DNA-binding protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC http.segdata.uspto.gov/sequence
 XX
 S0 Sequence 79 AA;

Query Match 89.7%; Score 26; DB 5; Length 79;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
74 TYALH 78

DB

RESULT 26

ADC25346
ID ADC5346 standard; protein; 79 AA.

XX AC ADC5346;

XX DT 18-DEC-2003 (first entry)

XX DE Human extracellular matrix protein from gene 55.

XX Extracellular matrix protein; cytosolic; antibacterial; virucide;
XX neuroprotective; gynaecological; gastrointestinal; cardiac;
XX cardiovascular; nephrotoxic; antiinflammatory; muscular; Gen;
XX respiratory; immunosuppressive; cerebroprotective; vasotrophic;
XX neotrophic; antiallergic; cancer; bacterial infection; viral infection;
XX muscular disorder; immune system disorder; blood disorder;
XX pulmonary disorder; reproductive disorder; gastrointestinal disorder;
XX inflammatory disorder; cardiovascular disorder; renal disorder;
XX inflammatory disorder; proliferative disorder; human; gene therapy.

XX Homo sapiens.

XX US2003049650-A1.

XX PD 13-MAR-2003.

XX PF 07-MAR-2002; 2002US-00091483.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

XX PR 14-AUG-2000; 2000US-0225270P.

XX PR 14-AUG-2000; 2000US-0225447P.

XX PR 14-AUG-2000; 2000US-0225757P.

XX PR 14-AUG-2000; 2000US-0225758P.

XX PR 14-AUG-2000; 2000US-0225759P.

XX PR 18-AUG-2000; 2000US-0226279P.

XX PR 22-AUG-2000; 2000US-0226861P.

XX PR 22-AUG-2000; 2000US-0226868P.

XX PR 23-AUG-2000; 2000US-0227182P.

XX PR 30-AUG-2000; 2000US-0227009P.

XX PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0231415P.

PR 08-SEP-2000; 2000US-0232081P.

PR 08-SEP-2000; 2000US-0232082P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235835P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239335P.

PR 13-OCT-2000; 2000US-0239336P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249220P.
PR 17-NOV-2000; 2000US-0249221P.
PR 17-NOV-2000; 2000US-0249222P.
PR 17-NOV-2000; 2000US-0249223P.
PR 17-NOV-2000; 2000US-0249224P.
PR 17-NOV-2000; 2000US-0249225P.
PR 17-NOV-2000; 2000US-0249226P.
PR 17-NOV-2000; 2000US-0249227P.
PR 17-NOV-2000; 2000US-0249228P.
PR 17-NOV-2000; 2000US-0249229P.
PR 17-NOV-2000; 2000US-0249230P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 01-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764846.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-605749/57.
DR N-PSDB; ADCC25218.
XX
PT New DNA-binding proteins and gene encoding them, useful for diagnosing,
PT treating and/or preventing e.g. neurological, inflammatory, infectious,
PT cardiovascular, autoimmune, respiratory, neoplastic or digestive
PT diseases.
XX
XX
PS Claim 1; SEQ ID NO 193; 226pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (cDNA)
CC encoding a human extracellular matrix protein, representing one of 161
CC novel genes. Also included are recombinant vectors, host cells
CC (expressing the protein), the extracellular matrix proteins (including
CC their fragments, epitopes and homologues), an isolated antibody that
CC binds specifically to the protein, diagnosing a pathological condition or
CC susceptibility to a pathological condition (comprising determining the
CC presence or absence of a mutation in the nucleic acid and diagnosing a
CC condition based on the presence or absence of the mutation), diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC (comprising determining the presence or amount of expression of the
CC protein in a biological sample and diagnosing a condition based on the
CC presence or amount of expression of the protein), preventing, treating or
CC ameliorating a medical condition by administering the nucleic acid or
CC protein to a mammalian subject, identifying a binding partner to the
CC protein, the gene corresponding to the cDNA sequence, and identifying an
CC activity in a biological assay (comprising expressing the nucleic acid in
CC a cell, isolating the supernatant, detecting an activity in a biological
CC assay and identifying the protein in the supernatant having the
CC activity). The nucleic acids and proteins display the following
CC activities Cytostatic, antibacterial, Virucide, Neuroprotective,
CC Gynaecological, Gastrointestinal-Gen, Cardiant, Cardiovascular-Gen,
CC
Query Match 89.7%; Score 26; DB 7; Length 79;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 27
ABG68752
ID ABG68752 standard; protein; 89 AA.
XX
XX
AC ABG68752;
XX
DT 07-OCT-2002 (first entry)
XX
XX Cytochrome P450 3A5 exon 11-13 altern. 2 with CYP3A43 exon 1.
DE
XX
XX Cytochrome P450; CYP3A41; CYP3A42; CYP3A43; CYP3A4; CYP3A5; CYP3A7;
KM drug metabolism; drug design; drug screening.
XX
XX Homo sapiens.
OS
XX
XX W0200244213-A1.
PN
XX
PD 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-SE002631.
PF
XX
XX 28-NOV-2000; 2000SE-00004366.
PR 11-JUN-2001; 2001SE-00002061.
XX
XX
PA (ZAPH/) ZAPHIROPOULOS P. G.
PA (FINT/) FINTA C.
XX
XX Zaphiropoulos PG, Finta C;
PI
XX
XX WPI; 2002-557532/59.
DR N-PSDB; ABK97691.
XX
XX
PT Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets
PT of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug
PT metabolism, in drug design and drug screening.
XX
XX
XX Claim 1; Page 96-97; 131pp; English.
XX
XX The invention describes a cytochrome P450 protein (I) in which CYP3A43
CC exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub
CC fragments, variants and multiples of (I) having essentially the same
CC characteristics. (I) is useful as a medicament, and for evaluating drug
CC metabolism, in drug design, and drug screening, and in tests for
CC adjusting the dose of drugs. This is the amino acid sequence of a novel
CC cytochrome P450 protein
XX
XX
SQ Sequence 89 AA;
XX
Query Match 89.7%; Score 26; DB 5; Length 89;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
DB 69 TYALH 73
XX
XX
RESULT 28
ABP01422
ID ABP01422 standard; protein; 162 AA.
XX
XX
AC ABP01422;
XX
XX
DT 24-JUN-2002 (first entry)
XX
XX Human ORFX protein sequence SEQ ID NO:2826.
DE
XX
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KM hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;
KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 OS Homo sapiens.
 PN WO200192523-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US010836.
 XX
 PR 30-MAY-2000; 2000US-0206132P.
 PR 29-AUG-2000; 2000US-0228716P.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shimkets RA, Leach MD;
 DR N-PSDB; ABN17174.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX
 PS Disclosure; SEQ ID NO 2826; 1037pp; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 162 AA;
 Query Match 89.7%; Score 26; DB 5; Length 162;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 |||:
 146 TYALH 150
 DB
 RESULT 29
 ABG68756
 ID ABG68756 standard; protein; 173 AA.
 AC ABG68756;
 XX
 XX 07-OCT-2002 (first entry)
 DT
 XX

DE Cytochrome P450 CYP3A43 exon 1-CYP3A4 exon 11-13 #1.
 XX
 XX Cytochrome P450; CYP3A1; CYP3AP2; CYP3A43; CYP3A4; CYP3A5; CYP3A7;
 KW drug metabolism; drug design; drug screening.
 KW
 OS Homo sapiens.
 PN WO200244213-A1.
 XX
 PD 06-JUN-2002.
 XX
 PF 28-NOV-2001; 2001WO-SE002631.
 XX
 PR 28-NOV-2000; 2000SE-00004366.
 PR 11-JUN-2001; 2001SE-00002061.
 XX
 PA (ZAPH/) ZAPHIROPOULOS P G.
 PA (FINV/) FINTA C.
 PI Zaphiropoulos PG, Finca C;
 DR N-PSDB; ABK97695.
 DR WPI: 2002-557532/59.
 XX
 PT Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets
 PT of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug
 PT metabolism, in drug design and drug screening.
 XX
 PS Claim 3; Fig 14; 131pp; English.
 XX
 CC The invention describes a cytochrome P450 protein (I) in which CYP3A43
 CC exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub
 CC fragments, variants and multiples of (I) having essentially the same
 CC characteristics. (I) is useful as a medicament, and for evaluating drug
 CC metabolism, in drug design, and drug screening, and in tests for
 CC adjusting the dose of drugs. This is the amino acid sequence of a novel
 CC cytochrome P450 protein
 XX
 SQ Sequence 173 AA;
 Query Match 89.7%; Score 26; DB 5; Length 173;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 |||:
 69 TYALH 73
 DB
 RESULT 30
 ADE08218
 ID ADE08218 standard; protein; 194 AA.
 AC ADE08218;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX
 DB Novel protein (useful for identifying genetic disorders) #373.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 PN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0338739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 XX

PR 14-MAR-2002; 2002US-0355384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ,
XX
DR WPI: 2003-569235/53.
DR N-PSDB: ADE07307.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Claim 20; SEQ ID NO 1284; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 194 AA;
XX
Query Match 89.7%; Score 26; DB 7; Length 194;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
DB 20 TYSWH 24
XX
RESULT 31
ADE08219
ID ADE08219 standard; protein; 205 AA.
XX
AC ADE08219;
XX
DT 29-JAN-2004 (first entry)
XX
DS Novel protein (useful for identifying genetic disorders) #374.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX

PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ,
XX
DR WPI: 2003-569235/53.
DR N-PSDB: ADE07308.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Claim 20; SEQ ID NO 1285; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 205 AA;
XX
Query Match 89.7%; Score 26; DB 7; Length 205;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
DB 20 TYSWH 24
XX
RESULT 32
ABB91152
ID ABB91152 standard; protein; 213 AA.
XX
AC ABB91152;
XX
DT 31-MAY-2002 (first entry)
XX
DS Herbicidally active polypeptide SEQ ID NO 363.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP009892.
XX
PR 28-AUG-2001; 2001WO-EP009892.
XX
PA (FARB) BAYER AG.
XX
PI Tietjen K, Weidner M;
XX
DR WPI: 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
PS Claim 5; SEQ ID NO 363; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor

CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides

XX Sequence 213 AA;

Query Match 89.7%; Score 26; DB 5; Length 213;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:|
Db 202 TYALH 206

RESULT 33

ADA55412
ID ADA55412 standard; protein; 221 AA.

XX ADA55412;

XX 20-NOV-2003 (first entry)

XX Human protein, SEQ ID 2980.

XX Cytostatic; Anti-inflammatory; Osteoprotective; Neuroprotective; Nootropic;

XX Gene Therapy; human; secretory protein; membrane proteins; cancer;

XX Inflammatory disease; osteoporosis; neurological disease.

XX Homo sapiens.

XX EPI293569-A2.

XX 19-MAR-2003.

XX 21-MAR-2002; 2002EP-00006586.

XX 14-SEP-2001; 2001JP-00328381.

XX 24-JAN-2002; 2002US-0350435P.

XX (HELI-) HELIX RES INST.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isegai T, Sugiyama T, Otsuki T, Makamatsu A, Sato H, Iehli S;

XX Yamamoto U, Iseono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

XX Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;

XX WPI; 2003-395539/38.

XX N-PSDB; ADA53773.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory

XX and/or membrane proteins, useful for developing medicines for diseases in

XX which the gene is involved, or as target molecules for gene therapy.

XX Claim 14; SEQ ID NO 2980; 205pp; English.

XX The present invention relates to novel human secretory or membrane

XX proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-

XX ADA54071). The coding sequences are useful in the gene therapy of

XX diseases caused by abnormalities of the proteins, e.g. cancer,

XX inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 221 AA;

RESULT 34
ABP46042
ID ABP46042 standard; protein; 238 AA.
XX ABP46042;
XX 19-AUG-2002 (first entry)
XX Human Blys binding scFv SEQ ID 2053.
XX Blys, B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX Homo sapiens.
XX WO200202641-A1.
XX 10-JAN-2002.
XX 15-JUN-2001; 2001WO-US019110.
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240815P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Anticodex against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX Claim 1; Page 2847-2848; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention

XX Sequence 238 AA;

Query Match 89.7%; Score 26; DB 5; Length 238;
Best Local Similarity 80.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:|
Db 31 TYSWH 35

RESULT 35

ADG96869 standard; protein; 238 AA.

ADG96869;

11-MAR-2004 (first entry)

Single chain antibody that immunospecifically binds Blys SegID 2053.

antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;

B cell proliferation; differentiation; scFv; myasthenia gravis;

multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;

antiinflammatory; antisthmatic; antiallergic; cytostatic.

Unidentified.

WO200305579-A2.

10-JUL-2003.

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-0331469P.

19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator

(Blys), useful for detecting and treating diseases or disorders e.g.

rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 2053; 394bp; English.

This invention relates to novel antibodies that immunospecifically bind

to B lymphocyte stimulator (Blys). The Blys gene has been mapped to

chromosome 11q34 and encodes a protein that is a member of the tumour

necrosis factor superfamily and induces both in vivo and in vitro B cell

proliferation and differentiation. Specifically, it refers to single

chain antibody molecules (scFvs) derived, preferably, from the variable

heavy CDR3 region that immunospecifically bind to a polypeptide, or

fragment thereof, of either human, murine, rat or monkey Blys. The

present invention refers to the use of such antibodies in various methods

for the detection, diagnosis and prognosis of diseases related to the

aberrant expression or inappropriate function of Blys or its receptor. As

such, these compositions are useful for identifying immune disorders

including myasthenia gravis and multiple sclerosis, inflammatory

disorders e.g. asthma and rheumatoid arthritis, infectious diseases such

as AIDS and proliferative disorders including leukaemia, carcinoma and

lymphoma. Accordingly, they can be described as exhibiting various

activities such as antirheumatic, antiallergic, neuroprotective,

antiinflammatory, antisthmatic, antiallergic and cytostatic. This

polypeptide sequence is a single chain antibody that binds Blys of the

invention. NOTE: The sequence data for this patent did not form part of

the printed specification, but was obtained in electronic format

directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 238 AA;

Query Match 89.7%; Score 26; DB 7; Length 238;

Best Local Similarity 80.0%; Pred. No. 7.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TYAMH 5

31 TYSMH 35

RESULT 36

ABB49910 standard; protein; 242 AA.

ABB49910;

05-FEB-2002 (first entry)

Listeria monocytogenes protein #2614.

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

vitamin B12; bacterial infection; disease.

Listeria monocytogenes.

WO200177335-A2.

18-OCT-2001.

11-APR-2001; 2001WO-FR001118.

11-APR-2000; 2000FR-00004629.

(INSP) INST PASTEUR.

Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P,

Duesberg O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P,

Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA,

Domínguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A,

Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L,

Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N,

Madueno E, De Pablo B, Weiland J, Kaerst U, Entian K, Hauf J,

Rose M, Voss H;

WPI; 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment

and prevention of Listeria and related bacterial infections, and related

polypeptides.

Claim 6; SEQ ID NO 2615; 192bp; French.

The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

it are useful for selecting probes and primers for detecting genes in L.

monocytogenes and related organisms, and for studying genetic

polymorphisms and other genomes. The present invention is a protein

encoded by the genome sequence of the present invention. Proteins

expressed from the genome sequence are useful for raising specific

antibodies, identification of L. monocytogenes and related organisms, and

for biosynthesis and biodegradation, especially biosynthesis of Vitamin

B12. The genome sequence and proteins encoded by it are also useful for

selecting compounds that regulate gene expression and cell replication

and modulate L. monocytogenes-related diseases. In addition, the genome

sequence and proteins encoded by it are useful in pharmaceutical and

vaccine compositions for the treatment or prevention of infections by L.

monocytogenes and related organisms. Note: The sequence data for this

patent did not form part of the printed specification, but was obtained

in electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences

Sequence 242 AA;

Query Match 89.7%; Score 26; DB 5; Length 242;

Best Local Similarity 80.0%; Pred. No. 7.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TYAMH 5

191 TYSMH 195

RESULT 37

ABU17641
ID ABU17641 standard; protein; 304 AA.
XX AC ABU17641;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #3168.
XX KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Bacillus anthracis.
XX PN MO20027183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002MO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-023926/02.
XX DR N-PSDB; ACAA21511.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 45565; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs; or for screening homologous nucleic acids
XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
XX CC the target prokaryotic essential genes. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 304 AA;

Query Match 89.7%; Score 26; DB 6; Length 304;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 299 TYALH 303

RESULT 38

AAG91423
ID AAG91423 standard; protein; 370 AA.

XX AC AAG91423;
XX AC AAG91423;
XX DT 26-SEP-2001 (first entry)

XX DE C glutamicum protein fragment SEQ ID NO: 5177.
XX KM Corynebacterium; amino acid synthesis; vitamin; saccharide;
XX KM organic acid synthesis.

XX OS Corynebacterium glutamicum.
XX PN EP1108790-A2.
XX PD 20-JUN-2001.
XX PF 18-DEC-2000; 2000EP-00127688.
XX PR 16-DEC-1999; 99JP-00377484.
XX PR 07-APR-2000; 2000JP-00159162.
XX PR 03-AUG-2000; 2000JP-00280988.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX DR WPI; 2001-376931/40.
XX DR N-PSDB; AAH66642.

XX PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
XX PT mutation point of a gene, measuring expression of a gene, analyzing
XX PT expression profile or pattern of a gene and identifying homologous gene.
XX PS Claim 17; SEQ ID NO 5177; 246pp + Sequence Listing; English.

XX CC The present invention provides a number of nucleotide and protein
XX CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
XX CC are useful for identifying the mutation point of a gene derived from a
XX CC mutant of corynebacterium bacterium, measuring expression amount and analysing
XX CC the expression profile or expression pattern of a gene derived from
XX CC Corynebacterium bacterium, and identifying a homologue of a gene derived from
XX CC corynebacterium bacterium. Corynebacterium bacteria are useful for producing amino
XX CC acids, nucleic acids, vitamins, saccharides and organic acids,
XX CC particularly L-lysine. The present sequence is a protein described in the
XX CC exemplification of the invention. Note: The sequence data for this patent
XX CC did not form part of the printed specification, but was obtained in
XX CC electronic format directly from the European Patent Office
XX SQ Sequence 370 AA;

Query Match 89.7%; Score 26; DB 4; Length 370;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 172 TYALH 176

RESULT 39

AA090014
 ID AA090014 standard; protein, 370 AA.
 AC AA090014;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE C glutamicum protein fragment SEQ ID NO: 3768.
 XX
 KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
 XX organic acid synthesis.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN BP108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PP 18-DEC-2000; 2000EP-00127688.
 XX
 PR 16-DEC-1999; 99JP-00377484.
 PR 07-APR-2000; 2000JP-00159162.
 PR 03-AUG-2000; 2000JP-00280988.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 PI WPI; 2001-376931/40.
 DR N-PSDB; AAH65233.
 XX
 PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX
 PS Claim 17; SEQ ID NO 3768; 246pp + Sequence listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium, measuring expression amount and analyzing
 CC the expression profile or expression pattern of a gene derived from
 CC Corynebacterium bacterium, and identifying a homologue of a gene derived from
 CC corynebacterium bacterium. Corynebacterium bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described in the
 CC exemplification of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the European Patent Office
 XX
 SQ Sequence 370 AA;
 QY
 Db 1 TYAMH 5
 172 TYALH 176
 Query Match 89.7%; Score 26; DB 4; Length 370;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 40
 ABO63767
 ID ABO63767 standard; protein, 454 AA.
 XX
 AC ABO63767;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Klebsiella pneumoniae polypeptide seqid 10284.
 XX
 KW Recombinant expression vector; transcription regulatory element;

KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 XX Klebsiella pneumoniae.
 OS
 XX US6610836-B1.
 PN
 XX 26-AUG-2003.
 PD
 XX
 PP 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton GL, Osborne M;
 XX
 DR WPI; 2003-895346/82.
 DR N-PSDB; ACH97318.
 XX
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX
 PS Disclosure; SEQ ID NO 10284; 932pp; English.
 XX
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 454 AA;
 QY
 Db 1 TYAMH 5
 152 TYALH 156
 Query Match 89.7%; Score 26; DB 7; Length 454;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Search completed: March 31, 2005, 12:02:26
 Job time : 41.75 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:44 ; Search time 9.76562 Seconds
(without alignments)
36.220 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents: AA.*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	5	US-09-383-667-10	Sequence 10, App1
2	29	100.0	118	US-09-232-290-45	Sequence 45, App1
3	29	100.0	258	US-09-252-991A-26228	Sequence 26228, A
4	29	100.0	690	US-10-262-083-2	Sequence 2, App1
5	29	100.0	690	US-10-262-083-18	Sequence 18, App1
6	26	89.7	108	US-09-270-767-35497	Sequence 35497, A
7	26	89.7	108	US-09-270-767-50714	Sequence 50714, A
8	26	89.7	454	US-09-489-039A-10284	Sequence 10284, A
9	26	89.7	455	US-09-543-681A-8288	Sequence 8288, Ap
10	26	89.7	502	US-09-949-016-5992	Sequence 5992, Ap
11	26	89.7	507	US-09-949-016-7091	Sequence 7091, Ap
12	26	89.7	544	US-09-976-594-699	Sequence 699, App
13	26	89.7	544	US-09-919-039-270	Sequence 270, App
14	25	86.2	5	US-08-264-093-21	Sequence 21, App1
15	25	86.2	5	US-08-918-148-26	Sequence 26, App1
16	25	86.2	5	US-09-383-667-21	Sequence 21, App1
17	25	86.2	5	US-09-138-091A-26	Sequence 26, App1
18	25	86.2	5	US-09-424-840B-34	Sequence 34, App1
19	25	86.2	5	US-09-424-840B-91	Sequence 91, App1
20	25	86.2	5	US-09-830-748B-10	Sequence 10, App1
21	25	86.2	38	US-07-977-630-67	Sequence 67, App1
22	25	86.2	58	US-09-270-767-38850	Sequence 38850, A
23	25	86.2	58	US-09-270-767-54067	Sequence 54067, A
24	25	86.2	98	US-08-211-202-118	Sequence 118, App
25	25	86.2	114	US-09-726-219A-222	Sequence 222, App
26	25	86.2	116	US-08-211-202-141	Sequence 141, App
27	25	86.2	117	US-08-545-809A-91	Sequence 91, App1

28	25	86.2	117	3	US-09-025-769B-24	Sequence 24, App1
29	25	86.2	117	4	US-09-490-070A-24	Sequence 24, App1
30	25	86.2	117	4	US-09-490-153-24	Sequence 24, App1
31	25	86.2	117	4	US-09-490-324-24	Sequence 24, App1
32	25	86.2	118	3	US-08-545-809A-145	Sequence 145, App
33	25	86.2	118	4	US-09-248-796A-1439	Sequence 1439, A
34	25	86.2	119	1	US-08-331-398A-46	Sequence 46, App1
35	25	86.2	119	2	US-08-561-521-10	Sequence 10, App1
36	25	86.2	119	2	US-08-561-521-12	Sequence 12, App1
37	25	86.2	119	2	US-08-561-521-13	Sequence 13, App1
38	25	86.2	119	2	US-08-331-397B-46	Sequence 46, App1
39	25	86.2	119	2	US-08-759-804A-46	Sequence 46, App1
40	25	86.2	119	3	US-09-227-693-46	Sequence 46, App1
41	25	86.2	119	4	US-09-438-954-41	Sequence 41, App1
42	25	86.2	119	5	PCT-US95-01219-10	Sequence 10, App1
43	25	86.2	119	5	PCT-US95-01219-12	Sequence 12, App1
44	25	86.2	119	5	PCT-US95-01219-13	Sequence 13, App1
45	25	86.2	120	1	US-08-211-202-135	Sequence 135, App

ALIGNMENTS

```
RESULT 1
US-09-383-667-10
; Sequence 10, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip R.
; APPLICANT: Judge, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-10
;
;
;
Query Match      100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
DB      1 TYAMH 5

RESULT 2
US-09-232-290-45
; Sequence 45, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGGER, ANNEMARIE
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
; FILE REFERENCE: MORPHO/7
; CURRENT APPLICATION NUMBER: US/09/232,290A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: PCT/EP96/02230
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EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 118
TYPE: PRT
ORGANISM: Murine
US-09-232-290-45

Query Match 100.0%; Score 29; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 3
US-09-252-991A-26228
Sequence 26228, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26228
LENGTH: 258
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26228

Query Match 100.0%; Score 29; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 201 TYAMH 205

RESULT 4
US-10-262-083-2
Sequence 2, Application US/10262083
Patent No. 6830905
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: MAGASAKI, Hiroaki
APPLICANT: YUASA, Aki
APPLICANT: KATOKA, Jiro
APPLICANT: KITAMOTO, Katsuhiko
TITLE OF INVENTION: A No. 6830905e1 Glutaminase, its Gene and a Method of Producing I
FILE REFERENCE: 199438US-8222-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/262.083
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: JP 10/134080
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: JP 10/292443
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: JP 11/89157
PRIOR FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 690
TYPE: PRT
ORGANISM: Aspergillus oryzae
US-10-262-083-2

Query Match 100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 5
US-10-262-083-18
Sequence 18, Application US/10262083
Patent No. 6830905
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: MAGASAKI, Hiroaki
APPLICANT: YUASA, Aki
APPLICANT: KATOKA, Jiro
APPLICANT: KITAMOTO, Katsuhiko
TITLE OF INVENTION: A No. 6830905e1 Glutaminase, its Gene and a Method of Producing I
FILE REFERENCE: 199438US-8222-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/262.083
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: JP 10/134080
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: JP 10/292443
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: JP 11/89157
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 690
TYPE: PRT
ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match 100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 6
US-09-270-767-35497
Sequence 35497, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35497
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE: OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35497

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
64 TYALH 68

RESULT 7
US-09-270-767-50714
; Sequence 50714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50714
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE: OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50714

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
64 TYALH 68

RESULT 8
US-09-489-039A-10284
; Sequence 10284, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10284
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10284

Query Match 89.7%; Score 26; DB 4; Length 454;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
64 TYALH 68

DB 152 TYALH 156

RESULT 9
US-09-543-681A-8288
; Sequence 8288, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709, 1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8288
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8288

Query Match 89.7%; Score 26; DB 4; Length 455;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
225 TYALH 229

RESULT 10
US-09-949-016-5992
; Sequence 5992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5992
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5992

Query Match 89.7%; Score 26; DB 4; Length 502;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
398 TYALH 402

RESULT 11
US-09-949-016-7091
; Sequence 7091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7091
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7091

Query Match      89.7%; Score 26; DB 4; Length 507;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        |||:-|
Db      403 TYALH 407

RESULT 12
US-09-976-594-699
; Sequence 699, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 699
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
; US-09-976-594-699

Query Match      89.7%; Score 26; DB 4; Length 544;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        |||:-|
Db      485 TYALH 489

RESULT 13
US-09-919-039-270
; Sequence 270, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaseer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
```

```

; SOFTWARE: PERL Program
; SEQ ID NO 270
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
; US-09-919-039-270

Query Match      89.7%; Score 26; DB 4; Length 544;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        |||:-|
Db      485 TYALH 489

RESULT 14
US-08-264-093-21
; Sequence 21, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 MB storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
; US-08-264-093-21

Query Match      86.2%; Score 25; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        :|||:-|
Db      1 SYAMH 5

RESULT 15
US-08-918-148-26
```



```
; Sequence 26, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W. Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; PRIOR FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; NAME/KEY: 10D10scFv, 12B5scFv VH CDR1
; LOCATION: 1-5
; OTHER INFORMATION:
US-08-918-148-26
```

```
Query Match      86.2% Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 TYAMH 5
Db      1 TYGMH 5
```

```
RESULT 16
US-09-383-667-21
; Sequence 21, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/Xa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; PRIOR FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-21
```

```
Query Match      86.2% Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TYAMH 5
Db      1 SYAMH 5
```

```
RESULT 17
US-09-138-091A-26
; Sequence 26, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
```

```
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-138-091A-26
```

```
Query Match      86.2% Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 TYAMH 5
Db      1 TYGMH 5
```

```
RESULT 18
US-09-424-840B-34
; Sequence 34, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-34
```

```
Query Match      86.2% Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TYAMH 5
Db      1 SYAMH 5
```

```
RESULT 19
US-09-424-840B-91
; Sequence 91, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
```

PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 91
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-91

Query Match 86.2%; Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 1 SYAMH 5

RESULT 20
US-09-830-748B-10
Sequence 10, Application US/09830748B
Patent No. 6818749
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by The
APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Kamhathi Syed V.S.
APPLICANT: Padman, Eduardo A.
APPLICANT: Jeffery, Schilom
TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49
FILE REFERENCE: 4239-61725
CURRENT APPLICATION NUMBER: US/09/830,748B
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: PCT/US99/25552
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/106,757
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 60/106,534
PRIOR FILING DATE: 1998-10-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-830-748B-10

Query Match 86.2%; Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 1 SYAMH 5

RESULT 21
US-07-977-630-67
Sequence 67, Application US/07977630
Patent No. 5583038
GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING
DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland

STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,630
FILING DATE: No. 5583038member 17, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469201-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-977-630-67

Query Match 86.2%; Score 25; DB 1; Length 38;
Best Local Similarity 80.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 6 SYAMH 10

RESULT 22
US-09-270-767-38850
Sequence 38850, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38850
LENGTH: 58
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-38850

Query Match 86.2%; Score 25; DB 4; Length 58;
Best Local Similarity 80.0%; Pred. No. 77;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 47 TYTWH 51

RESULT 23
US-09-270-767-54067
Sequence 54067, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 54067
 LENGTH: 58
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-54067

Query Match 86.2%; Score 25; DB 4; Length 58;
 Best Local Similarity 80.0%; Pred. No. 77;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYAMH 5
 ||||
 Db 47 TYTWH 51

RESULT 24
 US-08-211-202-118
 Sequence 118, Application US/08211202
 Patent No. 5565332
 GENERAL INFORMATION:
 APPLICANT: HOOGENBOOM, Hendricus Reneerus Jacobus Matheus
 APPLICANT: BAIER, Michael
 APPLICANT: JESPER, Laurent Stephane Anne Therese
 APPLICANT: WINTER, Gregory Paul
 TITLE OF INVENTION: Production of chimeric antibodies - a
 TITLE OF INVENTION: combinatorial approach
 NUMBER OF SEQUENCES: 144
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
 ADDRESS: Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/211,202
 FILING DATE: 23-SEP-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120252.3
 FILING DATE: 23-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120377.8
 FILING DATE: 25-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206181.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/00883
 FILING DATE: 15-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 2811/31960
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 118:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-211-202-118

Query Match 86.2%; Score 25; DB 1; Length 98;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 ||||
 Db 31 SYAMH 35

RESULT 25
 US-09-726-219A-222
 Sequence 222, Application US/09726219A
 Patent No. 6806079
 GENERAL INFORMATION:
 APPLICANT: Cambridge Antibody Technology
 APPLICANT: Cambridge Antibody Technology Limited
 APPLICANT: Medical Research Council
 APPLICANT: Mc Cafferty, John
 APPLICANT: Pope, Anthony
 APPLICANT: Johnson, Kevin
 APPLICANT: Hooogenboom, Hendricus
 APPLICANT: Griffiths, Andrew
 APPLICANT: Jackson, Ronald
 APPLICANT: Holliger, Kasper
 APPLICANT: Marks, James
 APPLICANT: Jackson, Timothy
 APPLICANT: Chiswell, David
 APPLICANT: Winter, Gregory
 APPLICANT: Bonert, Timothy
 TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
 FIVE REFERENCE: 213839-00013
 CURRENT APPLICATION NUMBER: US/09/726,219A
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: GB 9015198.6
 PRIOR FILING DATE: 1990-07-10
 PRIOR APPLICATION NUMBER: GB 9022845.3
 PRIOR FILING DATE: 1990-10-19
 PRIOR APPLICATION NUMBER: GB 9022845.3
 PRIOR FILING DATE: 1990-10-19
 PRIOR APPLICATION NUMBER: GB 9024503.6
 PRIOR FILING DATE: 1990-11-12
 PRIOR APPLICATION NUMBER: GB 9104744.9
 PRIOR FILING DATE: 1991-03-06
 PRIOR APPLICATION NUMBER: GB 9110549.4
 PRIOR FILING DATE: 1991-05-15
 PRIOR APPLICATION NUMBER: PCT/GB91/01134
 PRIOR FILING DATE: 1991-07-10
 PRIOR APPLICATION NUMBER: US 07/971,857
 PRIOR FILING DATE: 1993-01-08
 PRIOR APPLICATION NUMBER: US 08/484,893
 PRIOR FILING DATE: 1995-06-07
 NUMBER OF SEQ ID NOS: 272
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 222
 LENGTH: 114
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: VH of bcry from mouse immunized with 2-phenyl-5-oxazolone
 US-09-726-219A-222

Query Match 86.2%; Score 25; DB 4; Length 114;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 ||||
 Db 31 SYAMH 35

RESULT 26
US-08-211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
; APPLICANT: BAIRER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Bortun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEFAX: 25-3856
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-141

Query Match 86.2%; Score 25; DB 1; Length 116;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
:||||
Db 31 SYAMH 35

RESULT 27
US-08-545-809A-91
; Sequence 91, Application US/08545809A

Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Yasuko
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-91

Query Match 86.2%; Score 25; DB 3; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
:||||
Db 50 SYAMH 54

RESULT 28
US-09-025-769B-24
; Sequence 24, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-24

Query Match 86.2% Score 25; DB 3; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
DB 31 SYAMH 35

RESULT 29
US-09-490-070A-24
Sequence 24, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McCulliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-490-070A-24

Query Match 86.2% Score 25; DB 4; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
DB 31 SYAMH 35

RESULT 30
US-09-490-153-24
Sequence 24, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-490-153-24

Query Match 86.2% Score 25; DB 4; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5

Db :|||
31 SYAMH 35

RESULT 31

US-09-490-324-24
Sequence 24, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

APPLICANT: Knappik, Achim

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 145:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-809A-145

Query Match

Best Local Similarity 86.2%; Score 25; DB 3; Length 118;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:|||
Db 51 SYAMH 55

RESULT 33

US-09-248-796A-14399

Sequence 14399, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14399

LENGTH: 118

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-14399

Query Match

Best Local Similarity 86.2%; Score 25; DB 4; Length 118;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:|||
Db 57 SYAMH 61

RESULT 34
US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331.398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-398A-46
Query Match 86.2%; Score 25; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 35
US-08-561-521-10
Sequence 10, Application US/085615121
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VIA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-10
Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 36
US-08-561-521-12
Sequence 12, Application US/085615121
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VIA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-12

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 31 SYAMH 35

RESULT 37
US-08-561-521-13
Sequence 13, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
ADHESION MOLECULE VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-13

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 31 SYAMH 35

RESULT 38
US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES
THEREOF
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
Db 31 SYAMH 35

RESULT 39

US-08-759-804A-46
Sequence 46, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
NUMBER OF SEQUENCES: 68
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56PL/CL Variable Heavy chain (V-H)"
US-08-759-804A-46

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
Db 31 SYAMH 35

RESULT 40
US-09-227-693-46
Sequence 46, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADILAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
NUMBER OF SEQUENCES: 50
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION:
OTHER INFORMATION: 56PL/CL VH region"

US-09-227-693-46

Query Match 86.2%; Score 25; DB 3; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
Db 31 SYAMH 35

Search completed: March 31, 2005, 12:13:24
Job time : 10.7656 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 12:10:00 ; Search time 27.9688 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	11	US-10-468-543-91	Sequence 91, Appl
2	29	100.0	151	US-10-424-599-231272	Sequence 231272, A
3	29	100.0	206	US-10-282-1224-52731	Sequence 92731, A
4	29	100.0	278	US-10-359-493-9985	Sequence 9985, Ap
5	29	100.0	690	US-10-262-083-2	Sequence 2, Appl
6	29	100.0	690	US-10-262-083-2	Sequence 18, Appl
7	26	89.7	11	US-10-468-543-35	Sequence 35, Appl
8	26	89.7	59	US-10-424-599-217913	Sequence 217913, A
9	26	89.7	60	US-10-424-599-188252	Sequence 188252, A
10	26	89.7	61	US-10-437-963-109084	Sequence 109084, A
11	26	89.7	67	US-09-864-761-44407	Sequence 44407, A
12	26	89.7	67	US-10-424-599-190876	Sequence 190876, A
13	26	89.7	73	US-10-424-599-192746	Sequence 192746, A

14	26	89.7	73	US-10-424-599-205833	Sequence 205833, A
15	26	89.7	77	US-10-424-599-245586	Sequence 245586, A
16	26	89.7	79	US-09-764-846-193	Sequence 193, App
17	26	89.7	79	US-10-091-483-193	Sequence 193, App
18	26	89.7	85	US-10-767-701-48571	Sequence 48571, A
19	26	89.7	98	US-10-424-599-214193	Sequence 214193, A
20	26	89.7	137	US-10-424-599-227653	Sequence 227653, A
21	26	89.7	141	US-10-424-599-143644	Sequence 143644, A
22	26	89.7	168	US-10-767-701-39988	Sequence 39988, A
23	26	89.7	221	US-10-094-749-2980	Sequence 2980, Ap
24	26	89.7	238	US-09-880-748-2053	Sequence 2053, Ap
25	26	89.7	238	US-10-293-418-2053	Sequence 2053, Ap
26	26	89.7	304	US-10-282-1224-45565	Sequence 45565, A
27	26	89.7	370	US-09-738-626-3768	Sequence 3768, Ap
28	26	89.7	370	US-09-738-626-3768	Sequence 3768, Ap
29	26	89.7	420	US-10-425-114-54469	Sequence 54469, A
30	26	89.7	542	US-10-425-114-54414	Sequence 54414, A
31	26	89.7	544	US-09-919-039-270	Sequence 270, App
32	26	89.7	591	US-10-618-941-125	Sequence 125, App
33	26	89.7	619	US-10-424-599-155796	Sequence 155796, A
34	26	89.7	659	US-10-369-493-8287	Sequence 8287, Ap
35	26	89.7	678	US-10-369-493-19452	Sequence 19452, A
36	26	89.7	801	US-10-282-1224-58937	Sequence 58937, A
37	26	89.7	886	US-10-424-599-165676	Sequence 165676, A
38	26	89.7	929	US-10-060-841-3	Sequence 3, Appl
39	26	89.7	929	US-10-288-798-11	Sequence 11, Appl
40	26	89.7	929	US-10-362-892-11	Sequence 11, Appl
41	26	89.7	929	US-10-618-941-105	Sequence 105, App
42	26	89.7	929	US-09-972-656-38	Sequence 38, Appl
43	26	86.2	5	US-10-320-094-5	Sequence 5, Appl
44	26	86.2	5	US-10-399-701-4	Sequence 4, Appl
45	26	86.2	9	US-10-884-830-308	Sequence 308, App

ALIGNMENTS

RESULT 1
US-10-468-543-91
Sequence 91, Application US/10468543
Publication No. US20040091938A1
GENERAL INFORMATION:
APPLICANT: Irimura, Tatsuro
APPLICANT: Matsunoto, Mariko
APPLICANT: Yim, Mijung
APPLICANT: Ono, Takashi
TITLE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same
FILE REFERENCE: 03-786
CURRENT APPLICATION NUMBER: US/10/468, 543
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: JP 2001-044221
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Generated from randomly recombinant DNA part of MAH.
US-10-468-543-91

Query Match 100.0%; Score 29; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Cy 1 TYAMH 5
DB 2 TYAMH 6

RESULT 2
US-10-424-599-231272

Sequence 231272, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 231272
LENGTH: 151
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(151)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_50860C.1.pep
US-10-424-599-231272

Query Match 100.0%; Score 29; DB 15; Length 151;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 120 TYAMH 124

RESULT 3
US-10-282-122A-52731
Sequence 52731, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zvekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52731
LENGTH: 206
TYPE: PRT
ORGANISM: Clostridium botulinum
US-10-282-122A-52731

Query Match 100.0%; Score 29; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 30 TYAMH 34

RESULT 4
US-10-369-493-9985
Sequence 9985, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9985
LENGTH: 278
TYPE: PRT
ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-9985

Query Match 100.0%; Score 29; DB 15; Length 278;
Best Local Similarity 100.0%; Pred. No. 1,2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 220 TYAMH 224

RESULT 5
US-10-262-083-2
Sequence 2, Application US/10262083
Publication No. US20030170670A1
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoto
APPLICANT: NAGASAKI, Hitoeaki
APPLICANT: YUASA, Aki
APPLICANT: KITAMOTO, Katsuhiko
TITLE OF INVENTION: A No. US20030170670A1el Glutaminase, its Gene and a Method of Pro
FILE REFERENCE: 199438US-8222-10-0-PCF
CURRENT APPLICATION NUMBER: US/10/262,083
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: JP 10/134080
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/256974
PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: JP 10/292443
 PRIOR FILING DATE: 1998-10-14
 PRIOR APPLICATION NUMBER: JP 11/89157
 PRIOR FILING DATE: 1999-03-30
 PRIOR APPLICATION NUMBER: PCT/JP99/02455
 PRIOR FILING DATE: 1999-05-12
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 690
 TYPE: PRT
 ORGANISM: Aspergillus oryzae
 US-10-262-083-2

Query Match 100.0%; Score 29; DB 14; Length 690;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
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 Db 423 TYAMH 427

RESULT 6
 US-10-262-083-18
 Sequence 18, Application US/10262083
 Publication No. US20030170670A1
 GENERAL INFORMATION:
 APPLICANT: KOIBUCHI, Kyoto
 APPLICANT: NAGASAKI, Hiroaki
 APPLICANT: YUASA, Aki
 APPLICANT: KATAOKA, Jiro
 APPLICANT: KITAMOTO, Katsuhiko
 TITLE OF INVENTION: A NO. US20030170670A1 Glutaminase, its Gene and a Method of Pro
 FILE REFERENCE: 199438US-8222-10-0-PCT
 CURRENT FILING DATE: 2002-10-02
 PRIOR APPLICATION NUMBER: US/09/674,507
 PRIOR FILING DATE: 2000-11-15
 PRIOR APPLICATION NUMBER: JP 10/134080
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: JP 10/258974
 PRIOR FILING DATE: 1998-09-11
 PRIOR APPLICATION NUMBER: JP 10/292443
 PRIOR FILING DATE: 1998-10-14
 PRIOR APPLICATION NUMBER: JP 11/89157
 PRIOR FILING DATE: 1999-03-30
 PRIOR APPLICATION NUMBER: PCT/JP99/02455
 PRIOR FILING DATE: 1999-05-12
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 18
 LENGTH: 690
 TYPE: PRT
 ORGANISM: Aspergillus oryzae
 US-10-262-083-18

Query Match 100.0%; Score 29; DB 14; Length 690;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
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 Db 423 TYAMH 427

RESULT 7
 US-10-468-543-35
 Sequence 35, Application US/10468543
 Publication No. US20040091938A1
 GENERAL INFORMATION:
 APPLICANT: Iitamura, Tatsuro
 APPLICANT: Matsumoto, Mariko

APPLICANT: Yim, Mijung
 APPLICANT: Ono, Takashi
 TITLE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same
 FILE REFERENCE: 03-786
 CURRENT APPLICATION NUMBER: US/10/468,543
 PRIOR FILING DATE: 2003-08-20
 PRIOR APPLICATION NUMBER: JP 2001-044221
 PRIOR FILING DATE: 2001-02-20
 NUMBER OF SEQ ID NOS: 95
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 35
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Generated from randomly recombinant DNA part of MAH.
 US-10-468-543-35

Query Match 89.7%; Score 26; DB 15; Length 11;
 Best Local Similarity 80.0%; Pred. No. 26;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
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 Db 2 TYALH 6

RESULT 8
 US-10-424-599-217913
 Sequence 217913, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO: 217913
 LENGTH: 59
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_38802C.1.pcp
 US-10-424-599-217913

Query Match 89.7%; Score 26; DB 15; Length 59;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 10 TYSMH 14

RESULT 9
 US-10-424-599-188252
 Sequence 188252, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J
 APPLICANT: Kovalic, David K
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 285684
;; SEQ ID NO 188252
;; LENGTH: 60
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT3847_141004C.1.pcp
US-10-424-599-188252

Query Match 89.7%; Score 26; DB 15; Length 60;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 46 TYSMH 50

RESULT 10
US-10-437-963-109084
;; Sequence 109084, Application US/10437963
;; Publication No. US20040123343A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Wu, Wei
;; APPLICANT: Boukharov, Andrey A.
;; APPLICANT: Barbazuk, Brad
;; APPLICANT: Li, Ping
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 109084
;; LENGTH: 61
;; TYPE: PRT
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_13276C.1.pcp
US-10-437-963-109084

Query Match 89.7%; Score 26; DB 16; Length 61;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 43 TYALH 47

RESULT 11
US-09-864-761-44407
;; Sequence 44407, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wenheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecmiga-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366

;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonex Sequence Listing Engine vers. 1.1
;; SEQ ID NO 44407
;; LENGTH: 67
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC005020.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.58
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.7
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
;; OTHER INFORMATION: SWISSPROT HIT: P20815, EVALUATE 3.00e-35
;; OTHER INFORMATION: EST_HUMAN HIT: A1861809.1, EVALUATE 2.00e-34
US-09-864-761-44407

Query Match 89.7%; Score 26; DB 9; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 48 TYALH 52

RESULT 12
US-10-424-599-190876
;; Sequence 190876, Application US/10424599
;; Publication No. US20040031072A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT APPLICATION NUMBER: US/10/424,599
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 190876
LENGTH: 67
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_14380C.1.pdp
US-10-424-599-190876

Query Match 89.7%; Score 26; DB 15; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
|||:|
Db 25 TYALH 29

RESULT 13
US-10-424-599-192746
Sequence 192746, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192746
LENGTH: 73
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_16071C.1.pdp
US-10-424-599-192746

Query Match 89.7%; Score 26; DB 15; Length 73;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
|||:|
Db 12 TYSMH 16

RESULT 14
US-10-424-599-205833
Sequence 205833, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205833
LENGTH: 73
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27896C.1.pdp
US-10-424-599-205833

Query Match 89.7%; Score 26; DB 15; Length 73;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
|||:|
Db 22 TYSMH 26

RESULT 15
US-10-424-599-245586
Sequence 245586, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245586
LENGTH: 77
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_63796C.1.pdp
US-10-424-599-245586

Query Match 89.7%; Score 26; DB 15; Length 77;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
|||:|
Db 12 TYALH 16

RESULT 16
US-09-764-846-193
Sequence 193, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT12
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 193
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-193

Query Match 89.7%; Score 26; DB 9; Length 79;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
|||:|
Db 74 TYALH 78

RESULT 17

US-10-091-483-193
; Sequence 193, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212C1
; CURRENT APPLICATION NUMBER: US/10/091,483
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 193
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-091-483-193

Query Match 89.7%; Score 26; DB 14; Length 79;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 74 TYALH 78

RESULT 18
US-10-767-701-48571
; Sequence 48571, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 48571
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-046-Q6-K1-A9.pep
US-10-767-701-48571

Query Match 89.7%; Score 26; DB 16; Length 85;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 1 TYALH 5

RESULT 19
US-10-424-599-214193
; Sequence 214193, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214193
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35443C.1.pep
US-10-424-599-214193

Query Match 89.7%; Score 26; DB 15; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 57 TYALH 61

RESULT 20
US-10-424-599-227653
; Sequence 227653, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 227653
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4759C.1.pep
US-10-424-599-227653

Query Match 89.7%; Score 26; DB 15; Length 137;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 16 TYALH 20

RESULT 21
US-10-424-599-143644
; Sequence 143644, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143644
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

NAME/KEY: unsure
LOCATION: (1)-(141)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_100724C.1.pep
US-10-424-599-143644

Query Match 89.7%; Score 26; DB 15; Length 141;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 83 TYALH 87

RESULT 22
US-10-767-701-39988
Sequence 39988, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5335)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 2004-01-29
SEQ ID NO 39988
LENGTH: 168
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28WAY03-C3913_1.pep
US-10-767-701-39988

Query Match 89.7%; Score 26; DB 16; Length 168;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 77 TYALH 81

RESULT 23
US-10-094-749-2980
Sequence 2980, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYU
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749

CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2980
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2980

Query Match 89.7%; Score 26; DB 15; Length 221;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 162 TYALH 166

RESULT 24
US-09-880-748-2053
Sequence 2053, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2053
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2053

Query Match 89.7%; Score 26; DB 10; Length 238;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 TYSMH 35

RESULT 25
US-10-293-418-2053
Sequence 2053, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2053
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2053

Query Match 89.7%; Score 26; DB 15; Length 238;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 31 TYSMH 35

RESULT 26
US-10-282-122A-45565
Sequence 45565, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hagelbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45565

LENGTH: 304
TYPE: PRT
ORGANISM: Bacillus anthracis
US-10-282-122A-45565

Query Match 89.7%; Score 26; DB 15; Length 304;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 299 TYALH 303

RESULT 27
US-09-738-626-3768
Sequence 3768, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3768
LENGTH: 370
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3768

Query Match 89.7%; Score 26; DB 9; Length 370;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 172 TYALH 176

RESULT 28
US-09-738-626-5177
Sequence 5177, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125

;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 5177
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5177

Query Match 89.7%; Score 26; DB 9; Length 370;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 172 TYALH 176

RESULT 29
US-10-425-114-54469
;; Sequence 54469, Application US/10425114
;; Publication No. US2004003488A1
;; GENERAL INFORMATION:
;; APPLICANT: Liu, Jingdong
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Screen, Steven E.
;; APPLICANT: Tabaska, Jack E.
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;; FILE REFERENCE: 38-21(53313)B
;; CURRENT APPLICATION NUMBER: US/10/425,114
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 73128
;; SEQ ID NO 54469
;; LENGTH: 420
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Clone ID: LIB4651-038-H5_F11.pep
US-10-425-114-54469

Query Match 89.7%; Score 26; DB 15; Length 420;
Best Local Similarity 80.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 361 TYALH 365

RESULT 30
US-10-425-114-54114
;; Sequence 54114, Application US/10425114
;; Publication No. US2004003488A1
;; GENERAL INFORMATION:
;; APPLICANT: Liu, Jingdong
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Screen, Steven E.
;; APPLICANT: Tabaska, Jack E.
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;; FILE REFERENCE: 38-21(53313)B

;; CURRENT APPLICATION NUMBER: US/10/425,114
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 73128
;; SEQ ID NO 54114
;; LENGTH: 542
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Clone ID: LIB4119-111-F11_F11.pep
US-10-425-114-54114

Query Match 89.7%; Score 26; DB 15; Length 542;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 483 TYALH 487

RESULT 31
US-09-919-039-270
;; Sequence 270, Application US/09919039
;; Publication No. US20030108871A1
;; GENERAL INFORMATION:
;; APPLICANT: Kaser, Matthew R.
;; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;; FILE REFERENCE: PA-0035 US
;; CURRENT APPLICATION NUMBER: US/09/919,039
;; CURRENT FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: 60/222,113
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 401
;; SOFTWARE: PERL Program
;; SEQ ID NO 270
;; LENGTH: 544
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. US20030108871A1 4113161CD1
US-09-919-039-270

Query Match 89.7%; Score 26; DB 10; Length 544;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 485 TYALH 489

RESULT 32
US-10-618-941-125
;; Sequence 125, Application US/10618941
;; Publication No. US20040197792A1
;; GENERAL INFORMATION:
;; APPLICANT: WHITE, DAVID
;; APPLICANT: MANNING, GERRARD
;; APPLICANT: CAENEPEEL, SEAN
;; TITLE OF INVENTION: NOVEL KINASES
;; FILE REFERENCE: 034536-0321
;; CURRENT APPLICATION NUMBER: US/10/618,941
;; CURRENT FILING DATE: 2003-07-15
;; PRIOR APPLICATION NUMBER: 60/395,632
;; PRIOR FILING DATE: 2002-07-15
;; NUMBER OF SEQ ID NOS: 143
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 125
;; LENGTH: 591
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-618-941-125

Query Match 89.7%; Score 26; DB 16; Length 591;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 532 TYALH 536

RESULT 33

US-10-424-599-155796
; Sequence 155796, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 155796
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_111703C.1.pep
US-10-424-599-155796

Query Match 89.7%; Score 26; DB 15; Length 619;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 242 TYSMH 246

RESULT 34

US-10-369-493-8287
; Sequence 8287, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8287
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Thermobifida fusca
US-10-369-493-8287

Query Match 89.7%; Score 26; DB 15; Length 659;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 354 TYALH 358

RESULT 35
US-10-369-493-19452

; Sequence 19452, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19452
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-10-369-493-19452

Query Match 89.7%; Score 26; DB 15; Length 678;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 515 TYALH 519

RESULT 36

US-10-282-122A-58937
; Sequence 58937, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zykend, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58937
LENGTH: 801
TYPE: PRT
ORGANISM: Helicobacter pylori
US-10-282-122A-58937

Query Match 89.7%; Score 26; DB 15; Length 801;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 95 TYSMH 99

RESULT 37
US-10-424-599-165676
Sequence 165676, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165676
LENGTH: 886
TYPE: PRT
ORGANISM: Glycine max
FEATURES:
NAME/KEY: unsure
LOCATION: (1) ..(886)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_120620C.1.pdp
US-10-424-599-165676

Query Match 89.7%; Score 26; DB 15; Length 886;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 158 TYALH 162

RESULT 38
US-10-060-841-3
Sequence 3, Application US/10060841
Publication No. US20020162127A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Nguyen, Chung-Thong
TITLE OF INVENTION: A HUMAN PROTEIN KINASE DOMAIN-CONTAINING PROTEIN
FILE REFERENCE: PB0179
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/335,941
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Aecmca Sequence Listing Engine
SEQ ID NO 3
LENGTH: 929
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-841-3

Query Match 89.7%; Score 26; DB 13; Length 929;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 249 TYALH 253

RESULT 39
US-10-288-798-11
Sequence 11, Application US/10288798
Publication No. US20030207299A1
GENERAL INFORMATION:
APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B;
APPLICANT: WALTA, Natinder K.; HARALTA, April J.A.;
APPLICANT: YAO, Monique G.; GANDHI, Ameena L.;
APPLICANT: GURURAJAN, Rajagopal; DING, Li;
APPLICANT: PATTERSON, Chandra; YUE, Henry;
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
APPLICANT: LU, Yan; TSON, Craig H.;
APPLICANT: AU-YOUNG, Janice; TRAN, Y. Tom;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
APPLICANT: THANGAVELOU, Kavitha; BURFORD, Neil
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0209 USA
CURRENT APPLICATION NUMBER: US/10/288,798
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: PCT/US01/27219
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/240,542
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/238,389
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/236,499
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/232,654
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/229,873
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 929
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030207299A1 7481989CD1
US-10-288-798-11

Query Match 89.7%; Score 26; DB 15; Length 929;
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||:
 Db 249 TYALH 253

RESULT 40
 US-10-362-892-11
 ; Sequence 11, Application US/10362892
 ; Publication No. US20040038881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
 ; APPLICANT: NGUYEN, Danielle B.; WALIA, Narinder K.
 ; APPLICANT: HAPALIA, April J.A.; YAO, Monique G.
 ; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
 ; APPLICANT: DING, Li; PATTERSON, Chandra S.
 ; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
 ; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
 ; APPLICANT: ELIOTT, Vicki S.; LU, Yan
 ; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
 ; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
 ; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
 ; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
 ; APPLICANT: LAI, Preeti G.; RAMKUMAR, Jayalaxmi
 ; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
 ; APPLICANT: POLICKY, Jennifer L.; THANAVEILU, Kavitha
 ; APPLICANT: BURFORD, Neil
 ; TITLE OF INVENTION: HUMAN KINASES
 ; FILE REFERENCE: PF-0209 USN
 ; CURRENT APPLICATION NUMBER: US/10/362, 892
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/US01/27219
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: US 60/229, 873
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: US 60/231, 357
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: US 60/232, 654
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: US 60/234, 902
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: US 60/236, 499
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: US 60/238, 389
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: US 60/240, 542
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 11
 ; LENGTH: 929
 ; TYPE: prt
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID NO. US20040038881A1 7481989CD1
 US-10-362-892-11

Query Match 89.7%; Score 26; DB 15; Length 929;
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||:
 Db 249 TYALH 253

Search completed: March 31, 2005, 12:46:06
 Job time : 28.9688 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 7.10938 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	122	1 M3HUGA	Ig heavy chain V-I
2	29	100.0	138	2 A35676	Ig heavy chain V-I
3	29	100.0	196	2 D71184	adenylate kinase (
4	29	100.0	249	2 B83290	conserved hypotet
5	29	100.0	1151	2 H71347	hypothetical prote
6	29	100.0	1377	2 I54632	tsh protein - Esch
7	26	89.7	95	2 T34500	hypothetical prote
8	26	89.7	196	2 I50675	retinol-binding pr
9	26	89.7	213	2 H86403	hypothetical prote
10	26	89.7	228	2 E90215	conserved hypotet
11	26	89.7	228	2 T22924	hypothetical prote
12	26	89.7	242	2 AD1165	B. subtilis YYPB p
13	26	89.7	242	2 AD1524	B. subtilis YYPB p
14	26	89.7	501	2 A29487	cytochrome P450 3A
15	26	89.7	501	2 A34236	cytochrome P450 3A
16	26	89.7	502	1 A34101	cytochrome P450 3A
17	26	89.7	504	2 A25222	cytochrome P450 3A
18	26	89.7	609	2 B82423	hypothetical prote
19	26	89.7	723	2 B84425	hypothetical prote
20	26	89.7	801	2 B64679	paralysed flagella
21	26	89.7	852	1 GNLJGA	pol polyprotein -
22	26	89.7	852	1 GNLJGA	pol polyprotein -
23	26	89.7	852	2 S29358	fix23-3 protein -
24	26	89.7	966	2 S18955	probable helicase
25	26	89.7	1265	2 T11705	hypothetical prote
26	26	89.7	1385	2 T11705	hypothetical prote
27	26	89.7	1506	2 T10886	integumentary mucr
28	26	89.7	6260	2 T30228	polyketide synthas
29	25	86.2	35	2 S26887	Ig heavy chain V r

30	25	86.2	35	2 S46473	Ig heavy chain V r
31	25	86.2	94	2 P10120	Ig heavy chain V-I
32	25	86.2	96	2 S17609	Ig heavy chain V r
33	25	86.2	97	2 S10385	Ig heavy chain V r
34	25	86.2	97	2 S26885	Ig heavy chain V r
35	25	86.2	97	2 S26886	Ig heavy chain V r
36	25	86.2	98	2 S29546	Ig heavy chain V r
37	25	86.2	102	2 S53076	probable membrane
38	25	86.2	104	2 P11653	Ig heavy chain V r
39	25	86.2	109	2 P11653	Ig heavy chain V r
40	25	86.2	109	2 P11646	Ig heavy chain V r
41	25	86.2	109	2 P11644	Ig heavy chain V r
42	25	86.2	111	2 P11645	Ig heavy chain V r
43	25	86.2	113	2 E33936	Ig heavy chain V r
44	25	86.2	114	2 P11667	Ig heavy chain V r
45	25	86.2	114	2 S46390	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
M3HUGA
Ig heavy chain V-III region (Ga) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A02052
R:Florent, G., Lehman, D., Putnam, F.W.
Biochemistry 13, 2482-2498, 1974
A>Title: The switch point in mu heavy chains of human IgM immunoglobulins.
A:Reference number: A02052; MUID:74175307; PMID:4208843
A:Accession: A02052
A:Molecule type: protein
A:Residues: 1-122 <F10>
A:Cross-References: UNIPROT:P01769
C:Comment: This chain was isolated from a Waldenström's macroglobulin.
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-References: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F:15-98/Domain: immunoglobulin homology <IM>
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:22-96/Disulfide bonds: #status predicted

Query Match      100.0%; Score 29; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
DB      31 TYAMH 35

RESULT 2
A35676
Ig heavy chain precursor V-D-J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 23-Jul-1999
C:Accession: A35676
R:White, M.B.; Word, C.J.; Humphries, C.G.; Blattner, F.R.; Tucker, P.W.
Mol. Cell. Biol. 10, 3690-3699, 1990
A>Title: Immunoglobulin D switching can occur through homologous recombination in human
A:Reference number: A35676; MUID:90287160; PMID:2113175
A:Accession: A35676
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <WH>
A:Cross-References: GB:M38066; NID:g185466; PID:AA52974.1; PID:g553407
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IM>
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Query Match 100.0%; Score 29; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 50 TYAMH 54

RESULT 3

D11184
adenylate kinase (EC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: D11184
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekit
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5: 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D11184
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <KAM>
A:Cross-references: UNIPROT:O59443; GB:AF000007; NID:g3236134; PIDN:BAA30867.1; PID:g325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1753
C:Keywords: phosphotransferase

Query Match 100.0%; Score 29; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 157 TYAMH 161

RESULT 4

B83290
conserved hypothetical protein PA2847 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83290
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yu, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406: 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STD>
A:Cross-references: UNIPROT:Q9HZZ6; GB:AE004711; GB:AE004091; NID:g9948927; PIDN:AA60623
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2847

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 192 TYAMH 196

RESULT 5

H71347

hypothetical protein TP0245 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: H71347
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McDo
rthy, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281: 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: H71347
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1151 <COL>
A:Cross-references: UNIPROT:O83273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AA65523;
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0245
C:Superfamily: syphilis spirochete hypothetical protein TP0245

Query Match 100.0%; Score 29; DB 2; Length 1151;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 700 TYAMH 704

RESULT 6

I54632
tsh protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54632
R:Provense, D.L.; Curtis, R.
Infect. Immun. 62: 1369-1380, 1994
A:Title: Isolation and characterization of a gene involved in hemagglutination by an avia
A:Reference number: I54632; MUID:94178945; PMID:8132344
A:Accession: I54632
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1377 <RES>
A:Cross-references: UNIPROT:Q47692; GB:I27423; NID:g469235; PIDN:AAA24698.1; PID:g469236
C:Superfamily: IGA-specific metalloendopeptidase

Query Match 100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 341 TYAMH 345

RESULT 7

T34500
hypothetical protein ZK1248.17 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34500
R:Latreille, P.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid ZK1248.
A:Reference number: Z21534
A:Accession: T34500
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-95 <LAT>
A:Cross-references: UNIPROT:Q23248; EMBL:U23244; PIDN:AACT1098.1; GSPDB:GNO0020; CESP:ZK
A:Experimental source: strain Bristol N2; clone ZK1248
C:Genetics:
A:Gene: CESP:ZK1248.17

A:Map position: 2
C:Superfamily: Caenorhabditis elegans major sperm protein

Query Match 89.7%; Score 26; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 12 TYSMH 16

RESULT 8
150675
retinol-binding protein precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: 150675; S42887
R:Vieira, A.V.; Kuchler, K.; Schneider, W.J.
DNA Cell Biol. 14, 403-410, 1995
A>Title: Retinol in avian oogenesis: molecular properties of the carrier protein.
A:Reference number: 150675; PMID:95267350; PMID:7748490
A:Accession: 150675
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-196 <VIR>
A:Cross-references: UNIPROT:P41263; EMBL:X77960; NID:g457778; PIDN:CAA54922.1; PID:g4577
C:Genetics:
A:Gene: RBP
C:Superfamily: lipocalin; lipocalin homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:36-195/Domain: lipocalin homology <LRP>
F:25-181,91-195,141-150/Disulfide bonds: #status predicted

Query Match 89.7%; Score 26; DB 2; Length 196;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 134 TYALH 138

RESULT 9
H86403
hypothetical protein F28U5.12 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86403
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federgruel, N.A.; Kaul, S.; White, O.; Alonso, Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hultar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Vener, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; PMID:21016719; PMID:11130712
A:Accession: H86403
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <STO>
A:Cross-references: UNIPROT:Q9CGN1; GB:AE005172; NID:g10998924; PIDN:AA626064.1; GSPDB:G
C:Genetics:
A:Map position: 1

Query Match 89.7%; Score 26; DB 2; Length 213;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5

Db 202 TYALH 206

RESULT 10
E30215
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E30215
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
A:Submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A39139
A:Accession: E30215
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <KUR>
A:Cross-references: UNIPROT:Q9UX67; GB:AE006641; NID:g13813846; PIDN:AAK40980.1; GSPDB:G
C:Genetics:
A:Gene: SS00678
C:Superfamily: hypothetical protein MU0570

Query Match 89.7%; Score 26; DB 2; Length 222;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 14 TYALH 18

RESULT 11
T22924
hypothetical protein F58B6.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22924
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: 219638
A:Accession: T22924
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-228 <WIL>
A:Cross-references: UNIPROT:Q20984; EMBL:Z70754; PIDN:CAA94778.1; GSPDB:GN00023; CESP:F5
A:Experimental source: clone F58B6
C:Genetics:
A:Gene: CESP:F58B6.8
A:Map position: 5
A:Intons: 153/2
C:Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2

Query Match 89.7%; Score 26; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 177 TYALH 181

RESULT 12
A01165
B. subtilis YVPB protein homolog lmo0724 [imported] - Listeria monocytogenes (strain EGD)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: A01165
R:Glaeser, P.; Frangoul, L.; Buchrisser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fshih, H. D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madeno, E.; Maitournam, A.; Ma
ok, C.; Schlueder, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <GUA>
A:Cross-references: UNIPROT:Q8Y918; GB:NC_003210; PIDN:CAC98802.1; PID:G16410113; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0724
C:Superfamily: *Bacillus subtilis* hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 13
AD1524
B. subtilis yvpB protein homolog lmo0732 [imported] - *Listeria innocua* (strain C11p11262
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1524
R:Glaser, P.; Rangel, L.; Buchriser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fehrl, H.
Science 294, 849-852, 2001
D.; Jones, L.M.; Karet, U.
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madeno, E.; Maitournam, A.; Ma
ok, C.; Schlueder, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <GUA>
A:Cross-references: UNIPROT:Q92PT0; GB:AL592022; PIDN:CAC95964.1; PID:G16413104; GSPDB:C
A:Experimental source: strain C11p11262
C:Genetics:
A:Gene: lmo0732
C:Superfamily: *Bacillus subtilis* hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 14
A29487
cytochrome P450 3A6 (version 1) - rabbit
N:Alternate names: cytochrome P450 3C
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29487
R:Delet, C.; Clair, P.; Dautat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
DNA 7, 39-66, 1988
A:Title: Complete sequence of cytochrome P450 3C cDNA and presence of two mRNA species
A:Reference number: A29487; MUID:88166352; PMID:3349903
A:Accession: A29487
A:Molecule type: mRNA
A:Residues: 1-501 <DAL>
A:Cross-references: UNIPROT:P11707; GB:M19139; NID:G165573; PIDN:AAA31430.1; PID:G165574

C:Genetics:
A:Gene: CYP3A6
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:301-462/Domin: cytochrome P450 homology <P45>
F:440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
Best Local Similarity 80.0%; Pred. No. 176+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 396 TYALH 400

RESULT 15
A34236
cytochrome P450 3A6 (version 2) - rabbit
N:Alternate names: cytochrome P450 3C
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A34236
R:Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;
J. Biol. Chem. 264, 16222-16228, 1989
A:Title: Regulation of the rabbit cytochrome P-450 3C gene. Age-dependent expression and
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
A:Reference number: A34236; MUID:89380226; PMID:2777787
A:Accession: A34236
A:Molecule type: mRNA
A:Residues: 1-501 <POT>
A:Cross-references: UNIPROT:P11707; GB:J05034; NID:G164829; PIDN:AAA31178.1; PID:G164830
C:Genetics:
A:Gene: CYP3A6
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:300-462/Domin: cytochrome P450 homology <P45>
F:440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
Best Local Similarity 80.0%; Pred. No. 176+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 396 TYALH 400

RESULT 16
A34101
cytochrome P450 3A5 - human
N:Alternate names: cytochrome P450 H1p2
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: *Homo sapiens* (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A34101; S06491; I52302
R:Aoyama, T.; Yamano, S.; Waxman, D.J.; Lapenson, D.P.; Meyer, U.A.; Fischer, V.; Tyndal
J. Biol. Chem. 264, 10388-10395, 1989
A:Title: Cytochrome P-450 hPCN3, a novel cytochrome P-450 IIA gene product that is diff
DNA-expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and cyclosporine.
A:Reference number: A34101; MUID:89278095; PMID:2732228
A:Accession: A34101
A:Molecule type: mRNA
A:Residues: 1-502 <AOY>
A:Cross-references: UNIPROT:P20815; GB:J04813; NID:G101345; PIDN:AAA02993.1; PID:G101346
R:Schneitz, J.D.; Molowa, D.T.; Guelstein, P.S.
Arch. Biochem. Biophys. 274, 355-365, 1989
A:Title: Characterization of a cDNA encoding a new member of the glucocorticoid-responsi
A:Reference number: S06491; MUID:90025114; PMID:2802615
A:Accession: S06491
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-304, 'P', 306-317, 'F', 319-323, 'D', 325-376, 'G', 378-502 <SCH>

R;Jounaidi, Y.; Guzelian, P.S.; Maurel, P.; Vilarem, M.J.
Biochem. Biophys. Res. Commun. 205, 1741-1747, 1994
A;Title: Sequence of the 5'-flanking region of CYP3A5: comparative analysis with CYP3A4
A;Reference number: 152302; MUID:95110318; PMID:811260
A;Accession: 152302
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-24 <RES>
A;Cross-references: GB:S74699; NID:9786472; PIDN:RAD14157.1; PID:94261857
C;Genetics:
A;Gene: GDB:CYP3A5
A;Cross-references: GDB:118783
A;Map position: 7q22.1-7q22.1
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;302-463/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 1; Length 502;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 398 TYALH 402

RESULT 17
A25222
Cytochrome P450 3A2 - rat
N;Alternate names: cytochrome P450C2, pregnenolone 16-alpha-carbonitrile-inducible; tes
N;Contents: oxidoreductase (EC 1.-.-.-)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text change 09-Jul-2004
C;Accession: A25222; S27108; S46938; EX0032; EX0034; S30379
R;Gonzalez, F.J.; Song, B.J.; Hardwick, J.P.
Mol. Cell. Biol. 6, 2969-2976, 1986
A;Title: Pregnenolone 16-alpha-carbonitrile-inducible P-450 gene family: gene conversion
A;Reference number: A25222; MUID:87064606; PMID:3785219
A;Accession: A25222
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-504 <GON>
A;Cross-references: UNIPROT:P05183; GB:M13646; NID:9203827; PIDN:AAA1051.1; PID:9203828
A;Note: the authors translated the codon GAC for residue 445 as Gly
R;Telhada, M.B.; Pereira, T.M.; Lechner, M.C.
Arch. Biochem. Biophys. 298, 715-725, 1992
A;Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3
A;Reference number: S27107; MUID:93037516; PMID:1417000
A;Accession: S27108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <TEL>
A;Cross-references: EMBL:X62087
R;Miyata, M.; Nagata, K.; Shimada, M.; Yamazoe, Y.; Kato, R.
submitted to the EMBL Data Library, May 1994
A;Description: Structure of a gene and cDNA of a major constitutive form of testosterone
A;Reference number: S46938
A;Accession: S46938
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-428, 'D', '430-444', 'G', '446-504 <MT>
A;Cross-references: EMBL:X79320; NID:9515381; PIDN:CAA5888.1; PID:9515382
R;Nagata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
Biochem. 107, 718-725, 1990
A;Title: Purification and characterization of four catalytically active testosterone 6be
nally related forms.
A;Reference number: PX0032; MUID:90375438; PMID:2398038
A;Accession: PX0032
A;Molecule type: protein
A;Residues: 1-21, 'X', '23-26', 'X', '28-29', 'X', '31-33 <NAG>
A;Experimental source: liver, Sprague-Dawley male rat
A;Accession: PX0034
A;Molecule type: protein

A;Residues: 1-27, 'X', '29', 'X', '31-33 <NA2>
R;Cooper, K.O.; Reik, L.M.; Jayoshi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, R.
Arch. Biochem. Biophys. 301, 345-354, 1993
A;Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3
A;Reference number: S30378; MUID:93213168; PMID:7681660
A;Accession: S30379
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25 <COO>
C;Genetics:
A;Gene: CYP3A2
A;Introns: 24/2
A;Note: this list of introns is incomplete
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;303-465/Domain: cytochrome P450 homology <P45>
F;443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 504;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 399 TYALH 403

RESULT 18
E82423
Hypothetical protein VCA0730 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence revision 20-Aug-2000 #text change 09-Jul-2004
C;Accession: E82423
R;Heldelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82423
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <HEL>
A;Cross-references: UNIPROT:Q9KLL3; GB:AE004402; GB:AE003853; NID:99658148; PIDN:AAF9662
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0730
A;Map position: 2

Query Match 89.7%; Score 26; DB 2; Length 609;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 321 TYALH 325

RESULT 19
A84425
Hypothetical protein At2g01460 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #text change 09-Jul-2004
C;Accession: A84425
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umeyam, L.; Tallon, L.
euss, D.; Merlan, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-723 <STO>

A:Cross-references: UNIPROT:Q9ZVF8, GB:AE002093, NID:93785975, PIDN:AA67322.1, GSPDB:GN
 C:Genetics:
 A:Gene: At2g01460
 A:Map position: 2

Query Match 89.7%; Score 26; DB 2; Length 723;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||:|
 Db 173 TYALH 177

RESULT 20
 B64679
 paralyse flagella protein - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: B64679

R:Tombs, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.; Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
 A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: B64679
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-801 <TOM>

A:Cross-references: UNIPROT:O25864, GB:AE00631, GB:AE00511, NID:92314421, PIDN:AA0831

C:Genetics:

A:Start codon: TTG

Query Match 89.7%; Score 26; DB 2; Length 801;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||:|
 Db 95 TYSMH 99

RESULT 21
 GNLJGA

pol polyprotein - bovine leukemia virus (strain Australia)

N:Contains: endonuclease (EC 3.1.1.-); RNA-directed DNA polymerase (EC 2.7.7.49)

C:Species: bovine leukemia virus, BLV

A>Note: host Bos sp. (cattle)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C:Accession: J00555

R:Collier, J.; Nelf, H.; Brandon, R.; Kumar, S.; Khan, S.; Daniel, R.C.W.; Lavin, M.F.

J. Gen. Virol. 71, 1737-1746, 1990

A>Title: Molecular cloning and sequencing of an Australian isolate of proviral bovine le

A:Reference number: J00554; MUID:90362060; PMID:2167927

A:Accession: J00555

A:Molecule type: DNA

A:Residues: 1-852 <COU>

A:Cross-references: UNIPROT:P25059, DDBJ:D00647, NID:92920795, PIDN:BA00544.1, PID:9221

A>Note: This reading frame extends between two stop codons and does not begin with a sta

A>Note: the authors translated the codon CCC for residue 514 as Gln

C:Comment: The precise boundary between RNA-directed DNA polymerase and endonuclease has

C:Genetics:

A:Gene: pol

C:Superfamily: pol polyprotein

C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse trans

Query Match 89.7%; Score 26; DB 1; Length 852;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5

Db 636 TYALH 640

RESULT 22

pol polyprotein - bovine leukemia virus

N:Contains: endonuclease (EC 3.1.1.-); RNA-directed DNA polymerase (EC 2.7.7.49)

C:Species: bovine leukemia virus, BLV

A>Note: host Bos sp. (cattle)

C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004

C:Accession: A03960

R:Sagata, N.; Yasunaga, T.; Tsubuku-Kawamura, T.; Ohishi, K.; Ogawa, Y.; Ikawa, Y.

Proc. Natl. Acad. Sci. U.S.A. 82, 677-681, 1985

A>Title: Complete nucleotide sequence of the genome of bovine leukemia virus: its evolu

A:Reference number: A94063; MUID:85140159; PMID:2983308

A:Accession: A03960

A:Molecule type: DNA

A:Residues: 1-852 <SAG>

A:Cross-references: UNIPROT:P03361

A>Note: the authors translated the codon TTC for residue 104 as Ser and CTA for residue

C:Comment: Specific enzymatic cleavages may yield mature proteins including reverse tran

C:Genetics:

A:Gene: pol

C:Superfamily: pol polyprotein

C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse trans

Query Match 89.7%; Score 26; DB 1; Length 852;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||:|
 Db 636 TYALH 640

RESULT 23
 S29358

pol protein - bovine leukemia virus

C:Species: bovine leukemia virus, BLV

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S29358

R:Rice, N.R.; Stephens, R.M.; Burny, A.; Gilden, R.V.

Virolgy 142, 357-377, 1985

A>Title: The gag and pol genes of bovine leukemia virus: nucleotide sequence and analysis

A:Reference number: S29356; MUID:86045859; PMID:2997990

A:Accession: S29358

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-852 <RIC>

A:Cross-references: UNIPROT:Q85491; EMBL:M10987

C:Superfamily: pol polyprotein

Query Match 89.7%; Score 26; DB 2; Length 852;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||:|
 Db 636 TYALH 640

RESULT 24
 S18955

fix23-3 protein - Rhizobium meliloti

C:Species: Rhizobium meliloti

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S18955

R:Petrovics, G.; Putnoky, P.; Kondorosi, A.

submitted to the EMBL data library, January 1992

A:Description: A fatty acid synthase like gene cluster of Rhizobium meliloti is involved

A:Reference number: S18953

A:Accession: S18955

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-966 <PER>
A:Cross-references: UNIPROT:Q52932; EMBL:X64131; NID:g1235585; PIDN:CAA5485.1; PID:g462

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 966;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 198 TYALH 202

RESULT 25

P84517
Probable helicase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84517
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nucleotide 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84517

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1265 <STO>
A:Cross-references: UNIPROT:Q9ZOR0; GB:AE002093; NID:g4263825; PIDN:AAD15468.1; GSPDB:GN
C:Genetics:
A:Gene: At2G14470
A:Map position: 2

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 1265;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 195 TYSMH 199

RESULT 26

T21706
hypothetical protein F33H1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21706
R:Wilkinson, J.
submitted to the EMBL Data Library, March 1995
A:Reference number: Z19462
A:Accession: T21706
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1385 <WTL>
A:Cross-references: UNIPROT:Q19991; EMBL:Z48783; PIDN:CAA86699.1; GSPDB:GN00020; CESP:F3
A:Experimental source: clone F33H1
C:Genetics:
A:Gene: CESP:F33H1.4
A:Map position: 2
A:Introns: 88/2; 699/1; 1021/3; 1330/3; 1350/3

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 1385;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 1131 TYALH 1135

RESULT 27

T30886
Integumentary mucin B.1 - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30886
R:Joda, W.; Hoffmann, W.
J. Biol. Chem. 272, 1805-1810, 1997
A:Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and prepr

A:Reference number: Z20920; MUID:97153143; PMID:8998864
A:Accession: T30886
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1506 <JOB>
A:Cross-references: UNIPROT:P79927; EMBL:X08296; NID:g1839051; PIDN:CAA69604.1; PID:g183
C:Genetics:
A>Note: FIM-B.1
A:Superfamily: pig submaxillary mucin

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 1506;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 527 TYSMH 531

RESULT 28

T30228
polyketide synthase - Streptomyces hygroscopicus

C:Species: Streptomyces hygroscopicus
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30228
R:Apaticio, J.F.; Molnar, I.; Schwecke, T.; Koenig, A.; Haydock, S.F.; Khaw, L.E.; Staun
Gene 169, 9-16, 1996
A:Title: Organization of the biosynthetic gene cluster for rapamycin in Streptomyces hyg
A:Reference number: Z20782; MUID:96186896; PMID:8635756
A:Accession: T30228

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6260 <APA>
A:Cross-references: UNIPROT:Q54299; EMBL:X86780; NID:g987088; PID:g987102; PIDN:CAA60462
C:Genetics:
A:Gene: rapC

C:Keywords: carrier protein
F:55-451/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F:1536-1607/Domain: acyl carrier protein homology <ACP1>
F:1651-2042/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F:3123-3194/Domain: acyl carrier protein homology <ACP2>
F:3238-3632/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
F:3725-3999/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>
F:5114-5185/Domain: acyl carrier protein homology <ACP3>
F:5242-5638/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>
F:5759-6044/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2>
F:6135-6206/Domain: acyl carrier protein homology <ACP4>

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 6260;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 2611 TYALH 2615

RESULT 29

S26887
Ig heavy chain V region (DP-61) - human

C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26887
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26887
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-35 <TOM>
A:Cross-references: EMBL:Z12361; NID:9132941; PIDN:CAA78231.1; PID:932942
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 86.2%; Score 25; DB 2; Length 35;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 4 SYAMH 8

RESULT 30
S46473
Ig heavy chain V region (YAC-6) - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S46473
R:Cook, G.P.; Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Win
Nature Gene. 7, 162-168, 1994
A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A:Reference number: S46460; MUID:95004581; PMID:7920635
A:Accession: S46473
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-35 <COO>
A:Cross-references: EMBL:Z27505; NID:9505447; PIDN:CAA81825.1; PID:9505448
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 86.2%; Score 25; DB 2; Length 35;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 4 SYAMH 8

RESULT 31
P10120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: P10120
R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A:Reference number: P10116; MUID:88286083; PMID:2840480
A:Accession: P10120
A:Molecule type: mRNA
A:Residues: 1-94 <5'>
A:Cross-references: UNIPROT:O8WUK1; UNIPROT:O9UJ93
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A:Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2

Query Match 86.2%; Score 25; DB 2; Length 94;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5

Db 31 SYAMH 35

RESULT 32
S17609
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17609
R:Jackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17609
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 96;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 24 SYAMH 28

RESULT 33
S10385
Ig heavy chain V region (clone Re107) - little skate (fragment)
C:Species: Raja erinacea (little skate)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 20-Jun-2000
C:Accession: S10385
R:Harding, F.A.; Cohen, N.; Litman, G.W.
Nucleic Acids Res. 18, 1015-1020, 1990
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja e
A:Reference number: S08462; MUID:90192082; PMID:2107524
A:Accession: S10385
A:Molecule type: DNA
A:Residues: 1-97 <HAR>
A:Cross-references: EMBL:X15124; NID:964278; PIDN:CAA33218.1; PID:91334768
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 97;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 31 SYAMH 35

RESULT 34
S26885
Ig heavy chain V region (DP-44) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 23-Jul-1999
C:Accession: S26885; S36596
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM1>
A:Cross-references: EMBL:Z12344

R/Tomlinson, M.
submitted to the EMBL Data Library, June 1992
A:Reference number: S36536
A:Accession: S36536
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5, 'Q', 7-12, 'H', 14-97 <TOM2>
A:Cross-references: EMBL:Z12344; NID:g32908; PID:CAA78214.1; PID:g32909
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 97;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 35

S26886
Ig heavy chain V region (DP-45) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
A:Accession: S26886
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26886
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12345; NID:g32910; PID:CAA78215.1; PID:g32911
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 97;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 36

S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
A:Accession: S29546; S26888
R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29546
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12394; NID:g32843; PID:CAA78997.1; PID:g32844
A:Note: designated COS-8
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM2>
A:Cross-references: EMBL:Z12346; NID:g32912; PID:CAA78216.1; PID:g32913
A:Note: designated DP-46

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 37

S53076
probable membrane protein YMR254C - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YMR920.08c
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
A:Accession: S53076
R/Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53069
A:Accession: S53076
A:Molecule type: DNA
A:Residues: 1-102 <HUN>
A:Cross-references: UNIPROT:Q04838; EMBL:Z48639; NID:g732924; PID:g732932; GSPDB:GN00013
C:Genetics:
A:Gene: MIP8:YMR254C
A:Cross-references: SGD:S0004867
A:Map position: 13R
C:Superfamily: Saccharomyces probable membrane protein YMR254C
C:Keywords: transmembrane protein
F:2-18/Domain: transmembrane #status predicted <TM1>
F:46-62/Domain: transmembrane #status predicted <TM2>

Query Match 86.2%; Score 25; DB 2; Length 102;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 47 TYTMM 51

RESULT 38

PH1665
Ig heavy chain V region (clone 6B68) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
A:Accession: PH1665
R/Hillson, J.L.; Karr, N.S.; Opfinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1665
A:Molecule type: mRNA
A:Residues: 1-104 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 104;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 23 SYAMH 27

RESULT 39

PH1653
 IG heavy chain V region (clone 3G11) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C/Accession: PH1653
 R/Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
 A/Reference number: PH1642; MUID:93301610; PMID:8315388
 A/Accession: PH1653
 A/Molecule type: mRNA
 A/Residues: 1-109 <HIL>
 A/Experimental source: B cell
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 :|||
 Db 23 SYAMH 27

RESULT 40

PH1646
 IG heavy chain V region (clone 6H12) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
 C/Accession: PH1646
 R/Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
 A/Reference number: PH1642; MUID:93301610; PMID:8315388
 A/Accession: PH1646
 A/Molecule type: mRNA
 A/Residues: 1-109 <HIL>
 A/Cross-references: UNIPROT:Q8WUK1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 :|||
 Db 23 SYAMH 27

Search completed: March 31, 2005, 12:11:13
 Job time : 8.10938 secs


```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IGM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02052; M3HUGA.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid. Ig-like.
FT DOMAIN 1 112
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 1316 MW; 74E5B659E84100A CRC64;

Query Match 100.0%; Score 29; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 3
Q8PKV7 PRELIMINARY; PRT; 158 AA.
ID Q8PKV7;
AC Q8PKV7;
DT 01-OCT-2002 (TRENBLrel. 22. Created)
DT 01-OCT-2002 (TRENBLrel. 22. Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26. Last annotation update)
DE Hypothetical protein XAC2050.
GN OrderedLocustNames=XAC2050;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavaral F., Cardoso J., Chambergro F., Clapina L.P.,
RA Ciarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Guber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezsa R.I.D.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities.";

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RL Nature 417:459-463(2002).
DR EMBL; AE011840; AAM6912.1; -.
DR InterPro; IPR001412; CRNA-synt_1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 158 AA; 17289 MW; C1B1FB23AA6E930B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 132 TYAMH 136

RESULT 4
KADA_PVRHO STANDARD; PRT; 196 AA.
ID KADA_PVRHO
AC 059443;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN Name-Adk1; OrderedLocustNames=PH1753;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kousugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Oeuka R., Nakazawa H., Takamiya M., Ohtoku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki U., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the archaeal adenylate kinase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP000007; BAA30867.1; -.
DR PIR; D71184; D71184.
DR HSSP; P43410; 1K19.
DR HMAP; MF_00234; -.
KW ATP-binding; Complete proteome; Kinase; Transferase.
FT NP_BIND 9 17 ATP (Potential).
SQ SEQUENCE 196 AA; 22413 MW; 26C834A1BE9445DF CRC64;

Query Match 100.0%; Score 29; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 157 TYAMH 161

RESULT 5
Q9H2Z6

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ID Q9H2Z6 PRELIMINARY; PRT; 249 AA.
AC Q9H2Z6;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=EP2847;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Gardner L.L., Goulet L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Brady L.L., Coulter S.N., Folger K.R., Kas A., Ladwig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004711; AAG06235.1; -.
DR PIR; B83290; B83290.
DR InterPro; IPR002781; DUF81.
DR Pfam; PF01925; DUF81; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 249 AA; 25989 MW; 8B24827650F64D6A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 192 TYAMH 196

RESULT 6
Q962C9 PRELIMINARY; PRT; 356 AA.
AC Q962C9;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Transcription factor Cnox4-PC.
OS Podocoryne carnea.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydroactinidae; Podocoryne.
OX NCBI_TaxID=6096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21349874; PubMed=11456446; DOI=10.1006/dbio.2001.0299;
RA Yanze N., Spring J., Schmidl C., Schmid V.;
RT "Conservation of Hox/Parahox-related genes in the early development of
a cnidarian.";
RL Dev. Biol. 236:89-98(2001).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AY036893; AAK63185.1; -.
DR HSSP; P03089; IKZ2.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeobox, like.
DR Pfam; PF00047; HTH_lambrepreser.
DR PRINTS; PR00024; HOMEBOX_1.
DR PRINTS; PR00031; HTHREPRESSR.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 356 AA; 41170 MW; EAF5E2308D76C6B CRC64;
Query Match 100.0%; Score 29; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 103 TYAMH 107

RESULT 7
Q6N097 PRELIMINARY; PRT; 481 AA.
AC Q6N097;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein DKFZp686H20196.
GN Name=DKFZp686H20196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUB-Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambut R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
FOBO G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640619; CA845773.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 1,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 50 TYAMH 54

RESULT 8
Q68CN4 PRELIMINARY; PRT; 493 AA.
AC Q68CN4;
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209 (Fragment).
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Rectum tumor;
RA The German cDNA Consortium;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Oanger A., Fobo G., Han M., Wiemann S.;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR749861; CAH18705.1; -
DR InterPro: IPR003599; IG_1;
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; C1-act; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
FT NON_TER
SQ SEQUENCE 493 AA; 54117 MW; A1E4P5ED3FA8AB40 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 73 TYAMH 77

RESULT 9
Q83WR9 PRELIMINARY; PRT; 531 AA.
AC Q83WR9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tsh protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ABEC13;
RA Simoes R.C., Delicato E.R., Gaziri L.C.J., Vidotto M.C.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY280856; AAP33781.1; -
DR GO: GO:0004232; F:serine-type endopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000710; Peptidase S6.
DR InterPro: IPR009003; Pept_Ser_Cyt.
DR Pfam: PF02395; IGA1; 1.
DR PRINTS: PR00921; IGASERPTASE.
FT NON_TER
SQ SEQUENCE 531 AA; 56485 MW; 60AC4E859A7AFC03 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 341 TYAMH 345

RESULT 10
Q6A019 PRELIMINARY; PRT; 544 AA.
AC Q6A019;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)

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DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Probable acetyl-coenzyme A synthetase.
GN Name=acs; OrderedLocustNames=DP0825;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobacteraceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardoc T., Becker I., Amann U., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Kleink H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL: CR522870; CAG35554.1; -
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP_BINDING; 1.
KM Complete proteome.
SQ SEQUENCE 544 AA; 60412 MW; CAD62D99B4CCEBF7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 307 TYAMH 311

RESULT 11
Q9V6J4 PRELIMINARY; PRT; 648 AA.
ID Q9V6J4;
AC Q9V6J4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE CG3915-PB (GH27039p).
GN Name=Drl-2; ORFNames=CG3915;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abriil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck U., Brokstein P., Brotlier P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasner K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegyam C.,
 RA Kimali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mikhaylov G., Mikhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Neislo D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Massamman D.A., Weissstock G.M., Weissbach J.,
 RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weissstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceiniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mierra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
 RA Betencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez C., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munro J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceiniker S.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003820; AAF58429.3; -
 DR EMBL; BT004493; AAC42657.1; -
 DR HSSP; P08581; IRW.
 DR FlyBase; FBGN0033791; Dr1-2.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0004713; F:Protein-cytosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot. Kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR003306; WIF.
 DR Pfam; PF02019; WIF; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot. kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN; 1.
 DR PROSITE; PS50814; WIF; 1.
 DR Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 648 AA; 7139 MW; 1B4F6A0C84E457 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 648;
 Best Local Similarity 100.0%; Pred. NO. 1.de+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 DB 56 TYAMH 60
 RESULT 12
 Q9HGS1 PRELIMINARY; PRT; 690 AA.
 AC Q9HGS1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Glutaminease (EC 3.5.1.2).
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutroiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U212;
 RA Thammavongtham C., Turner G., Moir A.J., Tanticharoen M.,
 RA Cheevadhanarak S.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY005477; AAG02575.1; -
 DR GO; GO:0004359; F:glutaminease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 SQ SEQUENCE 690 AA; 76226 MW; 6546BE249D8D43C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 690;
 Best Local Similarity 100.0%; Pred. NO. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 DB 423 TYAMH 427
 RESULT 13
 Q9UVX9 PRELIMINARY; PRT; 690 AA.
 AC Q9UVX9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Glutaminease A.
 GN Name=gtaa;

```

OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI840;
RX MEDLINE=20406523; PubMed=10952006;
RA Koibuchi K., Nagasaki H., Yusa A., Kataoka J., Kitamoto K.;
RT "Molecular cloning and characterization of a gene encoding glutaminase
  from Aspergillus oryzae.";
RL Appl. Microbiol. Biotechnol. 54:59-68 (2000).
DR EMBL; AB029552; BA86934.1; -.
SQ SEQUENCE 630 AA; 76164 MW; E3D0B17841EEA00D CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 690;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 14
V222_FOWPV STANDARD; PRT; 747 AA.
ID V222_FOWPV
AC Q9513;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative ankylrin-repeat protein PPV222.
GN Name=PPV222;
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RX DOI=10.1128/JVI.74.8.3815-3831.2000;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC -1- SIMILARITY: Contains 14 ANK repeats.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AF198100; AAF4556.1; -.
DR HSP; Q60778; 1073.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00023; Ank; 13.
DR Pfam; PF00646; F-box; 1.
DR PRINTS; PR01415; ANKRIN.
DR SMART; SM00248; ANK; 15.
DR PROSITE; PS50297; ANK_RBP_REGION; 1.
DR PROSITE; PS50088; ANK_REPEAT; 7.
KM ANK repeat; Hypothetical protein; Repeat.
FT REPEAT 38 67 ANK 1.
FT REPEAT 103 132 ANK 2.
FT REPEAT 136 165 ANK 3.
FT REPEAT 169 198 ANK 4.
FT REPEAT 202 231 ANK 5.
FT REPEAT 234 263 ANK 6.
FT REPEAT 294 323 ANK 7.
FT REPEAT 328 357 ANK 8.

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FT REPEAT 361 393 ANK 9.
FT REPEAT 397 426 ANK 10.
FT REPEAT 430 460 ANK 11.
FT REPEAT 464 493 ANK 12.
FT REPEAT 495 524 ANK 13.
FT REPEAT 529 559 ANK 14.
SQ SEQUENCE 747 AA; 85303 MW; 55F90AF28553D28 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 1; Length 747;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 330 TYAMH 334

RESULT 15
Y245_TREPA STANDARD; PRT; 1151 AA.
ID Y245_TREPA
AC O83273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TP0245.
GN OrderedLocusNames=TP0245;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=965876; DOI=10.1126/science.281.5375.375;
RX Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R.J., Gwinn M.L., Hickey B.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardam J.M., McLeod M.P., Salzberg S.L., Petersen J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Uteirack T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
  agent spirochete.";
RL Science 281:375-388(1998).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB001206; AAC65239.1; -.
DR PIR; H71347; H71347.
DR TIGR; TP0245; -.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 1151 AA; 127556 MW; EDB6353C32CB4056 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 1; Length 1151;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 700 TYAMH 704

RESULT 16
O88093 PRELIMINARY; PRT; 1377 AA.
AC O88093;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

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DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Haemoglobin protease precursor.
GN Name=hbp;
OS Escherichia coli.
OC Plasmid pColy-K10.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EB1.
RX MEDLINE=98416173; PubMed=9743528;
RA Otto B.R., van Dooren S.J.M., Nuijens J.H., Luijckink J., Oudega B.;
RT "Characterization of a hemoglobin protease secreted by the pathogenic
RT Escherichia coli strain EB1."
RL J. Exp. Med. 188:1091-1103(1998).
DR EMBL; AJ223631; CAA11507.1; -.
DR MEROPS; S06.003; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto_transbeta.
DR InterPro; IPR011050; Pectin_lyas_like.
DR InterPro; IPR000710; Peptidase_S6.
DR Pfam; PF009003; Pept_Ser_Cys.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03395; IGA1; 1.
DR PRINTS; PR00921; IGASERPTASE.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
KW Plasmid; Protease; Signal.
FT SIGNAL.
SQ SEQUENCE 1377 AA; 148256 MW; BB16D98BEDAC0416 CRC64;

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Query Match 100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 1 TYAMH 5
DB 341 TYAMH 345

RESULT 17
ID 047692 PRELIMINARY; PRT; 1377 AA.
AC Q47692;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Tsh.
GN Name=tsh;
OS Escherichia coli.
OC Plasmid pAPBC-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=chi7122;
RX MEDLINE=94178945; PubMed=8132344;
RA Providence D.L., Curtiss R. III.;
RT "Isolation and characterization of a gene involved in hemagglutination
RT by an avian pathogenic Escherichia coli strain."
RL Infect. Immun. 62:1369-1380(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=chi7122;
RX MEDLINE=20316042; PubMed=10858231;
RX DOI=10.1128/JAI.68.7.4145-4154.2000;
RA Dozols C.M., Dho-Moulin M., Bree A., Fairbrother J.M., Desautels C.,
RA Curtiss R. III.;
RT "Relationship between the Tsh autotransporter and pathogenicity of

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RT avian Escherichia coli and localization and analysis of the Tsh
RT genetic region."
RL Infect. Immun. 68:4145-4154(2000).
DR EMBL; AF218073; AAA24698.1; -.
DR PIR; I54632; I54632.
DR MEROPS; S06.003; -.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto_transbeta.
DR InterPro; IPR011050; Pectin_lyas_like.
DR InterPro; IPR000710; Peptidase_S6.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03395; IGA1; 1.
DR PRINTS; PR00921; IGASERPTASE.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
KW Plasmid.
SQ SEQUENCE 1377 AA; 148226 MW; 237423644D9AE012 CRC64;

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Query Match 100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 1 TYAMH 5
DB 341 TYAMH 345

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RESULT 18
ID 06JUN6 PRELIMINARY; PRT; 7488 AA.
AC 06JUN6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Obsc.
OS Saccharopolyspora spinosa.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Saccharopolyspora.
OX NCBI_TaxID=60894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRL1.18395;
RA Zirkle R., Black T.A., Goriach J., Iygon J.M., Molnar I.;
RT "Analysis of a 108-kb region of the Saccharopolyspora spinosa Genome
RT covering the Obsecurin Polyketide Synthase Locus."
RL DNA Seq. 15:123-134(2004).
DR EMBL; AY466441; AAS00421.1; -.
DR HSSP; Q03133; IKEZ.
DR GO; GO:0004024; F:alcohol dehydrogenase activity; zinc-dependent; IEA.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016788; F:hydrolase activity; acting on ester bonds; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR001227; Ac_transferase.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR011032; GroES_like.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR006163; Pnpanteteh_bind.
DR InterPro; IPR006162; Pantetene_S.
DR Pfam; PF00698; ACYL_transf_1; 4.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF02801; ketoacyl-synt; 4.
DR Pfam; PF00550; PP-binding; 4.
DR Pfam; PF00975; Thioesterase; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 4.

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DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 4.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 4.
 DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
 DR Phosphopantetheine; Transferase.
 SQ SEQUENCE 7488 AA; 781833 MW; C54551IDF855B1A4 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 7488;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 7374 TYAMH 7378

RESULT 19

Q62XJ3 PRELIMINARY; PRT; 65 AA.
 AC Q62XJ3.
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=BL05084;
 OS Bacillus licheniformis DSM 13.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=279010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14580;
 RA Rey M.W., Ramaiva P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., de Leon A.L., Xiang H., Gueti V., Clausen I.G., Olsen P.B.,
 RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
 RA Sorkin A., Bolotin A., Lapidin A., Galleron N., Ehrlich S.D.,
 RA Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium Bacillus
 RT licheniformis and comparisons with closely related Bacillus species."
 RL Genome Biol. 5:R77-R77(2004).
 DR EMBL; CP000002; AA022515.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 65 AA; 7079 MW; 1D43A68FE26DC053 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 65;
 Best Local Similarity 80.0%; Pred. No. 90;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 33 TYALH 37

RESULT 20

Q23428 PRELIMINARY; PRT; 95 AA.
 AC Q23428.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein ZK1248.17;
 GN Name=ZK1248.17; ORFNames=ZK1248.17;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 CX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=98063613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Lactelle P.;
 RT "The sequence of C. elegans cosmid ZK1248."
 RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Central component in molecular interactions underlying
 sperm crawling. Forms an extensive filament system that extends
 from sperm villipoda, along the leading edge of the pseudopod (By
 similarity).
 CC -1- SIMILARITY: Contains 1 MSP domain.
 DR EMBL; U29244; AAC71098.1; -.
 DR PIR; T34500; T34500.
 DR HSSP; P53017; IGRW.
 DR WormBase; WBGene00022884; ZK1248.17.
 DR WormPep; ZK1248.17; CE02901.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000535; MSP.
 DR InterPro; IPR008962; PapD-like.
 DR Pfam; PF00635; Motile_Sperm; 1.
 DR PROSITE; PS50202; MSP; 1.
 KW Cyoskeleton; Hypothetical protein.
 SQ SEQUENCE 95 AA; 10727 MW; E8D70FF0395004A8 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 95;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 12 TYSMH 16

RESULT 21

Q6XNP8 PRELIMINARY; PRT; 108 AA.
 AC Q6XNP8.
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE ASR-like protein 1.
 GN Name=ASRBP1;
 OS Hevea brasiliensis (Para rubber tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Micondreae;
 OC Hevea.
 CX NCBI_TaxID=3981;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ko J.-H., Han K.-H.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY221984; AAP46155.1; -.
 DR GO; GO:0006950; P:response to stress; IEA.

DR InterPro; IPR003496; ABA_WDS.
DR Pfam; PF02496; ABA_WDS; 1.
SQ SEQUENCE 108 AA; 12124 MW; 368E3B9C50D47AE7 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 45 TYALH 49
RESULT 22
08ZZA5 PRELIMINARY; PRT; 138 AA.
AC 08ZZA5; 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein PAE0353.
GN OrderedLocusNames=PAE0353;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fltz-Gibson S.T., Ladner H., Kim U.-Y., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum".
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
KW EMBL; AE009763; AAL62736.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 138 AA; 15372 MW; 662A04E963ABE921 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 138;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 66 TYALH 70
RESULT 23
07Z447 PRELIMINARY; PRT; 160 AA.
AC 07Z447; 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cytochrome P450 (Fragment).
GN Name=CYP3A5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=2183017; PubMed=11726664; DOI=10.1074/jbc.M109175200;
RA Fita C., Zaphiropoulos P.G.;
RT "Intergenic mRNA molecules resulting from trans-splicing";
RL J. Biol. Chem. 277:5882-5890(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zaphiropoulos P.G.;
RL Submitted (MAY-2003) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AJ563378; CAD91647.1; -.
DR HSSP; P14779; 1BUT.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER
SQ SEQUENCE 160 AA; 18362 MW; A05FEDASB16A843 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 56 TYALH 60
RESULT 24
06BK2 PRELIMINARY; PRT; 169 AA.
AC 06BK2; 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Regulatory protein CII bacteriophage 186.
GN ORFNames=YR71769;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Camiel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinebusch B.J., Marteau M., Medigue C.,
RA Simonet M., Chenal-Franciaque V., Souza B., Dacheux D., Elliott J.M.,
RA Derblat A., Hauser L.J., Garcia B.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis".
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
KW EMBL; BX936398; CAH21008.1; -.
KW InterPro; IPR009679; Phage_CP76.
DR Pfam; PF06892; Phage_CP76; 1.
SQ SEQUENCE 169 AA; 17796 MW; 8DD659B642CB5D4 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 169;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 94 TYALH 98
RESULT 25
086SK1 PRELIMINARY; PRT; 173 AA.
AC 086SK1; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21839017; PubMed=11726664; DOI=10.1074/jbc.M109175200;
RA Finta C., Zaphiropoulos P.G.;
RT "Intergenic mRNA molecules resulting from trans-splicing.";
RL J. Biol. Chem. 277:5882-5890(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX Zaphiropoulos P.G.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AJ563378; CAD91347.1; -.
DR HSBP; P14779; 1B7.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002403; EP4501V.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00465; EP4501V.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Hypothetical protein.
SQ SEQUENCE 173 AA; 19718 MW; AF01A03594D95A13 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 173;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
||:|
Db 69 TYALH 73

RESULT 26

O6LMV3 PRELIMINARY; PRT; 175 AA.
AC O6LMV3;
DT 05-JUN-2004 (TREMblrel. 27, Created)
DT 05-JUN-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMblrel. 27, Last annotation update)
DE Putative autoinducer-2 production protein LuxS.
GN Name=S2901; OrderedCusNames=PBPA3045;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Verzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR318673; CAG21373.1; -.
DR GO; GO:0009372; P:quorum sensing; IEA.
DR InterPro; IPR003815; LuxS.
DR Pfam; PF02664; LuxS; 1.
DR PRINTS; PR01487; LUXSPROTEIN.
DR PRODOM; PD013172; LuxS; 1.
KW Complete proteome.
SQ SEQUENCE 175 AA; 19651 MW; 1191C0DCD26AB238 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 175;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
||:|
Db 133 TYSMH 137

RESULT 27
ID O67RR8 PRELIMINARY; PRT; 187 AA.
AC O67RR8;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=STH640;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM14863;
RA Ueda K., Yamashita A., Ishikawa J., Shinada M., Matsui T.,
RA Morimura K., Ikeda H., Hattori M., Bepko T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006840; BAD39625.1; -.
DR InterPro; IPR003848; DUF218.
DR Pfam; PF02698; DUF218; 1.
KW Hypothetical protein.
SQ SEQUENCE 187 AA; 21555 MW; 421C8F241F2A81B8 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 187;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
||:|
Db 180 TYALH 184

RESULT 28

RETB_CHICK STANDARD; PRT; 196 AA.
AC P41263;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Plasma retinol-binding protein precursor (PRBP).
GN Name=RPB4;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95267350; PubMed=7748490;
RA Vieira A.V., Kuchler K., Schneider W.J.;
RT "Retinol in avian oogenesis: molecular properties of the carrier
RT protein";
RL DNA Cell Biol. 14:403-410(1995).
CC -1- FUNCTION: Delivers retinol from the liver stores to the peripheral
CC tissues. In plasma, the RBP-retinol complex interacts with
CC transthyretin, this prevents its loss by filtration through the
CC kidney glomeruli (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the lipocalin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X77960; CAA54922.1; -.
DR PIR; I50675; I50675.

DR PDB, 1IUU; X-ray; A=23-196.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocalin cytochrome P-450.
DR InterPro; IPR002449; Retinol-binding.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00179; LIPOCALIN.
DR PROSITE; PS00213; LIPOCALIN; 1.
KM 3D-structure; Lipocalin; Plasma; Retinol-binding; Signal; Transport;
Vitamin A.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 196 Plasma retinol-binding protein.
FT DISULFID 25 181 By similarity.
FT DISULFID 91 195 By similarity.
FT DISULFID 141 150 By similarity.
FT STRAND 26 26
FT HELIX 27 29
FT TURN 34 35
FT TURN 38 41
FT HELIX 43 51
FT STRAND 60 68
FT TURN 70 71
FT STRAND 74 83
FT TURN 85 86
FT STRAND 89 99
FT TURN 104 105
FT STRAND 106 113
FT STRAND 121 130
FT STRAND 135 144
FT TURN 146 147
FT STRAND 149 159
FT TURN 162 163
FT HELIX 167 178
FT TURN 179 181
FT TURN 183 184
FT TURN 187 188
SQ SEQUENCE 196 AA; 22515 MW; 5B9423A14578DA75 CRC64;
Query Match 89.7%; Score 26; DB 1; Length 196;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 134 TYALH 138
RESULT 29
Q9CKO5 PRELIMINARY; PRT; 202 AA.
ID Q9CKO5
AC Q9CKO5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PM1551.
GN OrderedLocusNames=PM1551;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.-J., Zhang Q., Li H.-L., Paustian M.L., Whitlam T.S., Kapur V.,
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
RL EMBL; AF006192; AAK03635.1; -.
DR HSSP; Q9ZV03; 1E6B.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR010987; GST_C_1like.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF02798; GST_N; 1.

KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 202 AA; 23181 MW; 5B6D95AE3FE02E73 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 202;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 172 TYALH 176
RESULT 30
Q9CG61 PRELIMINARY; PRT; 213 AA.
ID Q9CG61
AC Q9CG61
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F28L5.12.
GN Name=F28L5.12;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uteback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC079280; AAG50576.1; -.
DR PIR; H86403; H86403.
KM Hypothetical protein.
SQ SEQUENCE 213 AA; 25121 MW; D98C5F7BC5EC199C CRC64;
Query Match 89.7%; Score 26; DB 2; Length 213;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 202 TYALH 206
RESULT 31
Q9DG60 PRELIMINARY; PRT; 217 AA.
ID Q9DG60
AC Q9DG60
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Zinc finger protein Salt (Fragment).
GN Name=Salt;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Mhlanga M., Brewster R., Ruiz i Altaba A.;
Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF181559; AAG09433.1; -.
FT NON_TER 1
SQ SEQUENCE 217 AA; 23167 MW; 44D3828F471668E2 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 217;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5

Db 132 TYSMH 136

RESULT 32

09UX67 PRELIMINARY; PRT; 222 AA.

AC 09UX67
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Hypothetical protein ORF-c16.036 (Hypothetical protein SS00678).
GN Name-ORF-c16.036, OrderedLocNames=SS00678;
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
NCBI_TaxID=2287;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=P2.
RX MEDLINE=20165948; PubMed=10701121; DOI=10.1139/gen-43-1-116;
RA Charlebois R.L., Singh R.K., Chan-Weiher C.C.Y., Allard G., Chow C.,
RA Confalonieri F., Curtis B., Duguet M., Brauso G., Paquy D.,
RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
RA Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,
RA St Jean A., Van Der Oost J., Young F., Zivanovic Y., Doolittle W.F.,
RA Ragan M.A., Senen C.W.;
RT "Gene content and organization of a 281-kbp contig from the genome of
RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
RL Genome 43:116-136(2000).
[2]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Amey M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moers A., Brauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; Y18930; CAB57625.1; -;
DR EMBL; AE006695; AA40980.1; -;
DR PIR; E90215; E90215.
DR InterPro; IPR002761; DUF71.
DR Pfam; PF01902; ATP_bind_4; 1.
DR TIGRFAMs; TIGR00290; M0570_dom; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 222 AA; 25574 MW; C67F5F29712CE82P CRC64;

Query Match 89.7%; Score 26; DB 2; Length 222;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 14 TYALH 18

RESULT 33

Q20984 PRELIMINARY; PRT; 228 AA.

AC 020984
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Hypothetical protein F58B6.8.
GN ORFNames=F58B6.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
[2]

RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurtry A.A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z70754; CA9478.1; -;
DR PIR; T22924; T22924.
DR WormBase; WBGene00010257; F58B6.8.
DR WormPep; F58B6.8; CE06023.
KM Hypothetical protein.
SQ SEQUENCE 228 AA; 25181 MW; 55F66019EE3A882E CRC64;

Query Match 89.7%; Score 26; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 177 TYALH 181

RESULT 34

Q8SHP4 PRELIMINARY; PRT; 229 AA.

AC Q8SHP4
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Trichoderma reesei (Hypocrea jecorina).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocremycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=21950703; PubMed=11825887; DOI=10.1074/jbc.M107651200;
RA Chambergo F.S., Bonaccorsi E.D., Ferreira A.J.S., Ramos A.S.P.,
RA Ferreira J.R.J., Abrahao-Neto J., Farah J.P.S., El-Dorry H.;
RT "Elucidation of the metabolic fate of glucose in the filamentous
RT fungus trichoderma reesei using expressed sequence tag (EST) analysis
RT and cDNA microarrays.";
RL J. Biol. Chem. 277:13983-13988(2002).

DR EMBL; AF447590; AL74168.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0006314; P:intern homing; IEA.
DR InterPro; IPR001982; Endonuc_LAG/HNH.
DR Pfam; PF00961; LAGLIDADG_1; 2.

KM Hypothetical protein; Mitochondrion.
SQ SEQUENCE 229 AA; 26909 MW; BC5E7B377C19A3C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 229;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 46 TYALH 50

RESULT 35

Q8Y918

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ID 08Y918 PRELIMINARY; PRT; 242 AA.
AC Q8Y918;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Lmo0724 protein.
GN OrderedLocustNames=lmo0724;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangoul L., Buchrieser C., Rumnok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cheouani F., Couve E., de Daruvar A., Deloux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf U., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kuntz F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RL Science 294:849-852(2001).
DR EMBL; AL591976; CAC98802.1; -.
PIR; AD1165; AD1165.
DR L161165; LMO0724; -.
DR PROSITE; PS00639; TH1OL_PROTEASE_HIS; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 26837 MW; E2D06DB33570BB8D CRC64;

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 36
ID Q92DT0 PRELIMINARY; PRT; 242 AA.
AC Q92DT0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Lmo0732 protein.
GN OrderedLocustNames=lmo0732;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangoul L., Buchrieser C., Rumnok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cheouani F., Couve E., de Daruvar A., Deloux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf U., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kuntz F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RL Science 294:849-852(2001).
DR EMBL; AL596166; CAC95964.1; -.

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DR PIR; AD1524; AD1524.
DR L161165; LMO0732; -.
DR InterPro; IPR000169; Pept_cys_acsite.
DR PROSITE; PS00639; TH1OL_PROTEASE_HIS; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 26751 MW; 7AC7946460DF39A7 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 37
ID Q722H3 PRELIMINARY; PRT; 242 AA.
AC Q722H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=LMOF2365_0760;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Raeko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Fothergill H.A., Tran B., Katherlou S., Wonderling L.D., Uhlrich G.A.,
RA Bayles D.O., Luchanansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL; AE017324; AA03541.1; -.
DR InterPro; IPR000169; Pept_cys_acsite.
DR PROSITE; PS00639; TH1OL_PROTEASE_HIS; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 26802 MW; 8C6903FDD8926A32 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 38
ID Q8WRC3 PRELIMINARY; PRT; 244 AA.
AC Q8WRC3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Endonuclease.
GN Name=TRI1;
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenida; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22030828; PubMed=12034842; DOI=10.1093/nar/30.11.2524;

```

```

RA Multesich J.D., Gershan J.A., Lochowicz A.J., Li S., Karrer K.M.;
RT "A novel family of mobile genetic elements is limited to the germline
RL genome in Tetrahymena thermophila."
RL Nucleic Acids Res. 30:2524-2537(2002).
DR EMBL/AF451862; AAL73456.1; -.
DR GO:GO:0005634; C:nucleus; IEA.
DR GO:GO:0004519; F:endonuclease activity; IEA.
DR GO:GO:0003676; F:nucleic acid binding; IEA.
DR GO:GO:0003700; F:transcription factor activity; IEA.
DR GO:GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam: PF01844; HNH; 1.
DR Pfam: PF07463; NUDOD4; 1.
DR SMART; SM00507; HNH; 1.
DR Endonuclease.
KW SEQUENCE
SQ SEQUENCE 244 AA; 28678 MW; C4805D4E8E2CA4CB CRC64;

Query March 89.7%; Score 26; DB 2; Length 244;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 128 TYAMH 132

RESULT 39
Q885R2 PRELIMINARY; PRT; 248 AA.
AC Q885R2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Membrane protein, putative.
GN OrderedLocusNames=PSPT01769;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joarist V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwyn M.T., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidse T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AE016862; AA055289.1; -.
DR TIGR; PSPT01769; -.
DR InterPro; IPR002781; DUF81.
DR Pfam; PF01925; DUF81; 1.
KW Complete proteome.
SQ SEQUENCE 248 AA; 26313 MW; DCEADEE42B6161CE CRC64;

Query Match 89.7%; Score 26; DB 2; Length 248;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYALH 195

RESULT 40
Q708W1 PRELIMINARY; PRT; 266 AA.

```

```

AC Q708W1;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AGCP11755
GN Name=agCG48584; ORFNames=ENSGANG00000018095;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008933; EAA09904.1; -.
DR GO:GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR010233; UbiG_mtfase.
DR TIGRfams; TIGR01983; UbiG_1.
SQ SEQUENCE 266 AA; 30168 MW; 2F342C53863CFA08 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 266;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 258 TYALH 262

Search completed: March 31, 2005, 12:09:37
Job time : 35.3698 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 131.75 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88
Sequence: 1 IISYDGSKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	88	100.0	17	3	AA79069	Anti-Fact
2	87	98.9	118	5	ABB07230	Abp07230 Anti-IL-4
3	87	98.9	248	5	ABP45312	Abp45312 Human Bly
4	87	98.9	248	5	ABP44905	Abp44905 Human Bly
5	87	98.9	248	5	ABP44903	Abp44903 Human Bly
6	87	98.9	248	7	ADG95730	Adg95730 Single ch
7	87	98.9	248	7	ADG95732	Adg95732 Single ch
8	87	98.9	248	7	ADG96139	Adg96139 Single ch
9	87	98.9	251	5	ABP45103	Abp45103 Human Bly
10	87	98.9	251	7	ADG95930	Adg95930 Single ch
11	86	97.7	135	7	ADD28319	Add28319 Human het
12	85	96.6	119	5	ABB07186	Abb07186 sHlgM22 h
13	84	95.5	117	7	ABO33850	Ab033850 Anti-GPI-
14	84	95.5	112	7	ABO33836	Ab033836 Human ant
15	84	95.5	119	5	ABB07169	Abb07169 sHlgM22 h
16	84	95.5	119	8	AD126654	Ad126654 Human ant
17	83	94.3	17	3	AA79076	Anti-Fact
18	83	94.3	123	8	ADP22108	Adp22108 Human ant
19	83	94.3	125	7	ADP28443	Adp28443 Human ant
20	83	94.3	137	7	ADP28233	Adp28233 Human het
21	83	94.3	137	7	ADP28321	Adp28321 Human het
22	83	94.3	252	5	ABP45679	Abp45679 Human Bly
23	83	94.3	252	5	ADG96506	Adg96506 Single ch
24	83	94.3	470	7	ADP28467	Adp28467 Human ant
25	83	94.3	614	5	ABB06275	Abb06275 Plasmid s

26	82	93.2	17	2	AAW90298	Aaw90298 Human ant
27	82	93.2	17	3	AA79074	AA79074 Anti-Fact
28	82	93.2	17	3	AA79078	AA79078 Anti-Fact
29	82	93.2	17	5	AAO17790	Aao17790 CDR2 regl
30	82	93.2	17	7	ADJ32094	Adj32094 Human int
31	82	93.2	17	7	ADH89402	Adh89402 Human tra
32	82	93.2	17	8	ADP47199	Adp47199 Human pho
33	82	93.2	17	8	ADG82565	Adg82565 Anti-IL-2
34	82	93.2	17	8	ADG52370	Adg52370 Fab targe
35	82	93.2	17	8	ADG52400	Adg52400 Fab targe
36	82	93.2	17	8	ADG52430	Adg52430 Fab targe
37	82	93.2	17	8	ADG52388	Adg52388 Fab targe
38	82	93.2	17	8	ADG52420	Adg52420 Human ant
39	82	93.2	41	8	ADR68562	Adr68562 Human EPO
40	82	93.2	61	2	AA766975	Aar766975 HSV-neutr
41	82	93.2	62	2	AA766976	Aar766976 HSV-neutr
42	82	93.2	66	6	ABU56837	Abu56837 BONT/A HC
43	82	93.2	66	6	ABU56866	Abu56866 BONT/A HC
44	82	93.2	83	2	AAW62799	Aaw62799 Amino aci
45	82	93.2	95	3	AAW40127	Aaw40127 Anti-hlrl

ALIGNMENTS

RESULT 1
AA79069
ID AA79069 standard; peptide; 17 AA.

AA79069;
12-JUN-2000 (first entry)

Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.

Complementarily determining region 2; CDR2; antibody; Gla domain;
Factor IX/IXa; blood coagulation; deep venous thrombosis;
arterial thrombosis; unstable angina; post myocardial infarction;
coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
percutaneous transluminal coronary angioplasty; PTCA; inflammation;
septic shock; hypotension; adult respiratory distress syndrome; ARDS;
arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.
WO200012562-A1.
09-MAR-2000.
26-AUG-1999; 99WO-US019453.
28-AUG-1998; 98US-0098233P.
03-MAR-1999; 99US-0122767P.
(GENTH) GENENTECH INC.

Adams CM, Devaux B, Eaton DL, Hase PE, Judice JK, Kirchhofer D;
Suggett S;
WPI; 2000-256595/22.
Novel human anti-factor IX/IXa antibodies against IX/IXa gamma-
carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
stroke, and post myocardial infarction.
Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarily determining region 2 (CDR2) of
the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
antibody. Factor IXa is a vitamin K dependent plasma serine protease that
participates in the blood coagulation pathways. The Gla domain of factor
IXa and its zymogen factor IX contains important structural determinants
for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FII/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

CC Sequence 17 AA;

Query Match 100.0%; Score 88; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVK 17
Db 1 IISYDGSKKYYADSVK 17

RESULT 2
ABR07230 standard; protein, 118 AA.

AC ABR07230;
XX
XX 26-MAR-2002 (first entry)
XX
XX Anti-IL-4 receptor Mab 6-2 heavy chain variable region.
XX
XX Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
XX antiarthritic; dermatological; antitumor; antiinflammatory; cytostatic;
XX anticaking; immunosuppressive; tuberculostatic; ophthalmological;
XX antianemic; antithyroid.

XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 31..35
XX /note= "complementarity determining region (CDR) 1"
XX Region 50..66
XX /note= "complementarity determining region (CDR) 2"
XX Region 99..107
XX /note= "complementarity determining region (CDR) 3"
XX
XX WO200192340-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US017094.
XX
XX 26-MAY-2000; 2000US-00579808.
XX 19-SEP-2000; 2000US-00665343.
XX 15-FEB-2001; 2001US-00785934.
XX 01-MAY-2001; 2001US-00847816.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Plumeke JD;
XX
XX WPI; 2002-114332/15.
XX N-PSDB; ABA94330.
XX
XX Novel human antibody which binds human interleukin (IL)-4 receptor and is
XX capable of inhibiting IL-4 induced biological activity, functions as IL-4
XX antagonist and is useful for treating septic arthritis, scleroderma.
XX
XX Claim 4; Page 73; 85pp; English.
XX
XX The invention relates to a human antibody (an interleukin (IL)-4
XX antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of

CC inhibiting an IL-4-induced biological activity. (I) is also useful for
CC inhibiting both IL-4-induced biological activity and IL-13-induced
CC biological activity in vivo in a human, and for treating septic arthritis
CC in a human afflicted with septic arthritis. (I) is also used for treating
CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,
CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric
CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
CC inflammatory bowel disease, other disorders of the digestive system in
CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the
CC gastrointestinal tract), conditions in which IL-4-induced barrier
CC disruption plays a role (e.g. conditions characterized by decreased
CC epithelial barrier function in the lung or gastrointestinal tract),
CC scleroderma, hypertrophic scarring, Whipple's disease, benign prostatic
CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-
CC Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
CC autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,
CC Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
CC diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
CC antagonists also find use as adjuvants to allergy immunotherapy and as
CC vaccine adjuvants, especially when directing the immune response toward a
CC TH1 response would be beneficial in treating or preventing the disease.
CC The present sequence represents an anti-IL-4 receptor monoclonal antibody
CC (Mab) 6-2 heavy chain variable region

CC Sequence 118 AA;

Query Match 98.9%; Score 87; DB 5; Length 118;
Best Local Similarity 94.1%; Pred. No. 4.1e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVK 17
Db 50 IISYDGSKKYYADSVK 66

RESULT 3
ABP45312 standard; protein, 248 AA.

AC ABP45312;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1323.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineutrotic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruden SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX


```

DR      WPI, 2002-114799/15.
XX
XX      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT      diagnosis and treatment of cancers and immune disorders.
XX
XX      Claim 1; Page 1981-1982; 3148pp; English.
XX
XX      This invention describes novel antibodies that immunospecifically bind to
CC      B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC      tumour necrosis factor (TNF) super family and induces B cell
CC      proliferation and differentiation. The antibodies of the invention have
CC      cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC      antirheumatic and antiAIDS activity and can be used in vaccines to
CC      inhibit the expression and activity of Blys. The antibodies bind to Blys
CC      and so may be used to detect and quantitate the presence of Blys in
CC      biological samples and may be used in this way to diagnose disease
CC      associated with aberrant expression of Blys. They may also be
CC      administered to treat diseases associated with aberrant Blys expression
CC      and actively such as cancer, immune, and autoimmune disorders and
CC      diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC      immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC      acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC      the antibodies and fragments of the antibodies described in the method of
CC      the invention
XX
XX      Sequence 248 AA:
SQ
XX
XX      Query Match          98.9%; Score 87; DB 5; Length 248;
XX      Best Local Similarity 94.1%; Pred. No. 9.3e-06;
XX      Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
XX
XX      1 IISYDGSKKYYADSVYKG 17
XX      :|||||
XX      50 VISYDGSKKYYADSVYKG 66
XX
XX      RESULT 4
XX      ABP44905
XX      ID      ABP44905 standard; protein; 248 AA.
XX      AC      ABP44905;
XX      DT      19-AUG-2002 (first entry)
XX      DE      Human Blys binding scFv SEQ ID 916.
XX      EE
XX      FF      Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX      GG      tumour necrosis factor; B cell proliferation; B cell differentiation;
XX      HH      immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX      II      antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX      JJ      systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX      KK      common variable immunodeficiency; acquired immunodeficiency syndrome.
XX      LL      Homo sapiens.
XX      MM      WO200202641-A1.
XX      NN      10-JAN-2002.
XX      OO
XX      PP      15-JUN-2001; 2001WO-US019110.
XX      QQ
XX      RR      16-JUN-2000; 2000US-0212210P.
XX      SS      17-OCT-2000; 2000US-0240816P.
XX      TT      16-MAR-2001; 2001US-0276248P.
XX      UU      21-MAR-2001; 2001US-0277379P.
XX      VV      25-MAY-2001; 2001US-0293499P.
XX      WW
XX      XX      (HUMA-) HUMAN GENOME SCI INC.
XX      YY      (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX      ZZ
XX      AA      Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX      BB      WPI, 2002-114799/15.

```

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 1495-1496; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumor necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cysteistic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 SQ Sequence 248 AA;
 Query Match 98.9%; Score 87; DB 5; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0
 Oy 1 IISYDGSKKYADSYKG 17
 :|||||
 Db 50 VISYDGSKKYADSYKG 66
 RESULT 5
 ID ABP44903 standard; protein; 248 AA.
 XX ABP44903;
 AC
 XX
 DT 19-AUG-2002 (first entry)
 DE
 DE Human Blys binding scFv SEQ ID 914.
 DE
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KM tumor necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccinia; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 OS
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI, 114799/15.
 XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1492-1493; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and anti-AIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). AB4390-AB47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;
XX
Query Match 98.9%; Score 87; DB 5; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVK 17
Db 50 VISYDGSKKYYADSVK 66
XX
RESULT 6
ADG95730
ID ADG95730 standard; protein; 248 AA.
XX
AC ADG95730;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys Segid 914.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scfv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineoplastic; antirheumatic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cyostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PE 14-NOV-2002; 2002WO-US036496.
XX
PF 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 914; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scfvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineoplastic, antirheumatic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cyostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 248 AA;
XX
Query Match 98.9%; Score 87; DB 7; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVK 17
Db 50 VISYDGSKKYYADSVK 66
XX
RESULT 7
ADG95732
ID ADG95732 standard; protein; 248 AA.
XX
AC ADG95732;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys Segid 916.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scfv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineoplastic; antirheumatic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cyostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PE 14-NOV-2002; 2002WO-US036496.
XX
PF 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 916; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 8
ADG96139 ID ADG96139 standard; protein; 248 AA.

XX AC ADG96139;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys seqID 1323.

XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
KW antiinflammatory; antisthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX XX WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 1323; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antisthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 9
ABP45103 ID ABP45103 standard; protein; 251 AA.

XX AC ABP45103;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1114.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0273739P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX XX WPI; 2002-114799/15.

XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1, Page 1731-1732; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineuritic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABR43390-ABR47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 251 AA;
XX
Query March 98.9%; Score 87; DB 5; Length 251;
Best Local Similarity 94.1%; Pred. No. 9.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66
XX
RESULT 10
ADD28319
ID ADD28319 standard; protein; 251 AA.
XX
AC ADG95930;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds BLyS SegID 1114.
XX
KM antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KM B cell proliferation; differentiation; scfv; myasthenia gravis;
KM multiple sclerosis; aschma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antineuritic; antiallergic; neuroprotective;
KM antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (BLyS), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1114; 394dp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind

CC to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scfvs) derived, preferably, from the variable
CC heavy CD3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey BLyS. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of BLyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineuritic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BLyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 251 AA;
XX
Query March 98.9%; Score 87; DB 7; Length 251;
Best Local Similarity 94.1%; Pred. No. 9.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66
XX
RESULT 11
ADD28319
ID ADD28319 standard; protein; 135 AA.
XX
AC ADD28319;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:97.
XX
KM human heterodimeric antibody; human; antibody; binding affinity;
KM protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KM edema factor; lethal factor; virulence; antibacterial; immunotherapy;
KM anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KM Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO2003076568-A2.
XX
PD 18-SEP-2003.
XX
PF 11-FEB-2003; 2003WO-US004206.
XX
PR 11-FEB-2002; 2002US-0356086P.
XX
PR 29-APR-2002; 2002US-0376408P.
XX
PR 27-SEP-2002; 2002US-0414053P.
XX
PR 25-NOV-2002; 2002US-0428807P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Wild MA;
XX
DR WPI; 2003-722327/68.
XX
PT New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.

XX
PS Claim 11, SEQ ID NO 97; 67bp; English.
XX
CC The present invention describes a human heterodimeric antibody (I)
CC (Fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 135 AA;
SQ
Query Match 97.7%; Score 86; DB 7; Length 135;
Best Local Similarity 94.1%; Pred. No. 6.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
Db 52 LIISYDGSKKYYADSVKG 68
RESULT 12
ABB07186
ID ABB07186 standard; protein; 119 AA.
XX
AC ABB07186;
XX
DT 13-MAR-2002 (first entry)
XX
DE sH1GM22 heavy chain variable region clone B sequence.
XX
XX Neuromodulatory agent; central nervous system; CNS; sH1GM22; LYM 22; AKJR4;
KM ebvH1GM M815D10; ebv H1GM CB2B68; CB21E12; CB21E7; MS19E5; virucide;
KM antiParkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS Homo sapiens.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
XX
DR N-PSDB; ABA94243.
XX
XX Novel neuromodulatory agent (a human Igm monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Claim 23, Fig 17, 219pp; English.
XX
XX The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca²⁺-
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sH1GM22 (LYM 22), ebvH1GM M815D10, ebv H1GM
CC CB2B68, AKJR4, CB21E12, CB21E7 or MS19E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in

CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a post-
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neutral disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the sH1GM22 heavy
CC chain variable region clone B amino acid sequence
XX
SQ Sequence 119 AA;
SQ
Query Match 96.6%; Score 85; DB 5; Length 119;
Best Local Similarity 94.1%; Pred. No. 8.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
Db 50 IISYDGSKKYYADSVKG 66
RESULT 13
ABO33850
ID ABO33850 standard; peptide; 17 AA.
XX
AC ABO33850;
XX
DT 18-SEP-2003 (first entry)
XX
DE Anti-GPI-antibody heavy chain complementarity determining region #10.
XX
XX Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
KM anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;
KM autoimmune disease; rheumatoid arthritis; heavy chain variable region;
KM VH; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
OS US2002146753-A1.
XX
PN US2002146753-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001US-00828708.
XX
PR 06-APR-2001; 2001US-00828708.
XX
PA (DITZEL H. SCHALLER M.
XX
PA (DITZEL H. SCHALLER M.
XX
PA (BURTON D R.
XX
PA (SCHALLER M.
XX
PI Ditzel H, Burton DR, Schaller M;
XX
DR WPI; 2003-521517/49.
XX
XX Immunopolypeptide for diagnosis and treatment of human autoimmune
PT disease, e.g., human rheumatoid arthritis, comprises a polypeptide that
PT binds to human glucose-6-phosphate isomerase.
XX
PS Claim 3, Fig 4A; 47pp; English.
XX
XX The invention describes an immunopolypeptide comprising a polypeptide
CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and
CC compositions are used for diagnosis and treatment of human autoimmune
CC disease, e.g., human rheumatoid arthritis. This is the amino acid
CC sequence of human anti-GPI-antibody heavy chain variable region

CC complementarity determining region
XX
SQ Sequence 17 AA;

Query Match 95.5%; Score 84; DB 7; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 1 VISYDGNKKYYADSVKG 17

RESULT 14

ABO33836
ID ABO33836 standard; protein, 112 AA.

AC ABO33836;

XX 18-SEP-2003 (first entry)

XX Human anti-GPI-antibody heavy chain variable region #3.

XX Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;

KM anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;

KM autoimmune disease; rheumatoid arthritis; heavy chain variable region;

XX VH.

XX Homo sapiens.

XX US2002146753-A1.

XX 10-OCT-2002.

XX 06-APR-2001; 2001US-00828708.

XX 06-APR-2001; 2001US-00828708.

XX (DITZEL/) DITZEL H.

XX (BURTON/) BURTON D R.

XX (SCHALLER/) SCHALLER M.

XX Ditzel H, Burton DR, Schaller M;

XX WPI; 2003-521517/49.

XX Immunopolypeptide for diagnosis and treatment of human autoimmune

XX disease, e.g., human rheumatoid arthritis, comprises a polypeptide that

XX binds to human glucose-6-phosphate isomerase.

XX Claim 11; Fig 3AH; 47pp; English.

XX The invention describes an immunopolypeptide comprising a polypeptide

XX that binds to human glucose-6-phosphate isomerase (GPI). The methods and

XX compositions are used for diagnosis and treatment of human autoimmune

XX disease, e.g., human rheumatoid arthritis. This is the amino acid

XX sequence of human anti-GPI-antibody heavy chain variable region

XX Sequence 112 AA;

XX Query Match 95.5%; Score 84; DB 7; Length 112;

XX Best Local Similarity 88.2%; Pred. No. 1.2e-05;

XX Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17

:|||||:|||||

Db 43 VISYDGNKKYYADSVKG 59

RESULT 15

ABO7169
ID ABO7169 standard; protein, 119 AA.

AC ABO7169;

XX 13-MAR-2002 (first entry)

XX sHlgM22 heavy chain variable region clone A sequence.

XX Neuromodulatory; central nervous system; CNS; sHlgM22; LYM 22; AKR4;

KM ebvHlgM M6119D10; ebv HlgM CR2B68; CB21E12; MS119E5; Valructide;

XX antiparkinsonian; neuroprotective; nootropic; vulnerary.

XX Homo sapiens.

XX WO200185797-A1.

XX 15-NOV-2001.

XX 30-MAY-2000; 2000US-00568351.

XX 10-MAY-2000; 2000US-00568351.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

XX Rodriguez M, Miller DJ, Pease LR;

XX WPI; 2002-066596/09.

XX N-PSDB; ABA94216.

XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting

XX neurite outgrowth, regeneration, remyelination and neuroprotection in

XX central nervous system, useful to treat post-infectious

XX encephalomyelitis.

XX Claim 23; Fig 17; 21pp; English.

XX The invention provides a neuromodulatory agent (I) capable of promoting

XX neurite outgrowth, regeneration, remyelination and neuroprotection in

XX central nervous system (CNS). (I) is capable of inducing remyelination,

XX promoting cellular proliferation of glial cells, and promoting Ca2+

XX signaling with oligodendrocytes. An humanised antibody to (I) can be

XX selected from antibody sHlgM22 (LYM 22), ebvHlgM M6119D10, ebv HlgM

XX CR2B68, AKR4, CB21E12, CB21E7 or MS119E5. (I) is useful for stimulating

XX remyelination of CNS axons, stimulating proliferation of glial cells in

XX CNS axons, or treating demyelinating disease of CNS in a mammal in need

XX of such therapy. (I) is capable of binding to structures and cells within

XX CNS. (I) is preferably useful for treating a demyelinating disease of CNS

XX of a mouse infected with Strain DA of Theiler's murine encephalomyelitis

XX (TMSEV) or for treating a human being having multiple sclerosis, or a

XX human or domestic animal with a viral demyelinating disease, or a post-

XX neural disease of CNS. (I) is also useful for an in vitro method of

XX stimulating the proliferation of glial cells from mixed cell culture. (I)

XX is also useful for preventing remyelination of CNS axons. The antibodies

XX are useful for preventing infection by a bacterium, virus or like

XX pathogen that causes demyelination or other neurodegenerative condition

XX in a subject. Methods where (I) is administered to a patient are useful

XX for treating multiple sclerosis, Parkinson's disease, Alzheimer's

XX disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating

XX disease, CNS diseases, and other conditions in the CNS where nerves are

XX damaged as by trauma. The present sequence represents the sHlgM22 heavy

XX chain variable region clone A amino acid sequence

XX Sequence 119 AA;

XX Query Match 95.5%; Score 84; DB 5; Length 119;

XX Best Local Similarity 88.2%; Pred. No. 1.3e-05;

XX Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17

:|||||:|||||

Db 50 VISYDGSKKYYADSVKG 66

RESULT 16

AD126654

AD126654 standard; protein, 119 AA.
 AD126654;
 15-APR-2004 (first entry)
 Human anti IGM antibody SHIGM22 VH protein.
 Human; antibody; IGM; remyelination; neuronal growth; autoantibody;
 demyelination disease; multiple sclerosis; central nervous system; CNS;
 axon; glial cell proliferation;
 Theiler's murine encephalomyelitis virus infection; CNS injury;
 spinal cord injury.
 Homo sapiens.
 US2003185827-A1.
 02-OCT-2003.
 13-NOV-2001; 2001US-00010729.
 29-APR-1994; 94US-00236520.
 08-AUG-1996; 96US-00692084.
 07-JAN-1997; 97US-00779784.
 28-MAY-1999; 99US-00322862.
 30-MAY-2000; 2000US-00580787.
 05-DEC-2000; 2000US-00730473.
 (MAYO-) MAYO FOUND.
 Rodriguez M, Miller DJ, Pease LR;
 WPI; 2004-119219/12.
 N-PSDB; AD126655.
 New human immunoglobulin M antibody for treating or preventing a
 demyelinating disease of the central nervous system in a human or
 domestic animal, such as multiple sclerosis.
 Claim 7; Fig 35; 159pp; English.

The invention relates to an antibody (I) produced by injecting an
 immunocompetent host with an antibody peptide, and harvesting the
 antibody, where the peptide comprises a human anti-IGM antibody fragment
 given in the specification, or active fragments. Also included are
 stimulating remyelination of central nervous system (CNS) axons in a
 mammal (comprising administering a monoclonal antibody, or mixtures,
 monomers, active fragments, or recombinant antibodies derived from it,
 characterised by their ability to bind structures and cells within the
 CNS, including oligodendrocytes), stimulating the proliferation of glial
 cells in CNS axons in a mammal (comprising administering a monoclonal
 antibody, or mixtures, monomers, active fragments, or recombinant
 antibodies derived from it, characterised by their ability to bind
 structures and cells within the CNS), treating or preventing a
 demyelinating disease of the CNS in a mammal (comprising administering a
 monoclonal antibody, or mixtures, monomers, active fragments, or
 recombinant antibodies derived from it, characterised by their ability to
 bind structures and cells within the CNS, and to stimulate remyelination
 of axons of the CNS), stimulating, in vitro, the proliferation of glial
 cells from mixed cell culture, stimulating remyelination of CNS axons in
 a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 antibody (or a peptide analogue, hapten, or active fragment of it, where
 the DNA sequence consists of a sequence encoding an anti IGM antibody), a
 probe capable of screening for the antibody, an assay for screening drugs
 and other agents for the ability to modulate the production or mimic the
 activities of mAb SHIGM22, SHIGM46, or combinations of them, a
 recombinant virus transformed with recombinant antibody nucleic acids or
 vector, imaging a portion of the CNS using the antibody and diagnosing or
 monitoring demyelination and/or remyelination of the CNS comprising using
 CNS image. The antibody is used to stimulate remyelination of CNS axons,
 and to stimulate the proliferation of glial cells in CNS axons,
 optionally in vitro. The antibody is used to treat or prevent a

demyelinating disease of the CNS in a human or domestic animal, such as
 multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 preferably the mammal is a mouse infected with strain DA of Theiler's
 murine encephalomyelitis virus. The antibody is used to treat a spinal
 cord injury and used to screen drugs and other agents for the ability to
 modulate the production or mimic the activities of the antibody. The
 antibody can be used to image a portion of the CNS which can be used to
 diagnose or monitor demyelination and/or remyelination of the CNS. The
 present sequence is a variable region of a human anti-IGM antibody (or
 fragment).
 Sequence 119 AA;
 Query Match 95.5%; Score 84; DB 8; Length 119;
 Best Local Similarity 88.2%; Pred. No. 1.3e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IISYDGSKRYADSVKG 17
 :|||||:|||||
 Db 50 VISYDGSRKRYADSVKG 66
 RESULT 17
 AAY79076
 ID AAY79076 standard; peptide; 17 AA.
 XX
 AC AAY79076;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.
 XX
 KM Complementarity determining region 2; CDR2; antibody; Gla domain;
 KM factor IX/IXa; blood coagulation; deep venous thrombosis;
 KM arterial thrombosis; unstable angina; post myocardial infarction;
 KM coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 KM percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 KM septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 KM arterial fibrillation; disseminated intravascular coagulopathy; DIC.
 XX
 OS Homo sapiens.
 XX
 PN WO200012562-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-US019453.
 XX
 PR 28-AUG-1998; 98US-0098233P.
 PR 03-MAR-1999; 99US-0122767P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Devaux B, Eaton DJ, Hase PE, Judice JK, Kirchofer D;
 PI Suggett S;
 XX
 DR WPI; 2000-256595/22.
 PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 XX
 PS Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of
 the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
 antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 participates in the blood coagulation pathways. The Gla domain of factor
 IXa and its zymogen factor IX contains important structural determinants
 for interaction with high affinity binding sites on vascular endothelial
 cells and platelets. Compositions comprising the antibodies are used for
 the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 disorders in a mammal for which inhibiting a FIX/IXa mediated event is

CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX
 SQ Sequence 17 AA;

Query Match 94.3%; Score 83; DB 3; Length 17;
 Best Local Similarity 94.1%; Pred. No. 2.1e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 Db 1 IISYDGSNKYYADSVKG 17

RESULT 18
 ADP22108
 ID ADP22108 standard; protein; 123 AA.

XX
 AC ADP22108;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 XX Human anti-TNF α antibody heavy chain variable region SEQ ID NO:14.

XX human; monoclonal antibody; tumour necrosis factor- α ; TNF α ;
 KM anti-TNF α antibody; anabolic; antiarteriosclerotic; antirheumatic;
 KM antibacterial; antiinflammatory; antiproliferative; antineoplastic;
 KM eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KM neuroprotective; vasotropic; antiapoptotic; TNF α antagonist;
 KM TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KM bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KM prostate cancer; immuno-mediated inflammatory disease;
 KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KM reestenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KM septic shock; cachexia; anorexia; multiple sclerosis.

XX
 OS Homo sapiens.
 XX
 XX WO2004050683-A2.
 XX
 PD 17-JUN-2004.
 XX
 XX 02-DEC-2003; 2003WO-US038281.
 XX
 XX 02-DEC-2002; 2002US-0430729P.
 XX
 XX (ABGE-) ABGENIX INC.
 XX
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendrich W, Rathnaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX
 XX WPI: 2004-480601/45.
 DR N-PSDB; ADP22107.
 XX
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor- α , useful for treating neoplastic disease such
 PT as cancer, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 XX Example 10; SEQ ID NO 14; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor- α (TNF α) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid

CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M) the level of TNF α in a patient sample, comprising contacting with
 CC (1), and detecting the level of binding between the antibody and TNF α in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNF α induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNF α induced apoptosis by administering the human monoclonal antibody of
 CC (1). (I) has anabolic, antiarteriosclerotic, antirheumatic,
 CC antibacterial, antiinflammatory, antiproliferative, antineoplastic, eating-
 CC disorder, immunomodulator, immunosuppressive, nephrotropic, and can be used
 CC as neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNF α antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, reestenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNF α
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 123 AA;

Query Match 94.3%; Score 83; DB 8; Length 123;
 Best Local Similarity 94.1%; Pred. No. 1.9e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 Db 50 IISYDGSNKYYADSVKG 66

RESULT 19
 ADE28443
 ID ADE28443 standard; protein; 125 AA.

XX
 AC ADE28443;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 XX Human anti-CD40 antibody 22-1-1 variable region heavy chain protein.

XX anti-CD40 monoclonal antibody; CD40; cytotoxic; virucide; antibacterial;
 KM immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KM bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KM human; variable region heavy chain; 22-1-1.

XX
 OS Homo sapiens.
 XX
 XX WO2003040170-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX 08-NOV-2002; 2002WO-US036107.
 XX
 XX 09-NOV-2001; 2001US-0348980P.
 XX
 XX (PF12) PFIZER PROD INC.
 PA (ABGE-) ABGENIX INC.
 XX
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 PI WPI: 2003-441521/41.
 DR N-PSDB; ADE28442.
 XX
 XX New chimERIC or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or

PT viral infections.
XX
PS Claim 1; SEQ ID NO 50; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region heavy chain protein of the invention.
XX
SQ Sequence 125 AA;

Query Match 94.3%; Score 83; DB 7; Length 125;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVYKG 17
Db 50 IISYDGSNNKYADSVYKG 66

RESULT 20
ADD28233
ID ADD28233 standard; protein; 137 AA.
XX
AC ADD28233;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:11.
XX
KW human heterodimeric antibody; human; antibody; binding affinity;
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003076568-A2.
XX
PD 18-SEP-2003.
XX
PF 11-FEB-2003; 2003WO-US004206.
XX
PR 11-FEB-2002; 2002US-0356086P.
PR 29-APR-2002; 2002US-0376408P.
PR 27-SEP-2002; 2002US-0414053P.
PR 25-NOV-2002; 2002US-0428807P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Wild MA;
XX
DR WPI; 2003-722327/68.
XX
PT New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX
PS Claim 6; SEQ ID NO 11; 67pp; English.
XX
CC The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in

CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 137 AA;

Query Match 94.3%; Score 83; DB 7; Length 137;
Best Local Similarity 88.2%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVYKG 17
Db 52 IISYDGSNNKYADSVYKG 68

RESULT 21
ADD28321
ID ADD28321 standard; protein; 137 AA.
XX
AC ADD28321;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:99.
XX
KW human heterodimeric antibody; human; antibody; binding affinity;
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003076568-A2.
XX
PD 18-SEP-2003.
XX
PF 11-FEB-2003; 2003WO-US004206.
XX
PR 11-FEB-2002; 2002US-0356086P.
PR 29-APR-2002; 2002US-0376408P.
PR 27-SEP-2002; 2002US-0414053P.
PR 25-NOV-2002; 2002US-0428807P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Wild MA;
XX
DR WPI; 2003-722327/68.
XX
PT New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX
PS Claim 11; SEQ ID NO 99; 67pp; English.
XX
CC The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The

CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.

XX Sequence 137 AA;

Query Match 94.3%; Score 83; DB 7; Length 137;
Best Local Similarity 88.2%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 52 VISYDGSKKYYGDSVKG 68

RESULT 22
ADP45679
ID ABP45679 standard; protein; 252 AA.

XX AC ABP45679;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1690.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX MO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,

XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2419-2420; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX Sequence 252 AA;

Query Match 94.3%; Score 83; DB 5; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYGDSVKG 66

RESULT 23
ADG96506
ID ADG96506 standard; protein; 252 AA.

XX AC ADG96506;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 1690.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scFv; myasthenia gravis;
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
XX antiinflammatory; antialastmatic; antiallergic; cytostatic.

OS Unidentified.

XX MO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,

XX WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 1690; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CD3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antialastmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ Sequence 252 AA;

Query Match 94.3%; Score 83; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
DB 50 VISYDGSKKYYGDSVKG 66

RESULT 24
ADE28467
ID ADE28467 standard; protein; 470 AA.
XX
AC ADE28467;
XX
DT 29-JAN-2004 (first entry)
XX

DE Human anti-CD40 antibody 23-29-1 variable region heavy chain protein.

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; variable region heavy chain; 23-29-1.

XX Homo sapiens.

XX WO2003040170-A2.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-US036107.

XX PR 09-NOV-2001; 2001US-0348980P.

XX PA (PFIZ) PRIZER PROD INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX DR WPI; 2003-441521/41.

XX DR N-PSDB; ADE28466.

XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.

XX Claim 1; SEQ ID NO 74; 177bp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region heavy chain protein of the invention.

XX SQ Sequence 470 AA;

Query Match 94.3%; Score 83; DB 7; Length 470;
Best Local Similarity 94.1%; Pred. No. 8.4e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17

DB 69 IISYDGSNNKYADSVKG 85
|||||

RESULT 25
ABB06275
ID ABB06275 standard; protein; 614 AA.

AC ABB06275;

XX DT 24-MAY-2002 (first entry)

DE Plasmid scFv(CO046N2)-CL-GFP protein sequence.

XX Construction; scFv antibody; green fluorescent protein; GFP; immunoassay;
KW fluorescent protein; antigen binding; immunostaining; fusion protein;
KW immunological assay.

XX Homo sapiens.

XX Synthetic.

XX WO200196401-A1.

XX PD 20-DEC-2001.

XX PF 12-JUN-2001; 2001WO-JP004964.

XX PR 14-JUN-2000; 2000JP-00178880.

XX PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.

XX PI Morino K, Akahori Y, Iba Y, Shinohara M, Ukai Y, Kurosawa Y;

XX DR WPI; 2002-098056/13.

XX DR N-PSDB; ABL49526.

XX Producing scFv antibody fused to a fluorescent protein, useful for
PT immunoassay and immunostaining, comprises expressing a scFv gene
PT (extracted from selected clones) fused to a fluorescent protein gene.

XX Example; Fig 14; 105bp; Japanese.

XX The present invention describes a method for producing a scFv antibody
CC fused to a fluorescent protein. The method comprises constructing a scFv
CC antibody library composed of phage clones expressing scFv antibody on
CC their surface, screening this library with an antigen, extracting the
CC gene for scFv antibody from the selected phage clones and inserting it
CC into an expression vector that expresses the gene fused to a fluorescent
CC protein. Also described are: (1) a fusion protein comprising the scFv
CC antibody fused to a fluorescent protein; (2) immunological assays using
CC the fusion protein of (1); (3) an expression vector encoding the fusion
CC protein of (1); and (4) a kit for producing the fusion protein of (1).
CC The fusion protein can be used in immunoassays and immunostaining.
CC Immunological assays using the fusion protein do not require a secondary
CC or tertiary antibody. Direct intracellular and even in vivo assays are
CC possible. ABL49521 to ABL49591 and ABB06268 to ABB06276 represent
CC sequences used in the exemplification of the present invention

XX SQ Sequence 614 AA;

Query Match 94.3%; Score 83; DB 5; Length 614;
Best Local Similarity 88.2%; Pred. No. 0.00011;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
DB 53 VISYDGSKKYYADSVKG 69

RESULT 26
AAW90298
ID AAW90298 standard; protein; 17 AA.
XX

AC AAW90298;
 XX 07-SEP-1999 (first entry)
 XX
 XX Human anti-GPIIb/IIIa auto-antibody heavy chain protein CDR2 region 2.
 DE
 XX Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
 KW blood platelet membrane protein; predisposition; prevention; treatment;
 KW thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;
 KW thrombocyte; cardiac infarction; pulmonary embolism; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX WO9855619-A1.
 XX
 PD 10-DEC-1998.
 XX
 PD 05-JUN-1998; 98WO-EP003357.
 XX
 PF 06-JUN-1997; 97DE-01023904.
 PR 12-DEC-1997; 97DE-01055227.
 PR 08-MAY-1998; 98DE-01020663.
 XX
 PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
 XX
 PI Berchtold P, Escher RFA;
 XX
 DR WPI; 1999-105496/09.
 XX
 XX Nucleic acid encoding human autoantibodies against platelet glycoprotein
 PT IIL/IIla - used for diagnosis, treatment and prevention of autoimmune
 PT thrombocytopenic purpura and for modulation of fibrinogen binding.
 XX
 PS Claim 3b; Page 5; 93pp; German.
 XX
 CC This invention describes novel nucleic acid fragments that encode human
 CC auto-antibodies and anti-idiotypic antibodies against blood platelet
 CC membrane protein, GPIIb/IIIa. The products of the invention are used for
 CC diagnosis (including monitoring and determining predisposition),
 CC prevention and treatment of autoimmune thrombocytopenic purpura (AITP)
 CC and also for modulating binding of fibrinogen to thrombocytes
 CC (particularly to dissolve thrombi and/or prevent their formation, e.g. in
 CC cases of cardiac infarction or pulmonary embolism). Unlike murine
 CC antibodies, human antibodies (hAb) do not induce adverse side effects and
 CC persist for longer in vivo than small peptides. AAW90293-W90337 represent
 CC antibody fragments used in the method of the invention
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 93.2%; Score 82; DB 2; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 1 VISYDGSNKYYADSVKG 17
 RESULT 27
 AAY79074
 ID AAY79074 standard; peptide; 17 AA.
 XX
 AC AAY79074;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.
 XX
 XX Complementarity determining region 2; CDR2; antibody; Gla domain;
 KW factor IX/IXa; blood coagulation; deep venous thrombosis;
 KW arterial thrombosis; unstable angina; post myocardial infarction;
 KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;

KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
 XX
 OS Homo sapiens.
 XX
 XX WO200012562-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-US019453.
 XX
 PR 28-AUG-1998; 98US-0098233P.
 PR 03-MAR-1999; 99US-0122767P.
 XX
 XX (GERTH) GENENTECH INC.
 XX
 PA Adams CW, Devaux B, Baton DL, Haas PE, Judice JK, Kirchhofer D;
 PI Suggett S;
 XX
 DR WPI; 2000-256595/22.
 XX
 XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 XX
 PS Claim 2; Fig 2; 84pp; English.
 XX
 CC This sequence represents a complementarity determining region 2 (CDR2) of
 CC the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
 CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 CC participates in the blood coagulation pathways. The Gla domain of factor
 CC IXa and its zymogen factor IX contains important structural determinants
 CC for interaction with high affinity binding sites on vascular endothelial
 CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 93.2%; Score 82; DB 3; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 1 VISYDGSNKYYADSVKG 17
 RESULT 28
 AAY79078
 ID AAY79078 standard; peptide; 17 AA.
 XX
 AC AAY79078;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.
 XX
 XX Complementarity determining region 2; CDR2; antibody; Gla domain;
 KW factor IX/IXa; blood coagulation; deep venous thrombosis;
 KW arterial thrombosis; unstable angina; post myocardial infarction;
 KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
 XX

OS Homo sapiens.
 XX WO200012562-A1.
 XX
 XX 09-MAR-2000.
 PD
 XX 26-AUG-1999; 99WO-US019453.
 XX
 XX 28-AUG-1998; 98US-0098233P.
 PR 03-MAR-1999; 99US-0122767P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Adams CW, Devaux B, Eaton DL, Hase PE, Judice JK, Kirchhofer D,
 PI Suggett S;
 XX
 XX WPI; 2000-256595/22.
 DR
 XX
 XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 XX
 PS Claim 2; Fig 2; 84pp; English.

CC This sequence represents a complementarity determining region 2 (CDR2) of
 CC the heavy chain variable domain of a human anti-factor IX/IXa Glia domain
 CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 CC participates in the blood coagulation pathways. The Glia domain of factor
 CC IXa and its zymogen factor IX contains important structural determinants
 CC for interaction with high affinity binding sites on vascular endothelial
 CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS) arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 CC
 XX
 XX Sequence 17 AA;

Query Match 93.2%; Score 82; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVK 16
 |||||
 DB 1 IISYDGSKKYYADSVK 16

RESULT 29
 AA017790
 ID AA017790 standard; peptide; 17 AA.
 XX
 AC AA017790;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE CDR2 region of antibody for glycoprotein IIb/IIIa receptor #2.
 XX
 XX CDR2; complementarity determining region 2; antibody; metastasis;
 KM glycoprotein IIb/IIIa; GPIIb/IIIa; angiogenesis; cancer; cytostatic;
 KM antiangiogenic; vasotropic; intimal hyperplasia; vascular occlusion.
 XX
 OS Unidentified.
 XX
 PN DE10057443-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 20-NOV-2000; 2000DE-01057443.

XX 20-NOV-2000; 2000DE-01057443.
 PR
 XX
 XX (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
 PA
 XX
 XX Peter B, Escher RF;
 PI
 XX
 XX WPI; 2002-472625/51.
 DR
 XX
 XX Use of specific antibodies, or individual chains, for treating tumors and
 PT vascular occlusions, by inhibition of the GPIIb/IIIa receptor.
 PT
 XX
 XX Claim 3; Page 9; 10pp; German.

CC The present invention relates to the use of heavy or light chains or
 CC their functional derivatives or fragments, having specific CDR
 CC (complementarity determining region) sequences of antibodies. The
 CC peptides can be used for the combined inhibition of the binding of
 CC fibrinogen to thrombocytes and of vitronectin to endothelial cells, the
 CC inhibition of angiogenesis, the inhibition of tumour metastasis and/or
 CC the inhibition of intimal hyperplasia after vascular injury. They are
 CC useful for prevention and treatment of vascular occlusion and for
 CC treating tumours. The present sequence is a CDR2 region of the invention
 CC
 XX
 XX Sequence 17 AA;

Query Match 93.2%; Score 82; DB 5; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 :|||
 DB 1 VISYDGSKKYYADSVKG 17

RESULT 30
 ADJ32094
 ID ADJ32094 standard; peptide; 17 AA.
 XX
 AC ADJ32094;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human interferon-gamma antibody heavy chain CDR2 peptide SegID48.
 XX
 XX antibody; antigen binding domain; interferon-gamma; INF-gamma;
 KM antagonist antibody; antiinflammatory; immunosuppressive;
 KM autoimmune disease; inflammatory condition; human;
 KM complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 PN US2003099647-A1.
 XX
 PD 29-MAY-2003.
 XX
 PE 05-OCT-2001; 2001US-00972656.
 XX
 PR 05-OCT-2001; 2001US-00972656.
 XX
 PA (DESH/) DESHPANDE R V.
 PA (TSAI/) TSAI M.
 XX
 PI Deshpande RV, Tsai M;
 XX
 XX WPI; 2003-696068/66.
 DR
 XX
 XX New antibody or antigen binding domain, or its fragment, variant or
 PT derivative, which binds to an interferon-gamma protein, useful for
 PT preparing a composition for preventing or treating inflammatory or
 PT autoimmune disorders.
 XX
 PS Claim 14; SEQ ID NO 48; 113pp; English.

XX This invention relates to a novel antibody or antigen binding domain, or
CC its fragment, variant or derivative, which binds to an interferon-gamma
CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
CC useful for the development of compounds with an antiinflammatory or
CC immunosuppressive activity through action as interferon-gamma agonists. A
CC composition containing the antibody is useful for preventing or treating
CC an autoimmune disease and an inflammatory condition. The present sequence
CC is that of a peptide which represents a complementarily determining
CC region (CDR) of a human IFN-gamma antibody which may be part of the
CC invention.
XX Sequence 17 AA;
SQ

Query Match 93.2%; Score 82; DB 7; Length 17;
Best Local Similarity 88.2%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db :|||||
1 VISYDGSNKYYADSVKG 17

RESULT 31
ADH89402
ID ADH89402 standard; peptide; 17 AA.
XX
AC ADH89402;
XX
DT 15-APR-2004 (first entry)
XX
DE Human transferrin fusion protein-related CDR2 peptide SegID46.
XX
XX fusion protein; transferrin protein; glycosylation;
XX antibody variable region; cytostatic; antibacterial; virucide;
XX antiparasitic; immunosuppressive; antiarthritic; gene therapy;
XX septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
XX viral infection; parasitic infection; neoplasm; autoimmune disease;
XX arthritis; graft rejection.
XX
XX Unidentified.
XX
XX OS
XX
XX PN US2003226155-A1.
XX
XX PD 04-DEC-2003.
XX
XX PF 10-MAR-2003; 2003US-00384060.
XX
XX PR 30-AUG-2001; 2001US-0315745P.
XX
XX PR 30-NOV-2001; 2001US-0334059P.
XX
XX PR 30-AUG-2002; 2002US-00231494.
XX
XX PR 30-AUG-2002; 2002US-0406977P.
XX
XX PA (BIO-R-) BIOREXIS PHARM CORP.
XX
XX PI Sadeghi H, Prior CP, Turner A;
XX
XX WI; 2004-022093/02.
XX
XX DR
XX
XX PT New fusion protein comprising a transferrin protein exhibiting reduced
XX glycosylation fused to at least one antibody variable region, useful for
XX preparing a composition for treating e.g., septic shock, neoplasm or
XX autoimmune disease.
XX
XX Example 2; SEQ ID NO 46; 82pp; English.
XX
XX This invention relates to a novel fusion protein which comprises a
XX transferrin protein exhibiting reduced glycosylation fused to at least
XX one antibody variable region. The invention may be useful for the
XX development of compounds with cytostatic, antibacterial, virucide,
XX antiparasitic, immunosuppressive or antiarthritic activity. In addition,
XX the sequences disclosed may be useful for gene therapy. The fusion
XX protein is useful for preparing a composition for treating a disease or

CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a CDR 2 peptide which was used in the exemplification
CC of the invention.
XX
XX Sequence 17 AA;
SQ

Query Match 93.2%; Score 82; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db :|||||
1 VISYDGSNKYYADSVKG 17

RESULT 32
ADP47199
ID ADP47199 standard; peptide; 17 AA.
XX
AC ADP47199;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mAb heavy chain peptide #64.
XX
XX human; monoclonal antibody; phospholipase A2; PLA2;
XX inflammatory disorder; degenerative disorder;
XX joint inflammatory reaction; skin inflammatory reaction;
XX blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
XX Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
XX OS Homo sapiens.
XX
XX PN W02004050850-A2.
XX
XX PD 17-JUN-2004.
XX
XX PF 02-DEC-2003; 2003WO-US038234.
XX
XX PR 02-DEC-2002; 2002US-0430724P.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
XX Jia X, Nocerini MR;
XX
XX WI; 2004-46119/43.
XX
XX DR
XX
XX PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
XX Example 5; SEQ ID NO 114; 128pp; English.
XX
XX The invention comprises a human monoclonal antibody that binds to
XX phospholipase A2 (PLA2). The monoclonal antibody of the invention is
XX useful in the preparation of a medicament for the treatment of
XX inflammatory and degenerative disorders stemming from inflammatory
XX reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
XX amino acid sequence represents a human PLA2-specific monoclonal antibody
XX heavy chain peptide.
XX
XX Sequence 17 AA;
SQ

Query Match 93.2%; Score 82; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 Db 1 VISYDGSNKYYADSVKG 17

RESULT 33
 ADS82565
 ID ADS82565 standard; peptide; 17 AA.

AC ADS82565;

XX 16-DEC-2004 (first entry)

DE Anti-IL-21R antibody MW1 H2 CDR, SEQ ID 23.

XX Immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
 KW Antiinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy;
 KW antibody; Interleukin-21 receptor; Interleukin-21; IL-21;
 KW IL-21R; autoimmune disorder; rheumatoid arthritis;
 KW inflammatory bowel disease; Crohn's disease; transplant rejection;
 KW psoriasis; hyperproliferative disorder; MUII;
 KW complementarity determining region; CDR; heavy chain; H2 CDR.

XX Homo sapiens.

OS WO2004083249-A2.

PN 30-SEP-2004.

XX 12-MAR-2004; 2004WO-US007444.

XX 14-MAR-2003; 2003US-0454336P.

XX (AMHP) WYETH.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Young DA, Witters MJ, Valge-Archer V, Collins M, Williams AJ;

PI Mikek J;

XX WPI; 2004-691025/67.

DR N-PSDB; ADS82574.

XX New human antibodies that selectively bind to human interleukin-21
 PT receptor, useful for diagnosing, preventing or treating autoimmune
 PT disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.

XX Claim 4; SEQ ID NO 23; 143pp; English.

XX The present invention relates to human antibodies, or their antigen-
 CC binding fragments, that selectively bind to a human interleukin-21
 CC receptor (IL-21R). The antibodies of the invention are referred to as
 CC MDP, MDP-germline, MW1, 18G4, 18A5, 19F5, CP5G2 and R18. The antibodies
 CC selectively bind the extracellular domain of human IL-21R, or inhibit the
 CC binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an
 CC antibody or fragment of the invention are useful for diagnosing,
 CC preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
 CC inflammatory bowel disease, Crohn's disease, transplant rejection or
 CC psoriasis) or hyperproliferative disorders. The present sequence is an
 CC anti-IL-21R antibody heavy chain complementarity determining region of
 CC the invention.

XX Sequence 17 AA;

Qy Query Match 93.2%; Score 82; DB 8; Length 17;

Best Local Similarity 88.2%; Pred. No. 3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 Db 1 VISYDGSNKYYADSVKG 17

RESULT 34

ADS52370
 ID ADS52370 standard; peptide; 17 AA.

XX ADS52370;

XX 16-DEC-2004 (first entry)

DE Fab targeting HLA-A2/Tax11-19, T3F2, heavy chain CDR 2.

XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KW major histocompatibility complex; MHC class I; viral infection;
 KW human T lymphotropic virus-1 infection; viral oncoprotein;
 KW mycoplasma infection; bacterial infection; fungal infection;
 KW protozoal infection; phase display; heavy chain; CDR;
 KW complementarity determining region.

XX Homo sapiens.

OS US2004191260-A1.

PN 30-SEP-2004.

XX 26-MAR-2003; 2003US-00396578.

XX 26-MAR-2003; 2003US-00396578.

XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Reiter Y, Cohen C;

XX WPI; 2004-735863/72.

XX New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.

XX Claim 5; SEQ ID NO 21; 68pp; English.

XX The invention relates to a composition-of-matter comprising (a multimeric
 CC form of) an antibody or antibody fragment including an antigen-binding
 CC region capable of specifically binding an antigen-presenting portion of a
 CC complex composed of a human antigen-presenting molecule and an antigen
 CC derived from a pathogen. Also included are an isolated polynucleotide
 CC comprising a nucleic acid sequence encoding an antibody fragment (the
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule and an antigen derived from a
 CC pathogen), a nucleic acid construct comprising the isolated
 CC polynucleotide above (and a promoter sequence for directing transcription
 CC of the isolated polynucleotide in a host cell), a host cell comprising
 CC the nucleic acid construct above, a host virus comprising the nucleic
 CC acid construct above, a virus comprising a coat protein fused to the
 CC antibody fragment, detecting an antigen-presenting portion of a complex
 CC composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen, a method of diagnosing an infection by a pathogen in an
 CC individual, a method of killing or damaging a target cell
 CC expressing/displaying an antigen-presenting portion of a complex
 CC (composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC detectable moiety is a recognition sequence of a biotin protein ligase, a
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.

KW complementarity determining region.
 XX Homo sapiens.
 OS
 XX US2004191260-A1.
 PN
 XX 30-SEP-2004.
 PD
 XX 26-MAR-2003; 2003US-00396578.
 PE
 XX 26-MAR-2003; 2003US-00396578.
 PR
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 PA
 XX Reiter Y, Cohen C;
 PI
 XX WPI; 2004-735863/72.
 DR
 XX
 XX New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 PS
 PS Claim 5; SEQ ID NO 81; 68bp; English.

The invention relates to a composition-of-matter comprising (a multimeric form of) an antibody or antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. Also included are an isolated polynucleotide comprising a nucleic acid sequence encoding an antibody fragment (the antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen), a nucleic acid construct comprising the isolated polynucleotide above (and a promoter sequence for directing transcription of the isolated polynucleotide in a host cell), a host cell comprising the nucleic acid construct above, a host virus comprising the nucleic acid construct above, a virus comprising a coat protein fused to the antibody fragment, detecting an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen, a method of diagnosing an infection by a pathogen in an individual, a method of killing or damaging a target cell expressing/displaying an antigen-presenting portion of a complex (composed of a human antigen-presenting molecule and an antigen derived from a pathogen) and a method of detecting in a biological sample an antigen-presenting portion of a complex as described above. The target cell is a T lymphocyte or an antigen-presenting cell, which is a B cell or a dendritic cell. The composition-of-matter further comprises a detectable moiety attached to the antibody or antibody fragment. The detectable moiety is a recognition sequence of a biotin protein ligase, a biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a polystyrene tag. The biotin protein ligase is BirA, the fluorophore is phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is Pseudomonas exotoxin A or its portion, which is a translocation domain and/or an ADP-ribosylation domain. The human antigen-presenting molecule is a major histocompatibility complex (MHC), preferably MHC class I molecule, more preferably HLA-A2 molecule. The pathogen is viral, preferably a retrovirus, more preferably human T lymphotropic virus-1. The antigen derived from a pathogen is restricted by the antigen-presenting molecule and is a polypeptide selected from a segment of a viral oncoprotein or a segment of a Tax protein. A pharmaceutical composition comprising an active ingredient the composition-of-matter is useful in a method for treating a disease associated with a pathogen in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and protozoans. The composition-of-matter or the methods are useful for diagnosing an infection by a pathogen in an individual and for killing or damaging a target cell expressing or displaying an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. A phage displayed library of human Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated and tested for specific binding to HLA-A2/Tax 11-19, individual clones were then sequenced and their CDR (complementarity determining region) sequences compared. The present sequence is a CDR from the heavy chain of

CC an isolated Fab clone.
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 93.2%; Score 82; DB 8; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVKG 17
 :|||||
 Db 1 VISYDGSNRYADSVKG 17

RESULT 37
 ADS52388
 ID ADS52388 standard; peptide; 17 AA.
 XX
 XX ADS52388;
 AC
 XX
 XX 16-DEC-2004 (first entry)
 DT
 XX
 XX Fab targeting HLA-A2/Tax11-19, T3D1, heavy chain CDR 2.
 DE
 XX
 XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KW major histocompatibility complex; MHC class I; viral infection;
 KW human T lymphotropic virus-1 infection; viral oncoprotein;
 KW mycoplasma infection; bacterial infection; fungal infection;
 KW protozoan infection; phage display; heavy chain; CDR;
 KW complementarity determining region.
 OS
 XX Homo sapiens.
 XX
 XX US2004191260-A1.
 PN
 XX 30-SEP-2004.
 PD
 XX 26-MAR-2003; 2003US-00396578.
 PE
 XX 26-MAR-2003; 2003US-00396578.
 PR
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 PA
 XX Reiter Y, Cohen C;
 PI
 XX WPI; 2004-735863/72.
 DR
 XX
 XX New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 PS
 PS Claim 5; SEQ ID NO 39; 68bp; English.

The invention relates to a composition-of-matter comprising (a multimeric form of) an antibody or antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. Also included are an isolated polynucleotide comprising a nucleic acid sequence encoding an antibody fragment (the antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen), a nucleic acid construct comprising the isolated polynucleotide above (and a promoter sequence for directing transcription of the isolated polynucleotide in a host cell), a host cell comprising the nucleic acid construct above, a host virus comprising the nucleic acid construct above, a virus comprising a coat protein fused to the antibody fragment, detecting an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen, a method of diagnosing an infection by a pathogen in an individual, a method of killing or damaging a target cell expressing/displaying an antigen-presenting portion of a complex (composed of a human antigen-presenting molecule and an antigen derived

CC from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC detectable moiety is a recognition sequence of a biotin protein ligase, a
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP-ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
 CC The antigen derived from a pathogen is restricted by the antigen-
 CC presenting molecule and is a polypeptide selected from a segment of a
 CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
 CC composition comprising as an active ingredient the composition-of-matter
 CC is useful in a method for treating a disease associated with a pathogen
 CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
 CC protozoans. The composition-of-matter or the methods are useful for
 CC diagnosing an infection by a pathogen in an individual and for killing or
 CC damaging a target cell expressing or displaying an antigen-presenting
 CC portion of a complex composed of a human antigen-presenting molecule and
 CC an antigen derived from a pathogen. A phage displayed library of human
 CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC sequences compared. The present sequence is a CDR from the heavy chain of
 CC an isolated Fab clone.

SO Sequence 17 AA;

Query Match 93.2%; Score 82; DB 8; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKITYADSVKG 17
 :|||||
 Db 1 VISYDGSNKITYADSVKG 17

RESULT 38
 ADS84420
 ID ADS84420 standard; protein; 41 AA.

AC ADS84420;

DT 18-NOV-2004 (first entry)

DE Human anti-EPO-R antibody heavy chain variable region CDR SEQ ID NO:59.

human; erythropoietin receptor; EPO receptor;
 erythropoietin receptor binding antibody; EPO receptor binding antibody;
 anti-anaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;
 wound healing; neural cell damage protection;
 neural tissue damage protection; brain injury; spinal cord injury;
 stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody;
 complementarity determining region; CDR.

OS Homo sapiens.

PN WO2004035603-A2.

PD 29-APR-2004.

PF 14-OCT-2003; 2003WO-US032243.

PR 14-OCT-2002; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.

PA (ABBO) ABBOTT LAB.

XX

PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX WPI; 2004-348433/32.

PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.

PS Claim 40; SEQ ID NO 59; 192pp; English.

CC The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,
 CC complements and degenerate codon equivalents; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has anti-anaemic, neuroprotective and vulnary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody heavy
 CC chain variable region complementarity determining region (CDR), which is
 CC given in the exemplification of the present invention.

SO Sequence 41 AA;

Query Match 93.2%; Score 82; DB 8; Length 41;
 Best Local Similarity 88.2%; Pred. No. 8.1e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKITYADSVKG 17
 :|||||
 Db 11 VISYDGSNKITYADSVKG 27

RESULT 39
 ADR68562
 ID ADR68562 standard; peptide; 41 AA.

AC ADR68562;

DT 02-DEC-2004 (first entry)

DE Human EPO-R heavy chain variable region seqid 59.

anti-anaemic; respiratory; vulnary; gene therapy; vaccine;
 erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
 hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
 wound healing; neural tissue damage; tissue damage; brain injury;
 spinal cord injury; stroke; human; heavy chain variable region;
 anti-EPO-R-antibody.

OS Homo sapiens.

PN US2004175379-A1.

PD 09-SEP-2004.

PF 10-OCT-2003; 2003US-00684109.

XX

```

XX 14-OCT-2002; 2002US-0418031P.
PR
XX (DEVIR/) DEVRIES P J.
XX (OSTROM D H.
XX (REIL/) REILLY E B.
XX (GREEN L L.
XX (WIEL/) WIELER J.
XX
XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX WPI; 2004-661369/64.
XX
XX New antibody or its antibody fragment that activates an endogenous
XX activity or is capable of binding to a human erythropoietin receptor in a
XX mammal, useful for treating a mammal suffering aplasia or anemia.
XX
XX Claim 40; SEQ ID NO 59; 156bp; English.
XX
XX The invention describes an antibody or its fragment that activates an
XX endogenous activity or capable of binding to a human erythropoietin
XX receptor in a mammal, or that comprises at least one heavy or light chain
XX variable region having a sequence comprising 116 or 107 amino acids (SEQ
XX ID NO: 3 or 5) given in the specification or its fragment, but does not
XX interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
XX given in the specification. Also described are: a method of activating or
XX modulating an endogenous activity of a human erythropoietin receptor in a
XX mammal; a pharmaceutical composition comprising a therapeutic amount of
XX an antibody or antibody fragment above and a pharmaceutical excipient; an
XX isolated and purified polynucleotide sequence selected from 28 sequences
XX comprising 322-370 bp (seven SEQ ID NOS between SEQ ID NO: 2-56) given in
XX the specification, and their fragments, complements, and degenerate codon
XX equivalents; and an isolated and purified amino acid sequence selected
XX from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
XX SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
XX their fragments. The antibody or its antibody fragment that activates or
XX modulates the activity of the receptor is useful in a method of treating
XX a mammal suffering aplasia or anemia. The antibodies are also useful for
XX treating disorders characterised by decreased or subnormal levels of
XX oxygen in the blood or tissue such as hypoxemia or chronic tissue
XX hypoxia and/or diseases characterised by inadequate blood circulation or
XX reduced blood flow. They are also useful for promoting wound healing or
XX for protecting against neural cell and/or tissue damage, resulting from
XX brain/spinal cord injury, stroke and the like. The antibodies are also
XX useful for identifying or diagnosing mammals having dysfunctional
XX erythropoietin receptor. This is the amino acid sequence of a human
XX erythropoietin receptor (EPO-R) anti-EPO-R-antibody heavy chain variable
XX region.
XX
XX Sequence 41 AA;
XX
XX Query Match 93.2%; Score 82; DB 8; Length 41;
XX Best Local Similarity 88.2%; Pred. No. 8.1e-06;
XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 IISYDGSKKYYADSVKG 17
XX :|||||
XX Db 11 VISYDGSKKYYADSVKG 27
XX
XX RESULT 40
XX AAR76975
XX ID AAR76975 standard; peptide; 61 AA.
XX
XX AAR76975;
XX
XX 23-FEB-1996 (first entry)
XX
XX HSV-neutralising antibody clone Fab fragment heavy chain variable domain.
XX Herpes simplex virus; type I; type II; monoclonal antibody; diagnosis;
XX neutralisation; immunotherapy.
XX

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OS Homo sapiens.
XX
XX WO9518634-A1.
XX
XX 13-JUL-1995.
XX
XX 04-JAN-1995; 95WO-US000067.
XX
XX 04-JAN-1994; 94US-00178201.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Williamson RA, Burtoni R, Sanna PP;
XX WPI; 1995-254909/33.
XX
XX Human monoclonal antibodies that neutralise Herpes simplex virus (HSV)
XX types 1 and 2 - used for diagnosis and passive immunotherapy of HSV
XX infections.
XX
XX Example 4; Page 61; 100bp; English.
XX
XX AAR76965-R76579 are the Fab fragment heavy chain variable domains of
XX human anti-herpes monoclonal antibodies. These antibodies are capable of
XX neutralising both herpes simplex virus (HSV) types I and II by binding an
XX epitope present on glycoprotein D. The antibody may be used for detecting
XX HSV in vivo or in vitro; for passive immunotherapy (pref.
XX prophylactically) of HSV infection (eg. genital, oral or ocular herpes),
XX parv. as its Fab fragment and as a competitive reagent for detecting
XX neutralising anti-HSV antibodies in a sample. Anti-Idiotypic antibodies
XX raised against the mAb can be used for active immunotherapy of HSV
XX infection
XX
XX Sequence 61 AA;
XX
XX Query Match 93.2%; Score 82; DB 2; Length 61;
XX Best Local Similarity 88.2%; Pred. No. 1.3e-05;
XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 IISYDGSKKYYADSVKG 17
XX :|||||
XX Db 45 VISYDGSKKYYADSVKG 61
XX
XX Search completed: March 31, 2005, 12:02:28
XX Job time : 133.75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:44 ; Search time 33.2031 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-11
Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/ECTUS COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	17	4	US-09-383-667-11
2	83	94.3	17	4	US-09-383-667-18
3	82	93.2	17	4	US-09-383-667-16
4	82	93.2	17	4	US-09-383-667-20
5	82	93.2	17	4	US-09-424-840B-36
6	82	93.2	17	4	US-09-424-840B-95
7	82	93.2	17	4	US-09-424-840B-108
8	82	93.2	17	4	US-09-424-840B-97
9	82	93.2	98	1	US-08-211-202-118
10	82	93.2	115	4	US-09-726-219A-167
11	82	93.2	116	1	US-08-211-202-141
12	82	93.2	117	3	US-08-545-809A-115
13	82	93.2	119	1	US-08-331-398A-46
14	82	93.2	119	2	US-08-331-397B-46
15	82	93.2	119	2	US-08-759-804A-46
16	82	93.2	119	3	US-09-227-693-46
17	82	93.2	120	1	US-08-211-202-135
18	82	93.2	120	1	US-07-942-245-35
19	82	93.2	123	3	US-08-983-607-38
20	82	93.2	123	4	US-09-424-840B-6
21	82	93.2	128	1	US-08-478-039-96
22	82	93.2	128	1	US-08-476-349A-96
23	82	93.2	248	4	US-09-315-926A-80
24	81	92.0	17	4	US-09-424-840B-77
25	81	92.0	17	4	US-09-424-840B-111
26	81	92.0	124	4	US-09-424-840B-16
27	81	92.0	179	3	US-08-862-124-2

28	81	92.0	225	4	US-09-456-090A-102	Sequence 102, App
29	81	92.0	225	4	US-09-456-090A-108	Sequence 108, App
30	81	92.0	225	4	US-09-456-090A-110	Sequence 110, App
31	81	92.0	225	4	US-09-453-234-102	Sequence 102, App
32	81	92.0	225	4	US-09-453-234-108	Sequence 108, App
33	81	92.0	225	4	US-09-453-234-110	Sequence 110, App
34	81	92.0	287	3	US-08-862-124-17	Sequence 17, App
35	81	92.0	304	3	US-08-862-124-14	Sequence 14, App
36	79	89.8	17	4	US-09-560-198A-12	Sequence 12, App
37	79	89.8	17	4	US-09-424-840B-84	Sequence 84, App
38	79	89.8	17	4	US-09-424-840B-113	Sequence 113, App
39	79	89.8	123	4	US-09-560-198A-2	Sequence 2, App
40	79	89.8	123	4	US-09-560-198A-4	Sequence 4, App
41	79	89.8	123	4	US-09-560-198A-10	Sequence 10, App
42	79	89.8	123	4	US-09-424-840B-22	Sequence 22, App
43	77	87.5	126	1	US-08-276-852-81	Sequence 81, App
44	77	87.5	126	1	US-08-899-575-81	Sequence 81, App
45	77	87.5	126	1	US-08-899-575-81	Sequence 81, App

ALIGNMENTS

RESULT 1
US-09-383-667-11
; Sequence 11, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camella W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: Pl661R2
; CURRENT FILING DATE: 1999-08-26
; EARLIER FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-11
Query Match 100.0%; Score 88; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 IISYDGSKKYYADSVKG 17
Db 1 IISYDGSKKYYADSVKG 17
RESULT 2
US-09-383-667-18
; Sequence 18, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camella W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: Pl661R2

;; CURRENT APPLICATION NUMBER: US/09/383,667
;; EARLIER FILING DATE: 1999-08-26
;; EARLIER APPLICATION NUMBER: US 60/098,233
;; EARLIER FILING DATE: 1998-08-28
;; EARLIER APPLICATION NUMBER: US 60/122,767
;; EARLIER FILING DATE: 1999-03-03
;; NUMBER OF SEQ ID NOS: 32
;; SEQ ID NO 18
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-383-667-18

Query Match 94.3%; Score 83; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 8,1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 IISYDGSNNKYADSVKG 17

RESULT 3

US-09-383-667-16
;; Sequence 16, Application US/09383667
;; Patent No. 6624295
;; GENERAL INFORMATION:
;; APPLICANT: Adams, Camelia W.
;; APPLICANT: Devaux, Brigitte
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Haase, Philip B.
;; APPLICANT: Judice, J. Kevin
;; APPLICANT: Kirchofer, Daniel
;; APPLICANT: Suggett, Shelley
;; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
;; FILE REFERENCE: P1661R2
;; CURRENT APPLICATION NUMBER: US/09/383,667
;; CURRENT FILING DATE: 1999-08-26
;; EARLIER APPLICATION NUMBER: US 60/098,233
;; EARLIER FILING DATE: 1998-08-28
;; EARLIER APPLICATION NUMBER: US 60/122,767
;; EARLIER FILING DATE: 1999-03-03
;; NUMBER OF SEQ ID NOS: 32
;; SEQ ID NO 16
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-383-667-16

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1,2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGSNNKYADSVKG 17

RESULT 4

US-09-383-667-20
;; Sequence 20, Application US/09383667
;; Patent No. 6624295
;; GENERAL INFORMATION:
;; APPLICANT: Adams, Camelia W.
;; APPLICANT: Devaux, Brigitte
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Haase, Philip B.
;; APPLICANT: Judice, J. Kevin
;; APPLICANT: Kirchofer, Daniel
;; APPLICANT: Suggett, Shelley
;; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
;; FILE REFERENCE: P1661R2
;; CURRENT APPLICATION NUMBER: US/09/383,667

;; CURRENT FILING DATE: 1999-08-26
;; EARLIER APPLICATION NUMBER: US 60/098,233
;; EARLIER FILING DATE: 1998-08-28
;; EARLIER APPLICATION NUMBER: US 60/122,767
;; EARLIER FILING DATE: 1999-03-03
;; NUMBER OF SEQ ID NOS: 32
;; SEQ ID NO 20
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-383-667-20

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1,2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVK 16
Db 1 IISYDGSKKYYADSVK 16

RESULT 5

US-09-424-840B-36
;; Sequence 36, Application US/09424840B
;; Patent No. 6790938
;; GENERAL INFORMATION:
;; APPLICANT: Berchtold, Peter
;; APPLICANT: Escher, Robert F. A.
;; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
;; FILE REFERENCE: 100564-09049
;; CURRENT APPLICATION NUMBER: US/09/424,840B
;; CURRENT FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: DE 19820663.1
;; PRIOR FILING DATE: 1998-05-08
;; PRIOR APPLICATION NUMBER: DE 19755227.7
;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: DE 19723904.8
;; PRIOR FILING DATE: 1997-06-06
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 36
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-424-840B-36

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1,2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGSNNKYADSVKG 17

RESULT 6

US-09-424-840B-95
;; Sequence 95, Application US/09424840B
;; Patent No. 6790938
;; GENERAL INFORMATION:
;; APPLICANT: Berchtold, Peter
;; APPLICANT: Escher, Robert F. A.
;; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
;; FILE REFERENCE: 100564-09049
;; CURRENT APPLICATION NUMBER: US/09/424,840B
;; CURRENT FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: DE 19820663.1
;; PRIOR FILING DATE: 1998-05-08
;; PRIOR APPLICATION NUMBER: DE 19755227.7
;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: DE 19723904.8
;; PRIOR FILING DATE: 1997-06-06
;; NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-95

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 7
US-09-424-840B-97
Sequence 97, Application US/09424840B
Patent No. 6790338
GENERAL INFORMATION:
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 97
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-97

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 8
US-09-424-840B-108
Sequence 108, Application US/09424840B
Patent No. 6790338
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US/09/424.840B
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 108
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens

US-09-424-840B-108

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 9
US-08-211-202-118
Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211.202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-118

Query Match 93.2%; Score 82; DB 1; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
US-09-726-219A-167
; Sequence 167, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kaaper
; APPLICANT: Marks, James
; APPLICANT: Jackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT FILING DATE: US/09/726,219A
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167

Query Match 93.2%; Score 82; DB 4; Length 115;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 11
US-08-211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus
; APPLICANT: BAIRER, Michael

APPLICANT: JESPER, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSER: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BFO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-141

Query Match 93.2%; Score 82; DB 1; Length 116;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 12
US-08-545-809A-115
; Sequence 115, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tadaaki
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545, 809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-115

Query Match 93.2%; Score 82; DB 3; Length 117;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDSKKYYADSVKG 17
:|||||
Db 69 VISYDSNKYYADSVKG 85

RESULT 13
US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match 93.2%; Score 82; DB 1; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDSKKYYADSVKG 17
:|||||
Db 50 VISYDSNKYYADSVKG 66

RESULT 14
US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note="Human fetal immunoglobulin
; OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15
US-08-759-804A-46
; Sequence 46, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pal, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid

STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note="Human fetal immunoglobulin
; OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-759-804A-46

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 16
US-09-227-693-46
; Sequence 46, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119

OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL VH region"
US-09-227-693-46

Query Match 93.2%; Score 82; DB 3; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 17

US-08-211-202-135
Sequence 135, Application US/08211202
Patent No. 5565332

GENERAL INFORMATION:

APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus

APPLICANT: BAIRER, Michael

APPLICANT: JESPER, Laurent Stephane Anne Therese

APPLICANT: WINTER, Gregory Paul

TITLE OF INVENTION: Production of chimeric antibodies - a

NUMBER OF INVENTION: combinatorial approach

CORRESPONDENCE ADDRESSES: 144

ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &

ADDRESS: Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/211.202

FILING DATE: 23-SEP-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9120252.3

FILING DATE: 23-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9120377.8

FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206372.6

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/31960

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 135:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-211-202-135

Query Match 93.2%; Score 82; DB 1; Length 120;
Best Local Similarity 88.2%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 18

US-07-942-245-35
Sequence 35, Application US/07942245
Patent No. 5639641

GENERAL INFORMATION:

APPLICANT: PEDERSEN, Jan T.

APPLICANT: SEARLE, Stephen M.J.

APPLICANT: REES, Anthony R.

APPLICANT: ROGUSKA, Michael A.

APPLICANT: GUILD, Braydon C.

TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT

NUMBER OF INVENTION: ANTIBODIES

CORRESPONDENCE ADDRESSES: 522

ADDRESSEE: Sughrue, Miron, Zimm, Macpeak & Seas

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States

ZIP: 20037-3202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: HP 9000/700 Workstation

OPERATING SYSTEM: UNIX

SOFTWARE: In house

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/942.245

FILING DATE: 09-SEP-1992

CLASSIFICATION: 530

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

TELEX: 6491103

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-942-245-35

Query Match 93.2%; Score 82; DB 1; Length 120;

Best Local Similarity 88.2%; Pred. No. 9e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 19

US-08-983-607-38
Sequence 38, Application US/08983607
Patent No. 6140470

GENERAL INFORMATION:

APPLICANT: Aiah Garen

APPLICANT: Xiaohong Cai

TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-

TITLE OF INVENTION: bodies

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Department of Molecular Biophysics

ADDRESSEE: and Biochemistry, Yale University

STREET: 266 Whitney Avenue

US-08-983-607-38

CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983.607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
ORGANISM: immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: Cycles
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phase construct
CLONE: V575
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-38
Query Match 93.2%; Score 82; DB 3; Length 123;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDSKYYADSVKG 17
:|||||
Db 50 VISYDSNKYYADSVKG 66
RESULT 20
US-09-424-840B-6
Sequence 6, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GP11B/11IA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424.840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-6
Query Match 93.2%; Score 82; DB 4; Length 123;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDSKYYADSVKG 17
:|||||
Db 50 VISYDSNKYYADSVKG 66
RESULT 21
US-08-478-039-96
Sequence 96, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478.039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379.072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912.292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856.281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735.064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teekin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: RF SJ2
US-08-478-039-96
Query Match 93.2%; Score 82; DB 1; Length 128;
Best Local Similarity 88.2%; Pred. No. 9.6e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 22
US-08-476-349A-96
; Sequence 96, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabli
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Bsg., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: RF SJ2
US-08-476-349A-96

Query Match 93.2%; Score 82; DB 1; Length 128;
Best Local Similarity 88.2%; Pred. No. 9.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 23

US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAR1 amino acid sequence"
US-09-315-926A-80

Query Match 93.2%; Score 82; DB 4; Length 248;
Best Local Similarity 88.2%; Pred. No. 1.9e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 72 VISYDGSNKYYADSVKG 88

RESULT 24
US-09-424-840B-77
; Sequence 77, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 77
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-77

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 LISYDGSNKYYADSVKG 17

RESULT 25

US-09-424-840B-111
; Sequence 111, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424, 840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-111

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 LISYDGSKKYYADSVKG 17

RESULT 26
US-09-424-840B-16
; Sequence 16, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424, 840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-16

Query Match 92.0%; Score 81; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 LISYDGSKKYYADSVKG 66

RESULT 27
US-08-862-124-2
; Sequence 2, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.

APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-862-124-2

Query Match 92.0%; Score 81; DB 3; Length 179;
Best Local Similarity 88.2%; Pred. No. 2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 111 VISYDGSKKYYADSVKG 127

RESULT 28
US-09-456-090A-102
; Sequence 102, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nile
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456, 090A
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31H
US-09-456-090A-102

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 29
US-09-456-090A-108
; Sequence 108, Application US/09456090A
; Patent No. 6680209

GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 108
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-34H

US-09-456-090A-108

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 30
US-09-456-090A-110
; Sequence 110, Application US/09456090A
; Patent No. 6680209

GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 110
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-35H

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 31
US-09-453-234-102
; Sequence 102, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:

APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 102
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-31H

US-09-453-234-102

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 32
US-09-453-234-108
; Sequence 108, Application US/09453234
; Patent No. 6794132

GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 108
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-34H

US-09-453-234-108

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 33
US-09-453-234-110
; Sequence 110, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff

```

; APPLICANT: Lonberg, Nils
; APPLICANT: Bioscience Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIORITY FILING DATE: 1999-12-01
; PRIORITY APPLICATION NUMBER: US 60/157,415
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 110
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35H
US-09-453-234-110

Query Match          92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy      1  IISYDGSKKYYADSVKG 17
        :|||||
        50  IISYDGSKKYYADSVKG 66

Db
RESULT 34
US-08-862-124-17
; Sequence 17, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maltl, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-862-124-17

Query Match          92.0%; Score 81; DB 3; Length 287;
Best Local Similarity 88.2%; Pred. No. 3.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy      1  IISYDGSKKYYADSVKG 17
        :|||||
        209  VISYDGSKKYYADSVKG 225

Db
RESULT 35
US-08-862-124-14
; Sequence 14, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maltl, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-862-124-14

Query Match          97.0%; Score 81; DB 3; Length 304;
Best Local Similarity 88.2%; Pred. No. 3.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy      1  IISYDGSKKYYADSVKG 17
        :|||||
        209  VISYDGSKKYYADSVKG 225

Db
RESULT 36
US-09-560-198A-12
; Sequence 12, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Leonard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Bradlock, Peter SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
```



```
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 28111/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-198A-12

Query Match      89.8%; Score 79; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 IISYDSKKYADSVKG 17
Db      1 VISYDSIKYADSVKG 17

RESULT 37
US-09-424-840B-84
; Sequence 84, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Bertschold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR FILING DATE: 1997-12-12
; PRIOR FILING DATE: 19755227.7
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-84

Query Match      89.8%; Score 79; DB 4; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 IISYDSKKYADSVKG 17
Db      2 IISYDSKKYADSVKG 17

RESULT 38
US-09-424-840B-113
; Sequence 113, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Bertschold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
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; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-113

Query Match      89.8%; Score 79; DB 4; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 IISYDSKKYADSVKG 17
Db      2 IISYDSKKYADSVKG 17

RESULT 39
US-09-560-198A-2
; Sequence 2, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peter SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 28111/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-198A-2

Query Match      89.8%; Score 79; DB 4; Length 123;
Best Local Similarity 88.2%; Pred. No. 2.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 IISYDSKKYADSVKG 17
Db      50 VISYDSIKYADSVKG 66

RESULT 40
US-09-560-198A-4
; Sequence 4, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peter SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 28111/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; CURRENT FILING DATE: 2000-04-28
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; PRIOR APPLICATION NUMBER: US 60/131,983
 ; PRIOR FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-560-198A-4

Query Match 89.8%; Score 79; DB 4; Length 123;
 Best Local Similarity 88.2%; Pred. No. 2.8e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVKG 17
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 Db 50 VISYDGSIKYYADSVKG 66

Search completed: March 31, 2005, 12:13:25
 Job time : 34.2031 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 12:10:00 ; Search time 95.0938 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	87	98.9	248 10 US-09-880-748-916	Sequence 916, App
3	87	98.9	248 10 US-09-880-748-1323	Sequence 123, App
4	87	98.9	248 15 US-10-293-418-914	Sequence 914, App
5	87	98.9	248 15 US-10-293-418-916	Sequence 916, App
6	87	98.9	248 15 US-10-293-418-1323	Sequence 123, App
7	87	98.9	251 10 US-09-880-748-1114	Sequence 1114, App
8	87	98.9	251 15 US-10-293-418-1114	Sequence 1114, App
9	86	97.7	135 15 US-10-364-743-97	Sequence 97, App
10	84	95.5	17 9 US-09-828-708-24	Sequence 24, App
11	84	95.5	101 9 US-09-828-708-10	Sequence 10, App
12	84	95.5	119 14 US-10-010-729-7	Sequence 7, App
13	83	94.3	123 17 US-10-727-155-14	Sequence 14, App

14	83	94.3	125 15 US-10-292-088-58	Sequence 58, App
15	83	94.3	137 15 US-10-364-743-11	Sequence 11, App
16	83	94.3	137 15 US-10-364-743-99	Sequence 99, App
17	83	94.3	252 10 US-09-880-748-1690	Sequence 1690, App
18	83	94.3	252 15 US-10-293-418-1690	Sequence 1690, App
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21	82	93.2	17 15 US-10-384-060-46	Sequence 46, App
22	82	93.2	17 15 US-10-399-701-6	Sequence 6, App
23	82	93.2	17 16 US-10-396-578-21	Sequence 21, App
24	82	93.2	17 16 US-10-396-578-39	Sequence 39, App
25	82	93.2	17 16 US-10-396-578-51	Sequence 51, App
26	82	93.2	17 16 US-10-396-578-81	Sequence 81, App
27	82	93.2	17 17 US-10-726-332-114	Sequence 114, App
28	82	93.2	41 15 US-10-269-711-47	Sequence 47, App
29	82	93.2	41 15 US-10-269-711-48	Sequence 48, App
30	82	93.2	41 16 US-10-684-109-59	Sequence 59, App
31	82	93.2	83 14 US-10-078-958-7	Sequence 7, App
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35	82	93.2	98 14 US-10-194-975-24	Sequence 24, App
36	82	93.2	98 14 US-10-194-975-25	Sequence 25, App
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43	82	93.2	98 15 US-10-032-0378-80	Sequence 80, App
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45	82	93.2	98 15 US-10-029-9888-75	Sequence 75, App

ALIGNMENTS

RESULT 1
US-09-880-748-914
; Sequence 914, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 914
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-914

Query Match 98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
DB 50 IISYDGSKKYYADSVKG 66

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RESULT 2
US-09-880-748-916
; Sequence 916, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 916
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-916
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Query Match          98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      50 VISYDGSKKYYADSVKG 66
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RESULT 3
US-09-880-748-1323
; Sequence 1323, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1323
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1323
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Query Match          98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      50 VISYDGSKKYYADSVKG 66
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RESULT 4
US-10-293-418-914
; Sequence 914, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 914
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-914
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Query Match          98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      50 VISYDGSKKYYADSVKG 66
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RESULT 5
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; Sequence 916, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 916
; LENGTH: 248
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-916

Query Match 98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
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Db 50 VISYDGSKKYYADSVKG 66

RESULT 6
US-10-293-418-1323
Sequence 1323, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly's
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1323
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1323

Query Match 98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 50 VISYDGSKKYYADSVKG 66

RESULT 7
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Sequence 1114, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly's
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1114

Query Match 98.9%; Score 87; DB 10; Length 251;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
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Db 50 VISYDGSKKYYADSVKG 66

RESULT 8
US-10-293-418-1114
Sequence 1114, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly's
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1114

Query Match 98.9%; Score 87; DB 15; Length 251;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 9
US-10-364-743-97
Sequence 97, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowditch, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Tooshiaki
APPLICANT: No. US20040009178A1, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)

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; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
US-10-364-743-97

Query Match          97.7%  Score 86; DB 15; Length 135;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
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Db      52 LISYDGSKKYYADSVKG 68

RESULT 10
US-09-828-708-24
; Sequence 24, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-24

Query Match          95.5%  Score 84; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
       :|||||:|||||
Db      1 VISYDGNKKYYADSVKG 17

RESULT 11
US-09-828-708-10
; Sequence 10, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-10

Query Match          95.5%  Score 84; DB 9; Length 101;

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Best Local Similarity 88.2%; Pred. No. 2.2e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
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Db      43 VISYDGNKKYYADSVKG 59

RESULT 12
US-10-010-729-7
; Sequence 7, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; FILE REFERENCE: 1199-1-005C1P2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-729-7

Query Match          95.5%  Score 84; DB 14; Length 119;
Best Local Similarity 88.2%; Pred. No. 2.6e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
       :|||||:|||||
Db      50 VISYDGSKKYYADSVKG 66

RESULT 13
US-10-727-155-14
; Sequence 14, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaapal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendelcho
; APPLICANT: Palaniswami Rathnaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF

```

```
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-14

Query Match
Best Local Similarity 94.3%; Score 83; DB 17; Length 123;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVYKG 17
Db 50 IISYDGSNNKYADSVYKG 66

RESULT 14
US-10-292-088-58
Sequence 58, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VARE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PR/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-088-58

Query Match
Best Local Similarity 94.3%; Score 83; DB 15; Length 125;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVYKG 17
Db 50 IISYDGSNNKYADSVYKG 66

RESULT 15
US-10-364-743-11
Sequence 11, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: No. US20040009178A1, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
```

```
SEQ ID NO 11
LENGTH: 137
TYPE: PRT
ORGANISM: human
US-10-364-743-11

Query Match
Best Local Similarity 94.3%; Score 83; DB 15; Length 137;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVYKG 17
Db 52 VISYDGSKKYYGDSVYKG 68

RESULT 16
US-10-364-743-99
Sequence 99, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: No. US20040009178A1, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 99
LENGTH: 137
TYPE: PRT
ORGANISM: human
US-10-364-743-99

Query Match
Best Local Similarity 94.3%; Score 83; DB 15; Length 137;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVYKG 17
Db 52 VISYDGSKKYYGDSVYKG 68

RESULT 17
US-09-880-748-1690
Sequence 1690, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1690
LENGTH: 252
TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-09-860-748-1690

Query Match          94.3%; Score 83; DB 10; Length 252;
Best Local Similarity 88.2%; Pred. No. 8.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      50 VISYDGSKKYYGDSVKG 66

RESULT 18
US-10-293-418-1690
; Sequence 1690, Application US/10293418
; Publication No. US200302239661
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1690
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1690

Query Match          94.3%; Score 83; DB 15; Length 252;
Best Local Similarity 88.2%; Pred. No. 8.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      50 VISYDGSKKYYGDSVKG 66

RESULT 19
US-10-292-088-62
; Sequence 62, Application US/10292088
; Publication No. US200302110041
; GENERAL INFORMATION:
; APPLICANT: BEDIAN VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
```

```

; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-62

Query Match          94.3%; Score 83; DB 15; Length 470;
Best Local Similarity 94.1%; Pred. No. 0.00015;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      69 IISYDGSNKYYADSVKG 85

RESULT 20
US-09-972-656-48
; Sequence 48, Application US/0972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-48

Query Match          93.2%; Score 82; DB 10; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      1 VISYDGSNKYYADSVKG 17

RESULT 21
US-10-384-060-46
; Sequence 46, Application US/10384060
; Publication No. US2003026155A1
; GENERAL INFORMATION:
; APPLICANT: SADBAGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 33 CDR2 sequence
US-10-384-060-46
```


Query Match 93.2%; Score 82; DB 15; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 1 VISYDGSNNKYADSVKG 17

RESULT 22
US-10-399-701-6
; Sequence 6, Application US/10399701
; Publication No. US20040022791A1
; GENERAL INFORMATION:
; APPLICANT: ASAT AG
; TITLE OF INVENTION: Rekombinant anti-GPIIb/IIIa-antibodies as agents for
; TITLE OF INVENTION: Inhibiting angiogenesis
; FILE REFERENCE: 23600PMO_DRAS
; CURRENT APPLICATION NUMBER: US/10/399,701
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 100 57 443.2
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2-region of
US-10-399-701-6

Query Match 93.2%; Score 82; DB 15; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 1 VISYDGSNNKYADSVKG 17

RESULT 23
US-10-396-578-21
; Sequence 21, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-21

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||

DB 1 VISYDGSNNKYADSVKG 17

RESULT 24
US-10-396-578-39
; Sequence 39, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-39

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 1 VISYDGSNNKYADSVKG 17

RESULT 25
US-10-396-578-51
; Sequence 51, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 51
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-51

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 1 VISYDGSNNKYADSVKG 17

RESULT 26
US-10-396-578-81
; Sequence 81, Application US/10396578
; Publication No. US20040191260A1

GENERAL INFORMATION:
APPLICANT: Reiter, Yoram
APPLICANT: Cohen, Cyril J.
TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
FILE REFERENCE: 25563
CURRENT APPLICATION NUMBER: US/10/396,578
CURRENT FILING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-81

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 1 VISYDGSNKYYADSVKG 17

RESULT 27
US-10-726-332-114
Sequence 114, Application US/10726332
Publication No. US20050058649A1
GENERAL INFORMATION:
APPLICANT: Gregory M. Landes
APPLICANT: Mary Haak-Frendescho
APPLICANT: Ling Chen
APPLICANT: Yen-Wah R. Lee
APPLICANT: Weina Liang
APPLICANT: Xiao-Feng
APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocentini
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: ABGENIX.072A
CURRENT APPLICATION NUMBER: US/10/726,332
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: n/a
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 114
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-726-332-114

Query Match 93.2%; Score 82; DB 17; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 1 VISYDGSNKYYADSVKG 17

RESULT 28
US-10-269-711-47
Sequence 47, Application US/10269711
Publication No. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: DeVries, Peter J.

APPLICANT: Reilly, Edward B.
APPLICANT: Ostrow, Dave
APPLICANT: Weller, James
APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-711-47

Query Match 93.2%; Score 82; DB 15; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 11 VISYDGSNKYYADSVKG 27

RESULT 29
US-10-269-711-48
Sequence 48, Application US/10269711
Publication No. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: DeVries, Peter J.
APPLICANT: Ostrow, Dave
APPLICANT: Weller, James
APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-711-48

Query Match 93.2%; Score 82; DB 15; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 11 VISYDGSNKYYADSVKG 27

RESULT 30
US-10-684-109-59
Sequence 59, Application US/10684109
Publication No. US20040175379A1
GENERAL INFORMATION:
APPLICANT: DeVries, Peter J.
APPLICANT: Green, Larry L.
APPLICANT: Ostrow, David H.
APPLICANT: Reilly, Edward B.
APPLICANT: Weller, James
TITLE OF INVENTION: Erythropoietin Receptor Binding
TITLE OF INVENTION: Antibodies
FILE REFERENCE: 6989.US.02
CURRENT APPLICATION NUMBER: US/10/684,109

; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-59

Query Match 93.2%; Score 82; DB 16; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 11 VISYDGSNKYYADSVKG 27

RESULT 31
US-10-078-958-7
; Sequence 7, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AVA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (22)
; OTHER INFORMATION: Variable amino acid
US-10-078-958-7

Query Match 93.2%; Score 82; DB 14; Length 83;
Best Local Similarity 88.2%; Pred. No. 3.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 35 VISYDGSNKYYADSVKG 51

RESULT 32
US-10-884-830-653
; Sequence 653, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BEI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999

; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 653
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-653

Query Match 93.2%; Score 82; DB 16; Length 95;
Best Local Similarity 88.2%; Pred. No. 4.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 33
US-09-948-939-15
; Sequence 15, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lomborg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: heavy chain variable region predicted sequence for
US-09-948-939-15

Query Match 93.2%; Score 82; DB 9; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 34
US-10-194-975-23
; Sequence 23, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-23

Query Match 93.2%; Score 82; DB 14; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 35
US-10-194-975-24
; Sequence 24, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foece, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24

Query Match 93.2%; Score 82; DB 14; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 36
US-10-194-975-25
; Sequence 25, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foece, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-25

Query Match 93.2%; Score 82; DB 14; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 37
US-10-308-817-63
; Sequence 63, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:

; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-63

Query Match 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 38
US-10-308-817-64
; Sequence 64, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-64

Query Match 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 39
US-10-308-817-65
; Sequence 65, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-65

Query Match 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNNKYADSVKG 66

RESULT 40
US-10-032-037B-74
; Sequence 74, Application US/10032037B
; Publication No. US2004001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-74

Query March 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNNKYADSVKG 66

Search completed: March 31, 2005, 12:46:07
Job time : 96.0938 secs

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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 24.1719 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88
Sequence: 1 IISYDGSNKYYADSVKVG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	93.2	94	2	PL0120 Ig heavy chain V-I
2	82	93.2	97	2	S44115 Ig heavy chain V-I
3	82	93.2	98	2	PL0116 Ig heavy chain V-I
4	82	93.2	98	2	S29546 Ig heavy chain V-I
5	82	93.2	109	2	PH1646 Ig heavy chain V-I
6	82	93.2	109	2	PH1644 Ig heavy chain V-I
7	82	93.2	111	2	PH1643 Ig heavy chain V-I
8	82	93.2	111	2	PH1645 Ig heavy chain V-I
9	82	93.2	113	2	S38490 Ig heavy chain V-I
10	82	93.2	114	2	S46390 Ig heavy chain V-I
11	82	93.2	114	2	S46392 Ig heavy chain V-I
12	82	93.2	117	2	S36270 Ig heavy chain V-I
13	82	93.2	118	2	S31677 Ig heavy chain V-I
14	82	93.2	118	2	S31116 Ig heavy chain V-I
15	82	93.2	119	2	F36005 Ig heavy chain V-I
16	82	93.2	120	2	S31112 Ig heavy chain V-I
17	82	93.2	121	2	S19666 Ig heavy chain V-I
18	82	93.2	121	2	G36005 Ig heavy chain V-I
19	82	93.2	122	2	E36005 Ig heavy chain V-I
20	82	93.2	122	2	S31119 Ig heavy chain V-I
21	82	93.2	123	2	S38493 Ig heavy chain V-I
22	82	93.2	130	2	PL0098 Ig heavy chain V-I
23	82	93.2	132	2	S31603 Ig heavy chain V-I
24	82	93.2	134	2	S31679 Ig heavy chain V-I
25	82	93.2	139	2	S31674 Ig heavy chain V-I
26	82	93.2	137	2	S31701 Ig heavy chain V-I
27	82	93.2	137	2	PH1642 Ig heavy chain V-I
28	82	93.2	137	2	PH1642 Ig heavy chain V-I
29	82	93.2	137	2	PH1642 Ig heavy chain V-I

30	75	85.2	122	2	S31117 Ig heavy chain - h
31	75	85.2	128	2	A48797 Ig heavy chain V-I
32	75	85.2	133	2	A49028 Ig heavy chain V-I
33	75	85.2	133	2	S31510 Ig heavy chain - h
34	74	84.1	98	2	S29543 Ig heavy chain V-I
35	74	84.1	117	2	S36259 Ig heavy chain V-I
36	74	84.1	118	2	PH1662 Ig heavy chain V-I
37	74	84.1	122	1	M3HUM Ig heavy chain V-I
38	74	84.1	134	2	S31688 Ig heavy chain V-I
39	74	84.1	135	2	S31598 Ig heavy chain V-I
40	74	84.1	140	2	S70442 Ig heavy chain pre
41	73	83.0	151	2	A60943 Ig heavy chain pre
42	72	81.8	115	2	S36284 Ig heavy chain V-I
43	72	81.8	121	2	PH1661 Ig heavy chain V-I
44	71	80.7	118	2	PH1660 Ig heavy chain V-I
45	69	78.4	76	2	S31592 Ig heavy chain V-I

ALIGNMENTS

RESULT 1

PL0120

Ig heavy chain V-III region (TD-Vo) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C:Accession: PL0120

R:Bird, U.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A:Reference number: PL0116; MUID:88286083; PMID:2840480

A:Accession: PL0120

A:Molecule type: mRNA

A:Residues: 1-94 <BIR>

A:Cross-references: UNIPROT:Q8WTK1; UNIPROT:Q9UJ93

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL

A>Note: The sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F:31-35/Region: complementarity-determining 1

F:49-65/Region: complementarity-determining 2

Query Match 93.2%; Score 82; DB 2; Length 94;

Best Local Similarity 88.2%; Pred. No. 7.2e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSNKYYADSVKVG 17

Db 50 VISYDGSNKYYADSVKVG 66

RESULT 2

S44115

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C:Accession: S44115

R:Harwin, R.E.; Zhu, D.; Orecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

Submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A:Reference number: S44105

A:Accession: S44115

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-97 <HAM>

A:Cross-references: EMBL:Z31384; NID:q472969; PIDN:CAA63259.1; PID:q940526

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 82; DB 2; Length 97;

Best Local Similarity 88.2%; Pred. No. 7.5e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1  IISYDGSKKYYADSVKG 17
      :|||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 3
PL0116
Ig heavy chain V-III region (AM-Vx) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0116; S26892
R:Bid: J.; Gallil, N.; Link, M.; Stiles, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A:Reference number: PL0116; MUID:88286083; PMID:2840480
A:Accession: PL0116
A:Molecule type: mRNA
A:Residues: 1-98 <BIR>
A:Experimental source: B cells from patient AM with acute lymphoblastic leukemia, ALL
A>Note: the sequence shows the V region (AM-Vx) from a nonproductive DNA rearrangement
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26892
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12349; NID:G32918; PIDN:CAA78219.1; PID:G32919
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2

Query Match      93.2%; Score 82; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  IISYDGSKKYYADSVKG 17
      :|||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 4
S29546
Ig heavy chain V region (COS-8 / DF-46) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29546; S26888
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29546
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PID:G32844
A>Note: designated COS-8
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913
A>Note: designated DF-46
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 98;
```

```
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  IISYDGSKKYYADSVKG 17
      :|||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 5
PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1643
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A:Reference number: PH1642; MUID:93301610; PMID:8315368
A:Accession: PH1646
A:Molecule type: mRNA
A:Residues: 1-109 <HIL>
A:Cross-references: UNIPROT:Q8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  IISYDGSKKYYADSVKG 17
      :|||||
Db      42 VISYDGSNKYYADSVKG 58

RESULT 6
PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1644
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A:Reference number: PH1642; MUID:93301610; PMID:8315368
A:Accession: PH1644
A:Molecule type: mRNA
A:Residues: 1-109 <HIL>
A:Cross-references: UNIPROT:Q9YU93
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  IISYDGSKKYYADSVKG 17
      :|||||
Db      42 VISYDGSNKYYADSVKG 58

RESULT 7
PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1643
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A:Reference number: PH1642; MUID:93301610; PMID:8315368
A:Accession: PH1643
```


A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:Q8WTK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 8

PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1645
R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1645
A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:Q8WTK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 9

S38490
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38490
R:Markes, J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a F15-98/Domain: immunoglobulin homology <IMM>
A:Reference number: S38498
A:Accession: S38490
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z23030; NID:9414027; PIDN:CA86565.1; PID:9414028
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 113;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
S46390

Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46390
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31686; NID:9509782; PIDN:CA83491.1; PID:9135143
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 11

S46392
Ig heavy chain V region (VH-28) - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46392
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31688; NID:9499306; PIDN:CA83493.1; PID:9135145
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 12

S36270
Ig heavy chain V region (clone alpha-TNF-E1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36270
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries
A:Reference number: S36256; MUID:93176448; PMID:7679990
A:Accession: S36270
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-117 <GRI>
A:Cross-references: EMBL:Z18839; NID:933118; PIDN:CA879291.1; PID:9339898
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 13
S31677
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31677
R:Chislier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <CU>
A:Cross-references: EMBL:Z14172; NID:G31009; PIDN:CA478541.1; PID:G31010
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 82; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 14
S31116
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S31116
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman, E.; J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31116
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-118 <RAA>
A:Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15
F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C:Accession: F36005
R:Schröder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: F36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; GB:M34026
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 16
S31112
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31112
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman, E.; J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31112
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-120 <RAA>
A:Cross-references: EMBL:X62961
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 120;
Best Local Similarity 88.2%; Pred. No. 9.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 17
S19666
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Mark, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MAR>
A:Cross-references: EMBL:X61646; NID:G37688; PIDN:CA43827.1; PID:G1335369
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 121;
Best Local Similarity 88.2%; Pred. No. 9.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 18
G36005
Ig heavy chain V region (M74) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C:Accession: G36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: G36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; GB:M34031
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMTM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 121;
Best Local Similarity 88.2%; Pred. No. 9.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 19
E36005
Ig heavy chain V region (M72) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: E36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: E36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMTM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 122;
Best Local Similarity 88.2%; Pred. No. 9.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 20
S31119

Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S31119
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31119
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: UNIPROT:Q8WUK1; EMBL:X62970
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 122;
Best Local Similarity 88.2%; Pred. No. 9.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 21
S38493
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38493
R:Markis, J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a p
A:Reference number: S38488
A:Accession: S38493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <MAR>
A:Cross-references: EMBL:Z23036; NID:9414033; PIDN:CA80571.1; PID:9414034
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 123;
Best Local Similarity 88.2%; Pred. No. 9.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 22
P10098
Ig heavy chain precursor V-III region (FL2-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: P10098
R:Nickerson, K.G.; Berman, J.; Glickman, E.; Chess, L.; Alt, F.W.
J. Exp. Med. 169, 1391-1403, 1989
A:Title: Early human IgH gene assembly in Epstein-Barr virus-transformed fetal B cell li
B.
A:Reference number: P10098; MUID:89176893; PMID:2538551
A:Accession: P10098
A:Molecule type: DNA
A:Residues: 1-130 <NTIC>
A:Cross-references: UNIPROT:Q8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:17-120/Product: Ig heavy chain V-III region FL2-2 #status predicted <MAT>

F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 130;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 67 VISYDGSNKYYADSVKG 83

RESULT 23

S31603

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31603

R/Cislinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31603

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-132 <CUI>

A/Cross-references: EMBL:Z14168; NID:G30999; PIDN:CA78537.1; PID:G31000

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;30-113/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 132;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 65 VISYDGSNKYYADSVKG 81

RESULT 24

S31679

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31679

R/Cislinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31679

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-134 <CUI>

A/Cross-references: EMBL:Z14203; NID:G30965; PIDN:CA78572.1; PID:G30966

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 134;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 25

S31674

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31674

R/Cislinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31674

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-139 <CUI>

A/Cross-references: EMBL:Z14204; NID:G30967; PIDN:CA78573.1; PID:G30968

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 139;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 26

S31701

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31701

R/Cislinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31701

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-137 <CUI>

A/Cross-references: EMBL:Z14177; NID:G31020; PIDN:CA78546.1; PID:G31021

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 77; DB 2; Length 137;
Best Local Similarity 82.4%; Pred. No. 6.5e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 27

PH1642

Ig heavy chain V region (clone 5A10) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C/Accession: PH1642

R/Hillson, J.L.; Kaur, N.S.; Oppliger, I.R.; Mannik, M.; Saseo, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylococ

A/Reference number: PH1642; MUID:93301610; PMID:8315368

A/Accession: PH1642

A/Molecule type: mRNA

A/Residues: 1-108 <HIL>

A/Cross-references: UNIPROT:Q8WUK1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 108;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17

```
Db      42 VIWYDGSNKYYADSVKG 58
      : | | | | | | | | | |
RESULT 28
S46391
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46391
R:Rigini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46391
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31687; NID:G509784; PIDN:CA83492.1; PID:G1335144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      85.2%; Score 75; DB 2; Length 114;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      1 IISYDGSKKYYADSVKG 17
      : | | | | | | | | | |
Db      50 VIWYDGSNKYYADSVKG 66

RESULT 29
S31111
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31111
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat
Eur. J. Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31111
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62959
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      85.2%; Score 75; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      1 IISYDGSKKYYADSVKG 17
      : | | | | | | | | | |
Db      50 VIWYDGSNKYYADSVKG 66

RESULT 30
S31117
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat
Eur. J. Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
```

```
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: EMBL:X62967
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      85.2%; Score 75; DB 2; Length 122;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      1 IISYDGSKKYYADSVKG 17
      : | | | | | | | | | |
Db      50 VIWYDGSNKYYADSVKG 66

RESULT 31
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/VI6) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C:Accession: S48797; S26893
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A>Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <MAH>
A:Cross-references: EMBL:Z46379; NID:G587147; PIDN:CA86512.1; PID:G1340168
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A>Title: The repertoire of human germline VH sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12350; NID:G32922; PIDN:CA87820.1; PID:G32923
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      85.2%; Score 75; DB 2; Length 128;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      1 IISYDGSKKYYADSVKG 17
      : | | | | | | | | | |
Db      50 VIWYDGSNKYYADSVKG 66

RESULT 32
A49028
Ig heavy chain V-II region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49028
R:Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuurmat
Eur. J. Immunol. 21, 2355-2363, 1991
A>Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A:Reference number: A49028; MUID:92008140; PMID:1915549
A:Accession: A49028
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-133 <TIM>
A:Cross-references: GB:564471; NID:G236904; PIDN:AA82001.1; PID:G236905
A:Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A>Note: sequence extracted from NCBI backbone (NCBI:64471, NCBI:64470)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
```

Query Match 85.2%; Score 75; DB 2; Length 133;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 50 IISYDGSKKYVADSVKG 17
50 IIVYDGSNKYVADSVKG 66

RESULT 33

Ig heavy chain - human
S31510
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31510
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31510
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-133 <CH>
A:Cross-references: EMBL:X69865; NID:G33092; PIDN:CAA49499.1; PID:G33093
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 133;
Best Local Similarity 87.5%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 62 IISYDGSKKYVADSVKG 17
62 IISYDGSNKYVADSVKG 77

RESULT 34

Ig heavy chain V region (COS 3) - human (fragment)
S29543
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29543
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29543
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:G32836
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 51 IISYDGSKKYVADSVKG 17
51 IIVYDGSNKYVADSVKG 66

RESULT 35

Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
S36259
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36259
R:Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36259
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-117 <GRI>
A:Cross-references: EMBL:Z18850; NID:G33123; PIDN:CAA79302.1; PID:G939902
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 51 IISYDGSKKYVADSVKG 17
51 IIVYDGSNKYVADSVKG 66

RESULT 36

Ig heavy chain V region (clone TS2) - human (fragment)
PH1662
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1662
R:Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphyloc
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1662
A:Molecule type: mRNA
A:Residues: 1-118 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 118;
Best Local Similarity 76.5%; Pred. No. 0.00017;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 42 IISYDGSKKYVADSVKG 17
42 IIVYDGSNKYVADSVKG 58

RESULT 37

Ig heavy chain V-III region (Cam) - human (tentative sequence)
M3HUM
C:Species: Homo sapiens (man)
C:Date: 31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A02051
R:Lehman, D.W.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 3239-3243, 1980
A:Title: Amino acid sequence of the variable region of a human mu chain: location of a pr
A:Reference number: A02051; MUID:81013859; PMID:6774332
A:Accession: A02051
A:Molecule type: protein
A:Residues: 1-122 <LEH>
A:Cross-references: UNIPROT:P01768
C:Comment: This mu chain was isolated from the plasma of a patient with macroglobulinemia;
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F:15-98/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyroglutamic acid (Gln) #status experimental
F:22-96/Disulfide bonds: #status predicted

Query Match 84.1%; Score 74; DB 1; Length 122;
Best Local Similarity 70.6%; Pred. No. 0.00017;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 50 VISYGBBKYYABSVKG 66

RESULT 38

S31598
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31598
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
A:Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31598
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <CUI>
A:Cross-references: EMBL:Z14174; NID:G31013; PIDN:CAA78543.1; PID:G31014
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-114/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 134;
Best Local Similarity 87.5%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
:|||||:|||||
Db 67 IRYDGSNKKYADSVKG 82

RESULT 39

S31598
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31598
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
A:Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31598
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <CUI>
A:Cross-references: EMBL:Z14170; NID:G31001; PIDN:CAA78539.1; PID:G31002
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-114/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 135;
Best Local Similarity 87.5%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
:|||||:|||||
Db 67 IRYDGSNKKYADSVKG 82

RESULT 40

S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S70442
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70442

A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: UNIPROT:Q8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 140;
Best Local Similarity 87.5%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
:|||||:|||||
Db 70 IRYDGSNKKYADSVKG 85

Search completed: March 31, 2005, 12:11:13
Job time : 24.1719 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 112.891 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-11
Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	93.2	116	2 Q9UL93	Q9UL93 homo sapien
2	82	93.2	240	2 Q6SZC9	Q6SZC9 homo sapien
3	82	93.2	613	2 Q8WUK1	Q8WUK1 homo sapien
4	74	84.1	113	2 Q9UL90	Q9UL90 homo sapien
5	74	84.1	122	1 HV3G_HUMAN	P01768 homo sapien
6	71	80.7	417	2 Q6N093	Q6N093 homo sapien
7	70	79.5	493	2 Q68CN4	Q68CN4 homo sapien
8	69	78.4	147	2 Q9Y509	Q9Y509 homo sapien
9	67	76.1	482	2 Q7Z351	Q7Z351 homo sapien
10	67	76.1	493	2 Q8KCL6	Q8KCL6 homo sapien
11	66	75.0	122	2 Q9UL84	Q9UL84 homo sapien
12	65	73.9	119	1 HV3L_HUMAN	P01773 homo sapien
13	64	72.7	95	2 Q9ULB6	Q9ULB6 homo sapien
14	64	72.7	122	1 HV3H_HUMAN	P01769 homo sapien
15	64	72.7	470	2 Q6RJ44	Q6RJ44 homo sapien
16	64	72.7	478	2 Q6P181	Q6P181 homo sapien
17	63	71.6	119	1 HV3I_HUMAN	P01770 homo sapien
18	63	71.6	614	2 Q6DDQ7	Q6DDQ7 xenopus lae
19	62	70.5	121	1 HV3J_HUMAN	P01771 homo sapien
20	62	70.5	519	2 Q6N092	Q6N092 homo sapien
21	61	69.3	121	2 Q9UL71	Q9UL71 homo sapien
22	61	69.3	544	2 Q6RJ95	Q6RJ95 homo sapien
23	60	68.2	118	2 Q9UL72	Q9UL72 homo sapien
24	56	63.6	116	1 HV05_CARAU	P01781 carassius a
25	56	63.6	126	1 HV3K_HUMAN	P01772 homo sapien
26	55	62.5	593	2 Q6INM5	Q6INM5 xenopus lae
27	55	62.5	481	2 Q6N097	Q6N097 homo sapien
28	53	60.2	464	2 Q6MZU6	Q6MZU6 homo sapien
29	53	60.2	597	2 Q6EBB9	Q6EBB9 homo sapien
30	52.5	57.7	122	1 HV3A_HUMAN	P01762 homo sapien
31	52	59.1	115	1 HV3F_HUMAN	P01767 homo sapien

32	52	59.1	466	2 Q6IN78	Q6IN78 homo sapien
33	52	59.1	475	2 Q6MZQ6	Q6MZQ6 homo sapien
34	52	59.1	493	2 Q6GMX2	Q6GMX2 homo sapien
35	50	56.8	114	1 HV3B_HUMAN	P01763 homo sapien
36	50	56.8	119	2 Q920E7	Q920E7 mus musculi
37	50	56.8	196	2 Q6SZL8	Q6SZL8 mus musculi
38	50	56.8	585	2 Q6GPX4	Q6GPX4 xenopus lae
39	49	55.7	71	2 Q6GJ71	Q6GJ71 salmo trutt
40	49	55.7	87	2 Q9AV03	Q9AV03 oryza sativ
41	49	55.7	98	1 HV57_MOUSE	P18528 mus musculi
42	49	55.7	117	1 HV3C_HUMAN	P01764 homo sapien
43	49	55.7	480	2 Q6N094	Q6N094 homo sapien
44	49	55.7	1048	1 YC81_METTA	Q56777 methanococc
45	48.5	55.1	247	2 Q9VZF9	Q9VZF9 drosophila

ALIGNMENTS

```
RESULT 1
Q9UL93      PRELIMINARY; PRT; 116 AA.
ID   Q9UL93
AC   Q9UL93;
DT   01-MAY-2000 (TREMBLrel. 13, Created)
DT   01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.N.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; RAD56257.1; -.
DR   PIR; P1644; P1644.
DR   HSSP; P01772; 2PB4.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PSS0835; IG_LIKE; 1.
FT   NON_TER
FT   NON_TER
SQ   SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match      93.2%; Score 82; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY   1 IISYDGSKKYYADSVKG 17
DB   49 VISYDGSNKKYYADSVKG 65

RESULT 2
Q6SZC9      PRELIMINARY; PRT; 240 AA.
ID   Q6SZC9
AC   Q6SZC9;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
DE   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bipartite diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; IG_v.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 240;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 3
Q9WUK1 PRELIMINARY; PRT; 613 AA.
AC Q9WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martuna K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomihyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Kravinski M.I., Skalska V., Smalios D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; P36005; P36005.
DR PIR; G36005; G36005.
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DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSSP; P01861; IADO.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 613;
Best Local Similarity 88.2%; Pred. No. 6.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 IISYDGSKKYYADSVKG 17
Db 69 VISYDGSNKYYADSVKG 85

RESULT 4
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSSP; P01772; ZPB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12437 MW; ED57PDD19086D07F CRC64;

Query Match 84.1%; Score 74; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 IISYDGSKKYYADSVKG 17
Db 51 IRYDGSNKYYADSVKG 66

RESULT 5
HV3G HUMAN STANDARD; PRT; 122 AA.
ID HV3G HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-II region CAM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81013859; PubMed=6774332;
 RA Lehman D.W., Putnam F.W.;
 RT "Amino acid sequence of the variable region of a human mu chain:
 RT location of a possible JH segment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
 CC -1- MISCELLANEOUS: This mu chain was isolated from the plasma of a
 CC patient with macroglobulinemia.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02051; M3HUM.
 DR HSSP; P01772; 2F94.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region;
 KW Pyrolydione carboxylic acid.
 FT DOMAIN 1 112 Ig-like.
 FT MOD_RES 1 1 Pyrolydione carboxylic acid.
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
 Query Match 84.1%; Score 74; DB 1; Length 122;
 Best Local Similarity 70.6%; Pred. No. 0.0024;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVYKG 17
 Db 50 VISYGBBKYYABSVYKG 66
 RESULT 6
 OGN093 PRELIMINARY; PRT; 417 AA.
 AC QGN093.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686i04196 (Fragment).
 GN Name=DKFZp686i04196;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BX640623; CA645777.1; -.
 DR HSSP; P01861; 1AD0.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IGV; 2.
 DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 417 AA; 46061 MW; C4518B844CFB883C CRC64;
 Query Match 80.7%; Score 71; DB 2; Length 417;
 Best Local Similarity 70.6%; Pred. No. 0.0029;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVYKG 17
 Db 22 VIAYDGSYYADSVYKG 38
 RESULT 7
 O68CN4 PRELIMINARY; PRT; 493 AA.
 ID O68CN4
 AC O68CN4.
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFZp686E23209 (Fragment).
 GN Name=DKFZp686E23209;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Rectum tumor;
 RG The German cDNA Consortium;
 RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; CR749861; CAH18705.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IGV; 2.
 DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 493 AA; 54117 MW; A1B4F5ED3FA6AB40 CRC64;
 Query Match 79.5%; Score 70; DB 2; Length 493;
 Best Local Similarity 70.6%; Pred. No. 0.0052;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVYKG 17
 Db 92 VISYGBBKYYABSVYKG 108
 RESULT 8
 O9Y509 PRELIMINARY; PRT; 147 AA.
 ID O9Y509
 AC O9Y509.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VHS3 protein (Fragment).
 GN Name=VHS3;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vesco R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
R Lichtenstein A.K., Benson J.R.;
RT "A CD10-positive population of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1348-1353(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01842; 1AOK.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 76.4%; Score 69; DB 2; Length 147;
Best Local Similarity 76.5%; Pred. No. 0.002;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 IISYDGSKKYYADSVKG 17
DB 50 LISTDGSSTOYAGSVKG 66

RESULT 9
Q72351 PRELIMINARY; PRT; 482 AA.
AC Q72351
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
GN Name=DKFZp686N02209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Bloecher W., Newes H.W., Weil B., Amid C., Oeanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 482;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
DB 69 VISTDGNHKLXSDSVKG 85

RESULT 10
Q8NCL6 PRELIMINARY; PRT; 493 AA.

AC Q8NCL6;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein FJ991070.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074651; BAC11114.1; -.
DR HSSP; P01876; 1OW0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 493;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 IISYDGSKKYYADSVKG 17
DB 69 LIWYDGRKTYSDSVKG 85

RESULT 11
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 75.0%; Score 66; DB 2; Length 122;
Best Local Similarity 61.2%; Pred. No. 0.0053;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ISYDSSKKYVADSVKG 17
| | | | |
Db 51 ISNDGSKNFYVADSVKG 66

RESULT 12

HV3L HUMAN STANDARD; PRT; 119 AA.

AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_Taxid=9606;

SEQUENCE

RP MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.S.V., Low T.L.K.;
RT "Primary structure of a human IgM immunoglobulin. IV. Streptococcal
RT IgM1 protease, digestion, Fab and Fc fragments, and the complete amino
RT acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02056; A1H0B.

HSSP; P01772; 2FB4.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KM Direct protein sequencing; Glycoprotein; Immunoglobulin V region;

KW Pyrolydione carboxylic acid.

FT DOMAIN 1 112

FT MOD_RES 1 1

FT DISULFID 22 96

FT CARBOHYD 28 28

FT NON_TER 119 119

SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match

Best Local Similarity 70.6%; Score 65; DB 1; Length 119;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 IISYDSSKKYVADSVKG 17
: | | | | |
Db 50 LISYGSBZYVADSVKG 66

RESULT 13

Q9ULB6 PRELIMINARY; PRT; 95 AA.

AC Q9ULB6; (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_Taxid=9606;

SEQUENCE FROM N.A.

Tange Y., Kayano H.;

Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

EMBL; AB035268; BAA87067.1; -.

PIR; PH0872; PH0872.

DR PIR; S36280; S36280.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1 1

FT NON_TER 95 95

SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D2574A CRC64;

Query Match

Best Local Similarity 72.7%; Score 64; DB 2; Length 95;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISYDSSKKYVADSVKG 17
| | | | |
Db 50 IKDSEKRYVADSVKG 65

RESULT 14

HV3L HUMAN STANDARD; PRT; 122 AA.

AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region GA.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_Taxid=9606;

SEQUENCE.

RP MEDLINE=74175307; PubMed=420843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RT Biochemistry 13:2482-2498(1974).
CC -I- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02052; M3HGA.

HSSP; P01772; 2FB4.

DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region;

KW Pyrolydione carboxylic acid.

FT DOMAIN 1 112

FT MOD_RES 1 1

FT DISULFID 122 122

SQ SEQUENCE 122 AA; 13166 MW; 74E5B695E84100A CRC64;

Query Match

Best Local Similarity 72.7%; Score 64; DB 1; Length 122;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IISYDSSKKYVADSVKG 17
: | | | | |
Db 50 VISYGBZVYVADSVKG 66

RESULT 15

Q6PJA4 PRELIMINARY; PRT; 470 AA.

AC Q6PJA4; (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)


```

DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EFSDB CRC64;

Query Match 70.5%; Score 62; DB 2; Length 121;
Best Local Similarity 64.7%; Pred. No. 0.024;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IISYGSKKYYADSVKG 17
Db 50 VIVYNGSRTYYGDSVKG 66

RESULT 20
Q6N092 PRELIMINARY; PRT; 519 AA.
ID Q6N092
AC Q6N092;
DT 05-JUL-2004 (TRENBLrel. 27, Last Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686K18196 (Fragment).
GN Name=DKFZp686K18196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wandt R., Heubner D., Mewes H.W., Well B., Amid C., Oeanger A.,
RA Fodo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640624; CAE45778.1; -.
DR HSSP; P01842; IAK.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003597; IG_Cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 519 AA; 56423 MW; F839EF7F811B88D CRC64;

Query Match 70.5%; Score 62; DB 2; Length 519;
Best Local Similarity 78.6%; Pred. No. 0.12;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YDGSKKYYADSVKG 17
Db 96 FDGSNNYYADSVKG 109

RESULT 21
Q9UL71 PRELIMINARY; PRT; 121 AA.
ID Q9UL71
AC Q9UL71;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

```

```

DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01852; INF.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 121
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CFPA5D50736 CRC64;

Query Match 69.3%; Score 61; DB 2; Length 121;
Best Local Similarity 70.6%; Pred. No. 0.036;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IISYGSKKYYADSVKG 17
Db 50 LISGDSGTTYADSVKG 66

RESULT 22
Q6P395 PRELIMINARY; PRT; 544 AA.
ID Q6P395
AC Q6P395;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuk S., Caraminci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunarene P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman W., Nadeau A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;

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RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019046; AAH19046.1; -.
 DR HSSP: P01861; IADQ.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF07654; C1-sec; 3.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; IGC1; 3.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; Ig_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match 69.3%; Score 61; DB 2; Length 544;
 Best Local Similarity 70.6%; Pred. No. 0.19;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IISYDSKKYVADSVKG 17
 Db 69 VFSTYDSDDKYVAAVKG 85

RESULT 23
 ID Q9UL72 PRELIMINARY; PRT; 118 AA.
 AC Q9UL72;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernex S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035042; AAD56278.1; -.
 DR PIR: S21205; S21205.
 DR HSSP: P01783; IIGC.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12872 MW; BAD1A5944B2D5CCA CRC64;

Query Match 68.2%; Score 60; DB 2; Length 118;
 Best Local Similarity 62.5%; Pred. No. 0.051;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ISYDSKKYVADSVKG 17
 Db 50 VTYSGGSSYVADSVKG 65

RESULT 24
 ID HV05 CARAU STANDARD; PRT; 116 AA.
 AC P19181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5A precursor.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88144476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Warr G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 RT and family relationships of two genes and a pseudogene in a teleost
 RT fish";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 DR HSSP: P01783; IIGC.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 19
 FT CHAIN 20 116 Ig heavy chain V region 5A.
 FT DOMAIN 20 49 Framework-1.
 FT DOMAIN 50 54 Complementarity-determining-1.
 FT DOMAIN 55 68 Framework-2.
 FT DOMAIN 69 84 Complementarity-determining-2.
 FT DOMAIN 85 116 Framework-3.
 FT DISULFID 41 114 By similarity.
 FT NON_TER 116
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 63.6%; Score 56; DB 1; Length 116;
 Best Local Similarity 62.5%; Pred. No. 0.24;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDSKKYVADSVKG 17
 Db 69 VTYSGGSSYVADSVKG 84

RESULT 25
 ID HV3K HUMAN STANDARD; PRT; 126 AA.
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig heavy chain V-II region KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marquart M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 RT and 1.0-A resolution";
 RL J. Mol. Biol. 141:369-391(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02055; G1HOKL.
 DR PDB: 2FB4; X-ray; H=1-126.
 DR PDB: 2IG2; X-ray; H=-.

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DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; P:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW Pyroglutamate carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RSS 1 112 Pyroglutamate carboxylic acid.
FT DISULFID 22 96
FT STRAND 105 110
FT STRAND 3 7
FT STRAND 11 12
FT STRAND 14 15
FT STRAND 18 25
FT STRAND 29 31
FT STRAND 34 39
FT STRAND 41 42
FT STRAND 45 51
FT STRAND 53 54
FT STRAND 58 60
FT STRAND 62 64
FT HELIX 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT STRAND 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;

Query Match 63.6%; Score 56; DB 1; Length 126;
Best Local Similarity 70.6%; Pred. No. 0.26;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IISYDGRKKYADSVKG 17
Db 50 IIMDDGSDQHYADSVKG 66

RESULT 26
Q6INM5 PRELIMINARY; PRT; 593 AA.
AC Q6INM5;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE MG659066 protein.
GN Name=MG659066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RT Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strauberg R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072253; AAH72253.1; -.
DR HSSP; P01842; IAOK.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR001680; WD40.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 4.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
SQ SEQUENCE 593 AA; 65874 MW; BB314FF921E12FC CRC64;

Query Match 63.6%; Score 56; DB 2; Length 593;
Best Local Similarity 68.8%; Pred. No. 1.4;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGRKKYADSVKG 17
Db 68 INPDGSGTYADSVKG 83

RESULT 27
Q6N097 PRELIMINARY; PRT; 481 AA.
AC Q6N097;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686H20196.
GN Name=DKFZp686H20196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wandert R., Heubner D., Mewes H.W., Well B., Amid C., Oanger A.,
RA Fodor G., Han W., Wiemann S.;
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RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640619; CAB45773.1; -.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG_1like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52759 MW; 4722009E64BDF988 CRC64;

Query Match 62.5%; Score 55; DB 2; Length 481;
 Best Local Similarity 68.8%; Pred. No. 1.6;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
 Db 70 ISPDGSKYYARVYKG 85

RESULT 28
 06MZU6 PRELIMINARY; PRT; 464 AA.
 AC 06MZU6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686C15213.
 GN Name=DKFZp686C15213;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Human rectum tumor;
 RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amid C., Oeanger A.,
 RA Robo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640874; CAB45931.1; -.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG_1like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 60.2%; Score 53; DB 2; Length 464;
 Best Local Similarity 73.3%; Pred. No. 3.4;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SYDGSKKYYADSVKG 17
 Db 72 SRGGSYYEYADSVKG 86

RESULT 29
 096BB9

ID 096BB9 PRELIMINARY; PRT; 597 AA.
 AC 096BB9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHM protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feinberg E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski J., Smallos D.E., Scheraga J.E.,
 RA Jones S.J., Mair M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Tissue=Primary B-Cells;
 RA Straubeberg R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1; -.
 DR PIR; S05271; S05271.
 DR PIR; S24260; S24260.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3ADBCE263D9 CRC64;

Query Match 60.2%; Score 53; DB 2; Length 597;
 Best Local Similarity 68.8%; Pred. No. 4.5;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
 Db 70 ISGSGSYYADSVKG 85

RESULT 30
 HV3A_HUMAN STANDARD; PRT; 122 AA.
 ID HV3A_HUMAN
 AC P01762;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-III region TRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN TRO).
RX MEDLINE=76023781; PubMed=809331;
RA Kratzin H., Altevogt P., Ruban E., Kortt A., Starescuk K.,
Hiltschman N.;
RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro),
RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
RT structure of the complete IgA-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC -1- MISCELLANEOUS: The sequence of the C region is also given.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02045; A1HTR.
DR HSSP; P01783; 11GC.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR POSITE; PS50835; IG LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 108
FT MOD_RSS 1 1 Pyroliidone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13472 MW; 2821A11DA04D80F9 CRC64;
Query March 59.7%; Score 52.5; DB 1; Length 122;
Best Local Similarity 63.2%; Pred. No. 0.96;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;
Qy 2 ISY---DGSKKRYADSVKG 17
Db 48 VSYIGSGSSTLYVADSVKG 66
RESULT 31
HVA3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG heavy chain V-III region BJT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: The sequence of the alpha-2, A2m(2) allotype, C
CC region of this myeloma protein is also given.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02050; A2HUBU.
DR HSSP; P01783; 11GC.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR POSITE; PS50835; IG LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 111
FT NON_TER 115 115 Ig-like.

SO SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCFA CRC64;
Query Match 59.1%; Score 52; DB 1; Length 115;
Best Local Similarity 71.4%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 YDGSKKRYADSVKG 17
Db 52 YRGGTYVADSVKG 65
RESULT 32
O61N78 PRELIMINARY; PRT; 466 AA.
ID O61N78;
AC O61N78;
DT 05-JUL-2004 (TRENBERL 27, Created)
DT 05-JUL-2004 (TRENBERL 27, Last sequence update)
DT 05-JUL-2004 (TRENBERL 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Mullaby S.J.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalins D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; IADQ.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG CI.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF07654; CI-sec; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00406; IGV; 1.
DR POSITE; PS50835; IG LIKE; 4.
DR POSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDB81076E CRC64;
Query Match 59.1%; Score 52; DB 2; Length 466;
Best Local Similarity 62.5%; Pred. No. 5;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 2 ISYDGSKKRYADSVKG 17

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Db          69 VLYTGATYYADSVKG 84

RESULT 33
Q6MZ06      PRELIMINARY; PRT; 475 AA.
AC Q6MZ06;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein DKFP686G1190.
GN Name=DKFP686G1190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
  Han M., Wiemann S.;
RL EMBL; BX640947; CAE45972.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1ike.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match          59.1%; Score 52; DB 2; Length 475;
Best Local Similarity 68.8%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ISYDSKKYADSVKG 17
Db          70 ISSGVNTYYADSVKG 85

RESULT 34
Q6GMX2      PRELIMINARY; PRT; 493 AA.
AC Q6GMX2;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL EMBL; BC073771; AAH73771.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 52865 MW; 55B99305B286203 CRC64;

Query Match          59.1%; Score 52; DB 2; Length 493;
Best Local Similarity 68.8%; Pred. No. 5.4;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDSKKYADSVKG 17
Db          70 INSDGSTSYADSVKG 85

RESULT 35
HV3B_HUMAN  STANDARD; PRT; 114 AA.
ID HV3B_HUMAN
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
  (protein WEA) with antibody activity against 3,4-pyruvylated galactose
  in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
  against 3,4-pyruvylated galactose and isolated from a patient with
  Waldenstrom's macroglobulinemia.
CC -1- SIMILARITY: Contains 1 immunoglobulin-1like domain.
CC PIR; A02046; M3H06.
DR HSSP; P01772; 2FP4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez A.C., Skalkida J., Schmutz J., Myers R.M., Butterfield Y.S.,
  Krzywinski M.I., Skalkida J., Smalins D.E., Schnerch A., Schein J.E.,
  Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
  and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL EMBL; BC073771; AAH73771.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 52865 MW; 55B99305B286203 CRC64;

Query Match          59.1%; Score 52; DB 2; Length 493;
Best Local Similarity 68.8%; Pred. No. 5.4;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDSKKYADSVKG 17
Db          70 INSDGSTSYADSVKG 85

RESULT 35
HV3B_HUMAN  STANDARD; PRT; 114 AA.
ID HV3B_HUMAN
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
  (protein WEA) with antibody activity against 3,4-pyruvylated galactose
  in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
  against 3,4-pyruvylated galactose and isolated from a patient with
  Waldenstrom's macroglobulinemia.
CC -1- SIMILARITY: Contains 1 immunoglobulin-1like domain.
CC PIR; A02046; M3H06.
DR HSSP; P01772; 2FP4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.

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DR Pfam: PF00047; Ig; 1..
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 112 Ig-like.
FT NON_TER 1 114 Pyrolydione carboxylic acid.
SQ SEQUENCE 114 AA; 12256 MW; D88294F8A18A07B7 CRC64;

Query Match 56.8%; Score 50; DB 1; Length 114;
Best Local Similarity 68.8%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDGSKKYVADSVKG 17
Db 51 IGGSGSYTYYPDSYVG 66

RESULT 36
Q920E7 PRELIMINARY; PRT; 119 AA.
ID Q920E7
AC Q920E7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotypic heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AL09421.1; -.
DR PIR; C25913; C25913.
DR HSSP; P01783; IIGC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 119
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 13025 MW; FEE904044381CA7C CRC64;

Query Match 56.8%; Score 50; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 2.5;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDGSKKYVADSVKG 17
Db 51 IGGSGSYTYYPDSYVG 66

RESULT 37
O65ZL8 PRELIMINARY; PRT; 196 AA.
ID O65ZL8
AC O65ZL8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Vh7183-DSP2-JH3-CH1 protein (Fragment).
GN Name=Vh7183-DSP2-JH3-CH1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c;
RA MEDLINE=95362300; PubMed=7635518;
RA Komori T., Sugiyama H.;
RA "An aberrant splicing using a 3' cryptic splice site within the CH1
```

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RT exon induces truncated mu-chain production.";
RL Immunology 85:166-170(1995).
DR EMBL; S79401; AAB35023.2; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 196
FT NON_TER 196
SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match 56.8%; Score 50; DB 2; Length 196;
Best Local Similarity 68.8%; Pred. No. 4.2;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDGSKKYVADSVKG 17
Db 70 IGGSGSYTYYPDSYVG 85

RESULT 38
O6GPX4 PRELIMINARY; PRT; 585 AA.
ID O6GPX4
AC O6GPX4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitsuki S., Cacinici P., Prange C.,
RA Baha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Roark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaracne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalka U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL
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DR EMBL; BC072981; AAT72981.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 4.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; Igc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
DR Hypothetical protein.
KW SEQUENCE 585 AA; 64853 MW; 05A3D91B29E566A3 CRC64;

Query Match          56.8%; Score 50; DB 2; Length 585;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YDGSKKYYADSVKG 17
DB 71 YDASKINADSLKG 84

RESULT 39
09GJ71 PRELIMINARY; PRT; 71 AA.
AC 09GJ71;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-JUN-2001 (TREMBLrel. 16, Last sequence update)
DE MHC class II alpha chain (fragment).
GN Name=atr-DAA;
OS Salmo trutta (Brown trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8032;
RN [1]
RP SEQUENCE FROM N.A.
RA Stet R.J.M., Jordan W.C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293950; CAC08187.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 71
SQ SEQUENCE 71 AA; 7699 MW; 0E3D9764E397FF72 CRC64;

Query Match          55.7%; Score 49; DB 2; Length 71;
Best Local Similarity 61.5%; Pred. No. 2.1;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 DGSKKYYADSVKG 17
DB 14 DGEKWTADPTKG 26

RESULT 40
09AV03 PRELIMINARY; PRT; 87 AA.
AC 09AV03; Q7XDS;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein OsJNBa0026012.3.
GN ORFNames=OsJNBa0026012.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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OC Euhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Uterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569 (2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC078829; AAK13161.1; -.
DR EMBL; AB017105; AAP54276.1; -.
DR Gramene; Q7XDS; -.
DR Gramene; Q9AV03; -.
KW Hypothetical protein.
SQ SEQUENCE 87 AA; 10264 MW; B9FE244022DAE718 CRC64;

Query Match          55.7%; Score 49; DB 2; Length 87;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVK 16
DB 9 ISYDGSKKYYADSVK 23

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Search completed: March 31, 2005, 12:09:38
 Job time : 114.057 secs

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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:42:18 ; Search time 85.25 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAPARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	11	3	AAV79070 Anti-fact
2	46	92.0	11	3	AAV79077 Anti-fact
3	37	74.0	408	8	Ad148827 Oil-asso
4	36	72.0	58	4	AAO13448 Human pol
5	36	72.0	652	8	AdS26132 Bacterial
6	36	72.0	652	8	AdS25655 Bacterial
7	36	72.0	655	8	AdS25373 Bacterial
8	36	72.0	656	8	AdS22602 Bacterial
9	35	70.0	708	5	ABR48560 Listeria
10	34	68.0	157	3	AAG18510 Zea may
11	34	68.0	159	3	AAG18509 Zea may
12	34	68.0	180	3	AAV37904 Amino aci
13	34	68.0	231	8	AdS28058 Bacterial
14	34	68.0	237	3	AAAG20306 Arabidops
15	34	68.0	237	3	AAAG51887 Arabidops
16	34	68.0	278	1	AAAP80850 Sequence
17	34	68.0	279	1	AAAP80274 Amino aci
18	34	68.0	279	2	AAAS4838 Thermicas
19	34	68.0	279	2	AAAM00768 Thermicas
20	34	68.0	279	2	AAAM00769 Thermicas
21	34	68.0	279	2	AAAM00774 Thermicas
22	34	68.0	279	2	AAAM00798 Thermicas
23	34	68.0	279	2	AAAM00770 Thermicas
24	34	68.0	279	2	AAAM00775 Thermicas
25	34	68.0	279	2	AAAM00780 Thermicas

26	34	68.0	279	2	AAAM00783 Thermicas
27	34	68.0	279	2	AAAM00792 Thermicas
28	34	68.0	279	2	AAAM00772 Thermicas
29	34	68.0	279	2	AAAM00784 Thermicas
30	34	68.0	279	2	AAAM00793 Thermicas
31	34	68.0	279	2	AAAM00796 Thermicas
32	34	68.0	279	2	AAAM00794 Thermicas
33	34	68.0	279	2	AAAM00785 Thermicas
34	34	68.0	279	2	AAAM00787 Thermicas
35	34	68.0	279	2	AAAM00789 Thermicas
36	34	68.0	279	2	AAAM00799 Thermicas
37	34	68.0	279	2	AAAM00803 Thermicas
38	34	68.0	279	2	AAAM00767 Thermicas
39	34	68.0	279	2	AAAM00771 Thermicas
40	34	68.0	279	2	AAAM00801 Thermicas
41	34	68.0	279	2	AAAM00790 Thermicas
42	34	68.0	279	2	AAAM00788 Thermicas
43	34	68.0	279	2	AAAM00797 Thermicas
44	34	68.0	279	2	AAAM00800 Thermicas
45	34	68.0	279	2	AAAM00800 Thermicas

ALIGNMENTS

RESULT 1
AAV79070
ID AAV79070 standard; peptide; 11 AA.
XX AAV79070;
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
XX
KW Complementarity determining region 3; CDR3; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
PN WO200012562-A1.
PD 09-MAR-2000.
XX
PF 26-AUG-1999; 99WO-US019453.
XX
PR 28-AUG-1998; 98US-0098233P.
PR 03-MAR-1999; 99US-0122767P.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Devaux B, Baton DL, Haase PE, Judice JK, Kirchhofer D;
PI Suggett S;
XX
DR WPI; 2000-256595/22.
XX
PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
PT stroke, and post myocardial infarction.
XX
PS Claim 2; Fig 2; 84pp; English.
XX
CC This sequence represents a complementarity determining region 3 (CDR3) of
CC the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
CC participates in the blood coagulation pathways. The Gla domain of factor
CC IXa and its zymogen factor IX contains important structural determinants
CC for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX
 SQ Sequence 11 AA;

QY Query Match 100.0%; Score 50; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ASIAARVLDY 11
 1 ASIAARVLDY 11

RESULT 2
 AAY79077
 ID AAY79077 standard; peptide; 11 AA.
 XX
 AC AAY79077;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
 XX
 KW Complementarity determining region 3; CDR3; antibody; Gla domain;
 KW factor IX/IXa; blood coagulation; deep venous thrombosis;
 KW arterial thrombosis; unstable angina; post myocardial infarction;
 KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
 XX
 OS Homo sapiens.
 XX
 PN WO200012562-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-US019453.
 XX
 PR 28-AUG-1998; 98US-0098233P.
 PR 03-MAR-1999; 99US-0122767P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CM, Devaux B, Eaton DL, Hase PE, Justice JK, Kirchofer D,
 PI Suggest S;
 XX
 DR WPI; 2000-256595/22.
 XX
 PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 XX
 PS Claim 2; Fig 2; 84pp; English.

CC This sequence represents a complementarity determining region 3 (CDR3) of
 CC the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
 CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 CC participates in the blood coagulation pathways. The Gla domain of factor
 CC IXa and its zymogen factor IX contains important structural determinants
 CC for interaction with high affinity binding sites on vascular endothelial
 CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is

CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX
 SQ Sequence 11 AA;

QY Query Match 92.0%; Score 46; DB 3; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 ASIAARVLDY 11
 1 ASIAARVLDY 11

RESULT 3
 ADJ48827
 ID ADJ48827 standard; protein; 408 AA.
 XX
 AC ADJ48827;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE O11-associated gene related protein #327.
 XX
 KW o11-associated gene; transgenic; enhanced seed oil; vegetable oil.
 XX
 OS Unidentified.
 XX
 PN US2004025202-A1.
 XX
 PD 05-FEB-2004.
 XX
 PF 14-MAR-2003; 2003US-00389566.
 PR 15-MAR-2002; 2002US-0365301P.
 PR 26-JUN-2002; 2002US-0391786P.
 PR 26-JUN-2002; 2002US-0392018P.
 XX
 PA (LAUR/) LAURIE C C.
 PA (RAVA/) RAVANELLO M.
 PA (SAVA/) SAVAGE T.
 PA (LEDE/) LEDEAUX J R.
 PA (ROGE/) ROGERS J A.
 XX
 PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
 XX
 DR WPI; 2004-142683/14.
 XX
 PT Novel recombinant DNA construct comprising a promoter functional in
 PT plants operably linked to an oil-associated gene for producing transgenic
 PT plant seed.
 XX
 PS Example 3; SEQ ID NO 831; 22pp; English.

CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in plants operably linked to an oil-associated gene.
 CC The construct is useful for transgenic plant seed which has in its genome
 CC the construct, that is functional in the plant to transcribe the oil-
 CC associated gene. The transgenic plant seed grows into a plant having
 CC enhanced seed oil as compared to wild type. The construct is useful for
 CC producing hybrid maize seed. The transgenic plant seed is useful for
 CC producing vegetable oil. The present sequence represents the amino acid
 CC sequence of an oil-associated gene related protein.

XX
 SQ Sequence 408 AA;

QY Query Match 74.0%; Score 37; DB 8; Length 408;
 Best Local Similarity 80.0%; Pred. No. 62;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 10
||:|||||
Db 275 ASIAARVLD 284

RESULT 4
AAO13448
ID AAO13448 standard; protein; 58 AA.
XX
XX AAO13448;
AC
XX 06-NOV-2001 (first entry)
DT
XX Human polypeptide SEQ ID NO 27340.
DE
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX MO200164835-A2.
PN
XX 07-SEP-2001.
PD
XX 26-FEB-2001; 2001WO-US004927.
PF
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
PS
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI: 2001-514838/56.
DR N-PSDB; AAI93379.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 27340; 1399pp + Sequence listing; English.
PS
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
XX
SQ Sequence 58 AA;
Query Match 72.0%; Score 36; DB 4; Length 58;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIAARVLDY 11
||:|||||
Db 12 SVAQARVLEY 21

RESULT 5
ADS26132
ID ADS26132 standard; protein; 652 AA.

XX
AC ADS26132;
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Bacterial polypeptide #15165.
DE
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polypeptide.
XX
XX Bacteria.
OS
XX US200333675-A1.
FN
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI
XX WPI: 2004-061375/06.
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 15165; 122pp; English.
PS
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 652 AA;
Query Match 72.0%; Score 36; DB 8; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11

Db 255 AATMAARADY 265

||:||||:|

RESULT 6
ADS25655
ID ADS25655 standard; protein; 652 AA.

XX
XX ADS25655;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #1468.

XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide..

XX
XX Bacteria.

XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.

XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.

XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.

XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.

XX
XX Claim 1; SEQ ID NO 14688; 122pp; English.

XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.

XX
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.

SO Sequence 652 AA;

Query Match 72.0%; Score 36; DB 8; Length 652;
Best Local Similarity 63.6%; Pred. NO. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AATMAARADY 11
||:||||:|

Db 255 AATMAARADY 265

RESULT 7
ADS25373
ID ADS25373 standard; protein; 655 AA.

XX
XX ADS25373;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #14406.

XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.

XX
XX Bacteria.

XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.

XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.

XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.

XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.

XX
XX Claim 1; SEQ ID NO 14406; 122pp; English.

XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.

XX
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactamannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX
SQ Sequence 655 AA;

QY Query Match 72.0%; Score 36; DB 8; Length 655;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 ASIAAARVLDY 11
255 AATAAARAIDY 265

RESULT 8
ID ADS22602 standard; protein; 656 AA.

XX
AC ADS22602;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #11635.

XX
KM Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactamannan;
KM bacterial polypeptide.

XX
OS Bacteria.

XX
PN US200323675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.

XX
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.

XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX
PS Claim 1; SEQ ID NO 11635; 122pp; English.

XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactamannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX
SQ Sequence 656 AA;

QY Query Match 72.0%; Score 36; DB 8; Length 656;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 ASIAAARVLDY 11
255 AATAAARAIDY 265

RESULT 9
ID ABB48560 standard; protein; 708 AA.

XX
AC ABB48560;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1264.

XX
KM Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KM vitamin B12; bacterial infection; disease.

XX
OS Listeria monocytogenes.

XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR001118.
XX
PR 11-APR-2000; 2000FR-00004629.

XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusanok C, Fsihi H, Deboux P;
PI Duesurget O, Cheroutan F, Medjari H, Glaser P, Kunst F, Cossart P;
PI Daniels U, Goebel W, Kreft U, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Trierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland U, Kaerst U, Entian K, Hauf U;
PI Rose M, Voss H;
XX
DR WPI; 2002-010914/01.

XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.

XX
PS Claim 6; SEQ ID NO 1265; 192pp; French.

XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGP-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins

```
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 708 AA;
QY 4 AAARVLDY 11
Db 697 AAARIDY 704
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Query Match 70.0%; Score 35; DB 5; Length 708;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
RESULT 10
ID AAG18510 standard; protein, 157 AA.
XX AAG18510;
XX
XX 17-OCT-2000 (first entry)
DE Zea mays protein fragment SEQ ID NO: 19948.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.
XX Zea mays subsp. mays.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
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XX 23-APR-1999; 99US-0130891P.
XX 26-APR-1999; 99US-0131449P.
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PR 29-SEP-1999; 99US-0156596P.
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Query Match 68.0%; Score 34; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVDY 11
Db 117 AARVDY 123

RESULT 11
AAG18509
ID AAG18509 strand; protein; 159 AA.
XX
AC AAG18509;
XX

DT 17-OCT-2000 (first entry)
XX

DE Zea mays protein fragment SEQ ID NO: 19947.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.

OS Zea mays subsp. mays.
XX

PN EP1033405-A2.
XX

PD 06-SEP-2000.
XX

PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
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PR 09-MAR-1999; 99US-0123548P.
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PR 29-MAR-1999; 99US-0126785P.
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PR 06-APR-1999; 99US-0128234P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 68.0%; Score 34; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
Db 119 AARVLDY 125

RESULT 12
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ID AAV37904 standard; protein, 180 AA.
AC AAV37904;
XX
XX AAV37904;
DT 07-OCT-1999 (first entry)
XX
XX Amino acid sequence of a Chlamydia trachomatis protein.
DE
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; peritphatitits;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis.
XX
XX Chlamydia trachomatis.
OS
XX W09928475-A2.
PN
XX 10-JUN-1999.
PD
XX
XX 27-NOV-1998; 98WO-1B001939.
PF
XX
XX 28-NOV-1997; 97ER-00015041.
PR 17-DEC-1997; 97ER-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX
XX (GEST) GENSET.
PA
XX Griffais R;
PI
XX WPI; 1999-371125/31.
DR
XX
XX Genome sequence of Chlamydia trachomatis.
PT
XX
XX Disclosure; Page 1426; 1755pp; English.
PS
XX
XX AAV37904 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC peritphatitits, Bartholinitis; pneumopathy in breast feeding infants; and
CC venereal lymphogranulomatosis. The polypeptides of the invention may be
CC of use in treating these diseases
XX
XX
SQ Sequence 180 AA;
Qy
Query Match 68.0%; Score 34; DB 2; Length 180;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IAAARVLDY 11
Db 140 IAAARVLDY 148

RESULT 13
ADS28058
ID ADS28058 standard; protein, 231 AA.

XX
AC ADS28058; -
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Bacterial polypeptide #17091.
DE
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
EN
XX
XX 18-DEC-2003.
PD
XX
XX 20-FEB-2003; 2003US-00369493.
PF
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XX 21-FEB-2002; 2002US-0360039P.
PR
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
PI
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PR microbial source, useful for producing plants with improved properties.
XX
XX
PS Claim 1; SEQ ID NO 17091; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX
SQ Sequence 231 AA;
Qy
Query Match 68.0%; Score 34; DB 8; Length 231;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10

Db 100 AT1PAAKLD 109

RESULT 14
AAG20306
ID AAG20306 standard; protein; 237 AA.

XX AAG20306;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 22440.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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XX 05-MAR-1999; 99US-0123180P.
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Query March Best Local Similarity 68.0%; Score 34; DB 3; Length 237;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
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Db 8 AARVLDY 14

RESULT 15
AAG51887
ID AAG51887 standard; protein; 237 AA.

XX XX
AC AAG51887;
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 65899.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
XX Epi1033405-A2.
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XX PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
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XX 23-MAR-1999; 99US-0125788P.
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PR 28-OCT-1999; 99US-0161922P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 68.0%; Score 34; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AARVLDY 11
Db 8 AARVLDY 14

RESULT 16

ID AAR0850 standard; protein: 278 AA.

XX AAR0850;
AC AAR0850;
XX 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 10-SEP-1990 (first entry)
XX

DE Sequence of subtilisin thermilase.
 XX Serine protease TW3; proteinase K; subtilisin thermilase.
 XX Unidentified.
 OS W08807581-A.
 XX
 XX W08807581-A.
 PD 06-OCT-1988.
 XX
 XX 28-MAR-1988; 88WO-US001040.
 PF
 XX 03-APR-1987; 87US-00035816.
 PR
 XX (AMGE-) AMGEN.
 PA
 XX Samal BB, Strabinsky Y;
 PI
 XX WPI; 1988-292865/41.
 DR
 XX
 XX New purified serine protease - isolated from culture medium of fungus
 PT Triticichum album or produced by recombinant DNA techniques.
 PT
 XX Disclosure; Fig 9a-9c; 74pp; English.
 XX
 XX Fig. 9 represents a comparison of the AA sequences of protease TW3 with
 CC those of proteinase K, subtilisin novo, subtilisin Carlsberg, subtilisin
 CC DY and thermilase. The AA sequence of the mature TW3 protein as
 CC determined from the nucleotide sequence has approximately 90% homology
 CC with that of proteinase K. There are certain positions where the TW3 AA
 CC sequence resembles that in subtilisin, but not to proteinase K. For
 CC example, at positions 143, a methionine residue occurs in all subtilisins
 CC as well as in protease TW3, while a leucine residue is present at that
 CC position in proteinase K. Similarly at position 219, an alanine residue
 CC is present in protease TW3 and subtilisin, but not in proteinase K. In
 CC addition, the AA fragment, Ser-Thr-, is absent from proteinase K while
 CC being present in the other enzymes (see AAP80847-49 and AAP80851) at
 CC position 226 and 227. Purified serine protease (SP), can be used in
 CC detergents and cleansers or spot removers, as a depilatory in tanning and
 CC also in the food industry for the prepn. of protein hydrolysates and in
 CC serology for the detection of incomplete antibodies. (Updated on 31-OCT-
 CC 2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX Sequence 278 AA;
 SQ
 Query Match 68.0%; Score 34; DB 1; Length 278;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAAARVLD 10
 DB 96 ASILAARVLD 105
 RESULT 17
 AAP80274
 ID AAP80274 standard; protein; 279 AA.
 XX
 AC AAP80274;
 XX
 XX 27-AUG-2003 (revised)
 DT 10-SEP-1990 (first entry)
 DT
 XX Amino acid sequence of Bacillus thermilase subtilisin.
 DE
 XX Enzyme mutant; catalytic function; Bacillus thermilase subtilisin.
 KW
 XX Bacillus sp.
 OS
 XX W08807578-A.
 PN
 XX 06-OCT-1988.
 PD

XX 30-MAR-1988; 88WO-US001078.
 PF
 XX 02-APR-1987; 87US-00034085.
 PR
 XX (GERTH) GENENTECH INC.
 PA
 XX Wells JA, Carter PJ;
 PI
 XX WPI; 1988-292862/41.
 DR
 XX
 XX Enzyme mutants with modified catalytic functional gp. - react with
 PT modified substrates which contain moiety to complement catalytic
 PT functionality.
 PT
 XX Disclosure; Fig 3b; 90pp; English.
 PS
 XX The patent is for a novel enzyme mutant (EM), not found in nature,
 CC derived by the replacement or modification, in a precursor enzyme, of at
 CC least one catalytic gp. of an amino acid residue which when in contact
 CC with a selected region of a polypeptide substrate, functions
 CC catalytically. The precursor enzyme may be, eg oxido-reductases,
 CC transferases, hydrolases, lyases, isomerases or ligases. EM have a
 CC catalytic preference for substrates which provide the replaced or
 CC modified functional gp. or its equivalent such that the substrate
 CC together with the enzyme mutant assists in its own catalysis. In Fig 3b
 CC B. amyloliquefaciens subtilisin and thermilase are aligned to compare
 CC conserved residues. (Updated on 27-AUG-2003 to correct OS field.)
 CC
 XX Sequence 279 AA;
 SQ
 Query Match 68.0%; Score 34; DB 1; Length 279;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAAARVLD 10
 DB 96 ASILAARVLD 105
 RESULT 18
 AAR54838
 ID AAR54838 standard; protein; 279 AA.
 XX
 AC AAR54838;
 XX
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 11-JAN-1995 (first entry)
 DT
 XX Thermilase (p229X).
 DE
 XX Subtilisin; mutant; variant; enzyme; protease; substrate; thermilase.
 KW
 XX Thermactinomyces vulgaris.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 229 /label= Ala, Leu, Met, Gln, Val, Ser
 FT /note= "pref. Ala"
 FT
 XX US5316941-A.
 PD 31-MAY-1994.
 XX
 XX 29-APR-1992; 92US-00876818.
 PF
 XX 06-JAN-1989; 89US-00294340.
 PR
 XX (GENV) GENENCOR INC.
 PA
 XX Graycar TP, Bott RR, Estell DA, Caldwell RM;
 PI
 XX

DR WPI; 1994-176274/21.

XX New DNA encoding subtilisin mutated at position - producing protease with
PT altered substrate specificity and reactivity.

XX
XX
PS Disclosure; Fig 3b; 13pp; English.

CC DNA encoding subtilisin in which the amino acid equiv. to Pro(225) of B.
CC amyloliquefactors subtilisin has been replaced by Ala, Leu, Met, Gln, Val
CC or Ser (pref. Ala) is claimed. Compared with wild-type subtilisin, the
CC variants have different catalytic and/or Michaelis constants, i.e.
CC different substrate reactivity and/or specificity, partic. at least a 2-
CC fold increase or decrease in the kcat/Km ratio. Changing Pro to Ala gives
CC a mutant enzyme with greater activity for ester as opposed to amide
CC substrates. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

XX
XX
SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 19
AAW00768
ID AAW00768 standard; protein; 279 AA.

XX
AC AAW00768;
XX
XX 20-NOV-1996 (first entry)

XX
DT
DE Thermilase G206N.

XX
XX Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT 66..73
FT Region /note= "loop 1"
FT 103..115
FT Region /note= "loop 2"
FT 134..141
FT Region /note= "loop 3"
FT 162..171
FT Region /note= "loop 4"
FT 191..195
FT Region /note= "loop 5"
FT 204..224
FT Region /note= "loop 6"
FT Misc-difference 206
FT /note= "G206N"

XX
FN W09628558-A1.

XX
PD 19-SEP-1996.

XX
PF 06-MAR-1996; 96WO-US003009.

XX
PR 09-MAR-1995; 95US-00401573.

XX
XX (PROC) PROCTER & GAMBLE CO.

XX
XX Brode PF, Barnett BL, Rubingh DN;

DR WPI; 1996-433830/43.

XX
XX New thermilase variants, partic. for cleaning compans. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.

XX
XX
PS Example 7; Page 7; 159pp; English.

CC AAW00766-W00803 represent thermilase variants of the invention.
CC Thermilase is a protease. These sequences are based on the wild type
CC Bacillus thermilase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermilase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermilase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermilase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates

SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 20
AAW00769
ID AAW00769 standard; protein; 279 AA.

XX
AC AAW00769;
XX
XX 20-NOV-1996 (first entry)

XX
DT
DE Thermilase T11N.

XX
XX Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT 66..73
FT Region /note= "loop 1"
FT 103..115
FT Region /note= "loop 2"
FT 111
FT Misc-difference 111
FT /note= "T11N"
FT 134..141
FT Region /note= "loop 3"
FT 162..171
FT Region /note= "loop 4"
FT 191..195
FT Region /note= "loop 5"
FT 204..224
FT Region /note= "loop 6"

XX
FN W09628558-A1.

```

XX 19-SEP-1996.
PD 06-MAR-1996; 96MO-US003009.
XX 09-MAR-1995; 95US-00401573.
XX (PROC ) PROCTER & GAMBLE CO.
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX
XX New thermilase variants, partic. for cleaning compsns. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 13; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermilase variants of the invention.
CC Thermilase is a protease. These sequences are based on the wild type
CC Bacillus thermilase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermilase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermilase in the catalytically productive adsorption of the enzyme
CC therefore have a significant effect on this adsorption. The thermilase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
XX Sequence 279 AA;
SQ
Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1 ASIAARVLD 10
Db 96 ASIAARVLD 105

RESULT 21
AAM00774
ID AAM00774 standard; protein; 279 AA.
XX
XX AAM00774;
AC
XX
XX 20-NOV-1996 (first entry)
DT
XX
XX Thermilase Y210G, T212P, P214G, S222D.
DB
XX
XX Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
XX subtilisin; cleaning composition; proteinaceous stain removal;
XX hard surface cleaning; dishwashing composition; oral cleaning;
XX denture cleaning; contact lens cleaning; fabric cleaner.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX FT 66..73
XX FT /note= "loop 1"
XX FT 103..115
XX FT /note= "loop 2"
XX FT 134..141
XX FT Region

```

```

FT FT /note= "loop 3"
FT FT 162..171
FT FT /note= "loop 4"
FT FT 191..195
FT FT /note= "loop 5"
FT FT 204..224
FT FT /note= "loop 6"
FT FT /note= "Y210G"
FT FT /note= "T212P"
FT FT /note= "P214G"
FT FT /note= "S222D"
FT FT
XX
XX W09628558-A1.
XX
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96MO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX
XX New thermilase variants, partic. for cleaning compsns. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 25; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermilase variants of the invention.
CC Thermilase is a protease. These sequences are based on the wild type
CC Bacillus thermilase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermilase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermilase in the catalytically productive adsorption of the enzyme
CC therefore have a significant effect on this adsorption. The thermilase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
XX Sequence 279 AA;
SQ
Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1 ASIAARVLD 10
Db 96 ASIAARVLD 105

RESULT 22
AAM00798
ID AAM00798 standard; protein; 279 AA.
XX
XX AAM00798;
AC
XX
XX

```

DT 20-NOV-1996 (first entry)
 XX Thermiltase Y218A.
 XX Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FT 66..73
 FT Region /note= "loop 1"
 FT 103..115
 FT Region /note= "loop 2"
 FT 134..141
 FT Region /note= "loop 3"
 FT 162..171
 FT Region /note= "loop 4"
 FT 191..195
 FT Region /note= "loop 5"
 FT 204..224
 FT Region /note= "loop 6"
 FT Misc-difference 218
 FT /note= "Y218A"
 FT
 XX
 XX W09628558-A1.
 XX 19-SEP-1996.
 XX
 XX 06-MAR-1996; 96WO-US003009.
 XX
 XX 09-MAR-1995; 95US-00401573.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 XX Brode PF, Barnett BL, Rubingh DN;
 XX WPI; 1996-433830/43.
 XX
 XX New thermiltase variants; partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 XX Example 71; Page ?; 159pp; English.
 XX
 CC AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 CC
 XX Sequence 279 AA;
 SO

Query Match 68.0%; Score 34; DB 2; Length 279;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 ||| |||
 Db 96 ASIILAVRVD 105
 RESULT 23
 ID AAM00770 standard; protein; 279 AA.
 XX AAM00770;
 XX
 AC 20-NOV-1996 (first entry)
 DT
 XX Thermiltase T217G + S222E.
 DE
 XX Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FT 66..73
 FT Region /note= "loop 1"
 FT 103..115
 FT Region /note= "loop 2"
 FT 134..141
 FT Region /note= "loop 3"
 FT 162..171
 FT Region /note= "loop 4"
 FT 191..195
 FT Region /note= "loop 5"
 FT 204..224
 FT Region /note= "loop 6"
 FT Misc-difference 217
 FT /note= "T217G"
 FT Misc-difference 222
 FT /note= "S222E"
 FT
 XX
 XX W09628558-A1.
 XX 19-SEP-1996.
 XX
 XX 06-MAR-1996; 96WO-US003009.
 XX
 XX 09-MAR-1995; 95US-00401573.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 XX Brode PF, Barnett BL, Rubingh DN;
 XX WPI; 1996-433830/43.
 XX
 XX New thermiltase variants; partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 XX Example 13; Page ?; 159pp; English.
 XX
 CC AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase

CC variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. These sequences have decreased adsorption to insoluble substrates, thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;
SQ
Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1 ASIAARVLD 10
||| |||
Db 96 ASILAVRLD 105

RESULT 24
AAW00775
ID AAW00775 standard; protein; 279 AA.
XX AAW00775;
XX 20-NOV-1996 (first entry)
XX Thermittase T195P.
XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermittase; hygiene;
XX subtilisin; cleaning composition; proteinaceous stain removal;
XX hard surface cleaning; dishwashing composition; oral cleaning;
XX denture cleaning; contact lens cleaning; fabric cleaner.

XX Synthetic.

XX Key Location/Qualifiers
XX Region 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT Misc-difference 195
FT /note= "T195P"
FT 204..224
FT Region /note= "loop 6"

XX W09628558-A1.

XX 19-SEP-1996.

XX 06-MAR-1996; 96WO-US003009.

XX 09-MAR-1995; 95US-00401573.

XX (PROC) PROCTER & GAMBLE CO.

XX Brode PF, Barnett BL, Rudinigh DN;

XX WPI; 1996-433830/43.

XX New thermittase variants, partic. for cleaning compens. - having amino
XX acid substns. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.

XX Example 29; Page 7; 159pp; English.

XX AAW00766-W00803 represent thermittase variants of the invention.
XX Thermittase is a protease. These sequences are based on the wild type

CC Bacillus thermittase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermittase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermittase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermittase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;
SQ
Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1 ASIAARVLD 10
||| |||
Db 96 ASILAVRLD 105

RESULT 25
AAW00780
ID AAW00780 standard; protein; 279 AA.

XX AAW00780;
XX 20-NOV-1996 (first entry)
XX Thermittase Y213S, T217G, G223E.

XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermittase; hygiene;
XX subtilisin; cleaning composition; proteinaceous stain removal;
XX hard surface cleaning; dishwashing composition; oral cleaning;
XX denture cleaning; contact lens cleaning; fabric cleaner.

XX Synthetic.

XX Key Location/Qualifiers
XX Region 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT 204..224
FT Region /note= "loop 6"
FT Misc-difference 213
FT /note= "Y213S"
FT Misc-difference 217
FT /note= "T217G"
FT Misc-difference 223
FT /note= "G223E"

XX W09628558-A1.

XX 19-SEP-1996.

XX 06-MAR-1996; 96WO-US003009.

XX 09-MAR-1995; 95US-00401573.

```

XX (PROC ) PROCTER & GAMBLE CO.
PA Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX New thermaltase variants, partic. for cleaning compans. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
PS Example 37; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermaltase variants of the invention.
CC Thermaltase is a protease. These sequences are based on the wild type
CC Bacillus thermaltase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermaltase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermaltase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermaltase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
SQ Sequence 279 AA;
XX
XX Query Match 68.0%; Score 34; DB 2; Length 279;
XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 ASIAAARVLD 10
Db 96 ASIAAARVLD 105
XX
RESULT 26
AAM00783 ID AAM00783 standard; protein; 279 AA.
XX
AC AAM00783;
XX
DT 20-NOV-1996 (first entry)
XX
DE Thermaltase N66S, S70E, G72N.
XX
XX Thermaltase; hydrolysis; enzyme; protease; Bacillus thermaltase; hygiene;
KM subtilisin; cleaning composition; proteinaceous stain removal;
KM hard surface cleaning; dishwashing composition; oral cleaning;
KM denture cleaning; contact lens cleaning; fabric cleaner.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 66..73
FT /note= "loop 1"
FT Misc-difference 66
FT /note= "specified as N66S, but the mutation should
FT actually be Q66S, as elsewhere in the specification
FT residue 66 is specified as Q"
FT Misc-difference 70
FT /note= "specified as S70E, but the mutation should
FT actually be G70E, as elsewhere in the specification
FT residue 70 is specified as G"
FT Misc-difference 72

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FT /note= "G72N"
FT Region 103..115
FT /note= "loop 2"
FT Region 134..141
FT /note= "loop 3"
FT Region 162..171
FT /note= "loop 4"
FT Region 191..195
FT /note= "loop 5"
FT Region 204..224
FT /note= "loop 6"
XX
XX W09628558-A1.
XX
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX
XX New thermaltase variants, partic. for cleaning compans. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 45; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermaltase variants of the invention.
CC Thermaltase is a protease. These sequences are based on the wild type
CC Bacillus thermaltase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermaltase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermaltase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermaltase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning,
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
SQ Sequence 279 AA;
XX
XX Query Match 68.0%; Score 34; DB 2; Length 279;
XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 ASIAAARVLD 10
Db 96 ASIAAARVLD 105
XX
RESULT 27
AAM00792 ID AAM00792 standard; protein; 279 AA.
XX
AC AAM00792;
XX
DT 20-NOV-1996 (first entry)
XX
DE Thermaltase I209A, A219B.
XX

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KM Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
 KM subtilisin; cleaning composition; proteolaceous stain removal;
 KM hard surface cleaning; dishwashing composition; oral cleaning;
 KM denture cleaning; contact lens cleaning; fabric cleaner.

OS Synthetic.

XX Key Location/Qualifiers
 FH Region 66..73
 FT /note= "loop 1"

FT Region 103..115
 FT /note= "loop 2"

FT Region 134..141
 FT /note= "loop 3"

FT Region 162..171
 FT /note= "loop 4"

FT Region 191..195
 FT /note= "loop 5"

FT Region 204..224
 FT /note= "loop 6"

FT Misc-difference 209
 FT /note= "I209A"

FT Misc-difference 219
 FT /note= "A219P"

XX WO9628558-A1.

PD 19-SEP-1996.

XX 06-MAR-1996; 96WO-US003009.

XX 09-MAR-1995; 95US-00401573.

XX (PROC) PROCTER & GAMBLE CO.

XX Brode PF, Barnett BL, Rubingh DN;

XX WPI; 1996-433830/43.

XX New thermilase variants, partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.

XX Example 60; Page ?; 159pp; English.

XX AA00766-W00803 represent thermilase variants of the invention.

XX Thermilase is a protease. These sequences are based on the wild type
 CC Bacillus thermilase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermilase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermilase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermilase
 CC variants can be used in cleaning compositions for proteolaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; length 279;

Best local similarity 80.0%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 ||| |||

DB 96 ASIAARVLD 105

RESULT 28

AA00772 ID AA00772 standard; protein; 279 AA.

XX AA00772;

DT 20-NOV-1996 (first entry)

XX Thermilase S207E, Y210S, G223N.

XX Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
 KM subtilisin; cleaning composition; proteolaceous stain removal;
 KM hard surface cleaning; dishwashing composition; oral cleaning;
 KM denture cleaning; contact lens cleaning; fabric cleaner.

XX Synthetic.

XX Key Location/Qualifiers
 FH Region 66..73
 FT /note= "loop 1"

FT Region 103..115
 FT /note= "loop 2"

FT Region 134..141
 FT /note= "loop 3"

FT Region 162..171
 FT /note= "loop 4"

FT Region 191..195
 FT /note= "loop 5"

FT Region 204..224
 FT /note= "loop 6"

FT Misc-difference 207
 FT /note= "S207E"

FT Misc-difference 210
 FT /note= "Y210S"

FT Misc-difference 223
 FT /note= "G223N"

XX WO9628558-A1.

PD 19-SEP-1996.

XX 06-MAR-1996; 96WO-US003009.

XX 09-MAR-1995; 95US-00401573.

XX (PROC) PROCTER & GAMBLE CO.

XX Brode PF, Barnett BL, Rubingh DN;

XX WPI; 1996-433830/43.

XX New thermilase variants, partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.

XX Example 19; Page ?; 159pp; English.

XX AA00766-W00803 represent thermilase variants of the invention.

XX Thermilase is a protease. These sequences are based on the wild type
 CC Bacillus thermilase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermilase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermilase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermilase

CC variants can be used in cleaning compositions for protease stain removal. The variants can be used in hard surface cleaning compositions, CC dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. CC These sequences have decreased adsorption to insoluble substrates. CC thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
||| |||
96 ASIAPARVLD 105

Db 96 ASIAPARVLD 105

RESULT 29
AAW00784 standard; protein; 279 AA.

XX AAW00784;
XX 20-NOV-1996 (first entry)
XX Thermolase S109E, T113G.
XX Thermolase; hydrolysis; enzyme; protease; Bacillus thermolase; hygiene;
KM subtilisin; cleaning composition; protease; stain removal;
KM hard surface cleaning; dishwashing composition; oral cleaning;
KM denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.

XX OS
XX Key Location/Qualifiers
XX Region 66..73
XX /note= "loop 1"
XX Region 103..115
XX /note= "loop 2"
XX Misc-difference 109
XX /note= "S109E"
XX Misc-difference 113
XX /note= "T113G"
XX Region 134..141
XX /note= "loop 3"
XX Region 162..171
XX /note= "loop 4"
XX Region 191..195
XX /note= "loop 5"
XX Region 204..224
XX /note= "loop 6"

XX PN W09628558-A1.
XX 19-SEP-1996.
XX 06-MAR-1996; 96WO-US003009.
XX 09-MAR-1995; 95US-00401573.
XX (PROC) PROCTER & GAMBLE CO.
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI, 1996-433830/43.
XX New thermolase variants, partic. for cleaning compns. - having amino
XX acid substns. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.
XX Example 46; Page 7; 159pp; English.

CC AAW00766-W00803 represent thermolase variants of the invention.
CC Thermolase is a protease. These sequences are based on the wild type
CC Bacillus thermolase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermolase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermolase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermolase
CC variants can be used in cleaning compositions for protease stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates.
CC thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
||| |||
96 ASIAPARVLD 105

Db 96 ASIAPARVLD 105

RESULT 30
AAW00793 standard; protein; 279 AA.

XX AAW00793;
XX 20-NOV-1996 (first entry)
XX Thermolase L216N.
XX Thermolase; hydrolysis; enzyme; protease; Bacillus thermolase; hygiene;
KM subtilisin; cleaning composition; protease; stain removal;
KM hard surface cleaning; dishwashing composition; oral cleaning;
KM denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.

XX OS
XX Key Location/Qualifiers
XX Region 66..73
XX /note= "loop 1"
XX Region 103..115
XX /note= "loop 2"
XX Region 134..141
XX /note= "loop 3"
XX Region 162..171
XX /note= "loop 4"
XX Region 191..195
XX /note= "loop 5"
XX Region 204..224
XX /note= "loop 6"

XX PN W09628558-A1.
XX 19-SEP-1996.
XX 06-MAR-1996; 96WO-US003009.
XX 09-MAR-1995; 95US-00401573.
XX /note= "specified as L216N, but the mutation should
XX actually be S216N, as elsewhere in the specification
XX residue 216 is specified as S"

XX (PROC) PROCTER & GAMBLE CO.
 PA Brode PF, Barnett BL, Rubingh DN;
 PI WPI; 1996-433830/43.
 XX
 DR New thermatase variants, partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 PS Example 60; Page 7; 159pp; English.
 XX
 CC AAM00766-W00803 represent thermatase variants of the invention.
 CC Thermatase is a protease. These sequences are based on the wild type
 CC Bacillus thermatase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermatase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermatase in the catalytically productive adsorption of the enzyme
 CC therefore have a significant effect on this adsorption. The thermatase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 XX
 SQ Sequence 279 AA;
 QY Query Match 68.0%; Score 34; DB 2; Length 279;
 Db Best Local Similarity 80.0%; Pred. NO. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAARVLD 10
 Db 96 ASIAARVLD 105
 XX
 XX RESULT 31
 XX AAM00796
 XX ID AAM00796 standard; protein; 279 AA.
 XX AC AAM00796;
 XX 20-NOV-1996 (first entry)
 XX DE Thermatase S109E.
 XX
 XX Thermatase; hydrolysis; enzyme; protease; Bacillus thermatase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 XX Synthetic.
 XX OS
 XX Key Location/Qualifiers
 XX FT 66.73
 XX FT Region /note= "loop 1"
 XX FT 103.115
 XX FT Region /note= "loop 2"
 XX FT Misc-difference 109
 XX FT /note= "S109E"
 XX FT 134.141
 XX FT Region /note= "loop 3"
 XX FT 162.171
 XX FT Region /note= "loop 4"
 XX FT 191.195
 XX FT Region

FT /note= "loop 5"
 FT Region 204.224
 FT /note= "loop 6"
 XX
 XX W09628558-A1.
 XX
 XX PD 19-SEP-1996.
 XX
 XX PD 06-MAR-1996; 96WO-US003009.
 XX
 XX PD 09-MAR-1995; 95US-00401573.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 XX Brode PF, Barnett BL, Rubingh DN;
 XX WPI; 1996-433830/43.
 XX
 XX New thermatase variants, partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 PS Example 67; Page 7; 159pp; English.
 XX
 CC AAM00766-W00803 represent thermatase variants of the invention.
 CC Thermatase is a protease. These sequences are based on the wild type
 CC Bacillus thermatase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermatase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermatase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermatase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 XX
 SQ Sequence 279 AA;
 QY Query Match 68.0%; Score 34; DB 2; Length 279;
 Db Best Local Similarity 80.0%; Pred. NO. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAARVLD 10
 Db 96 ASIAARVLD 105
 XX
 XX RESULT 32
 XX AAM00794
 XX ID AAM00794 standard; protein; 279 AA.
 XX AC AAM00794;
 XX 20-NOV-1996 (first entry)
 XX DE Thermatase W112C, T217G.
 XX
 XX Thermatase; hydrolysis; enzyme; protease; Bacillus thermatase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 XX Synthetic.
 XX OS
 XX Key Location/Qualifiers
 XX FT

CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 34
AAW00785
ID AAW00785 standard; protein: 279 AA.

AC AAW00785;

DT 20-NOV-1996 (first entry)

DE Thermitase G135Q, V138D, G139S.

XX
XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermitase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.

OS Synthetic.

XX
FH Key Location/Qualifiers

FT Region 66..73

FT Region /note= "loop 1"

FT Region 103..115

FT Region /note= "loop 2"

FT Region 134..141

FT Region /note= "loop 3"

FT Misc-difference 135

FT Misc-difference 138 /note= "G135Q"

FT Misc-difference 139 /note= "V138D"

FT Misc-difference 139 /note= "G139S"

FT Region 162..171

FT Region /note= "loop 4"

FT Region 191..195

FT Region /note= "loop 5"

FT Region 204..224

FT Region /note= "loop 6"

XX
PN W09628558-A1.

XX
PD 19-SEP-1996.

XX
PF 06-MAR-1996; 96WO-US003009.

XX
PR 09-MAR-1995; 95US-00401573.

XX
PA (PROC) PROCTER & GAMBLE CO.

XX
PI Brode PF, Barnett BL, Rubingh DN;

XX
DR WPI; 1996-433830/43.

XX
PT New thermitase variants, partic. for cleaning compns. - having amino

XX
PT acid substns. to provide decreased adsorption to and increased hydrolysis

XX
PT of bound substrates.

XX
PS Example 47; Page 7; 159pp; English.

XX
CC AAW00766-W00803 represent thermitase variants of the invention.

XX
CC Thermitase is a protease. These sequences are based on the wild type

CC Bacillus thermitase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermitase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermitase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermitase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 35

AAW00787
ID AAW00787 standard; protein: 279 AA.

AC AAW00787;

DT 20-NOV-1996 (first entry)

DE Thermitase S191E, S192D, F193D, T195P.

XX
XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermitase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.

OS Synthetic.

XX
FH Key Location/Qualifiers

FT Region 66..73

FT Region /note= "loop 1"

FT Region 103..115

FT Region /note= "loop 2"

FT Region 134..141

FT Region /note= "loop 3"

FT Region 162..171

FT Region /note= "loop 4"

FT Region 191..195

FT Region /note= "loop 5"

FT Misc-difference 191 /note= "S191E"

FT Misc-difference 192 /note= "S192D"

FT Misc-difference 193 /note= "F193D"

FT Misc-difference 195 /note= "T195P"

FT Region 204..224

FT Region /note= "loop 6"

XX
PN W09628558-A1.

XX
PD 19-SEP-1996.

XX
PF 06-MAR-1996; 96WO-US003009.

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XX 09-MAR-1995; 95US-00401573.
PR (PROC ) PROCTER & GAMBLE CO.
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI, 1996-433830/43.
XX New thermatase variants, partic. for cleaning compns. - having amino
PT acid subunits. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 48; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermatase variants of the invention.
CC Thermatase is a protease. These sequences are based on the wild type
CC Bacillus thermatase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermatase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermatase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermatase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
CC
XX Sequence 279 AA;
SQ
Query March 68.04; Score 34; DB 2; Length 279;
Best Local Similarity 80.04; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASIAAARVLD 10
Db 96 ASIILAVRLD 105
RESULT 36
AAM00789 standard; protein; 279 AA.
ID AAM00789;
AC AAM00789;
XX 20-NOV-1996 (first entry)
DT
XX Thermatase N68D, V138D, A164G, A168E, T217G.
DE
XX Thermatase; hydrolysis; enzyme; protease; Bacillus thermatase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 66..73
XX /note= "loop 1"
XX
XX Misc-difference 68
XX /note= "specified as N68D, but the mutation should
XX actually be G68D, as elsewhere in the specification
XX residue 68 is specified as G"
XX 103..115
XX /note= "loop 2"
XX 134..141
XX Region

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FT /note= "loop 3"
FT Misc-difference 138
FT /note= "V138D"
FT Region 162..171
FT /note= "loop 4"
FT Misc-difference 164
FT /note= "A164G"
FT Misc-difference 168
FT /note= "A168E"
FT Region 191..195
FT /note= "loop 5"
FT Region 204..224
FT /note= "loop 6"
FT Misc-difference 217
FT /note= "T217G"
FT
XX
XX W09628558-A1.
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX (PROC ) PROCTER & GAMBLE CO.
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI, 1996-433830/43.
XX
XX New thermatase variants, partic. for cleaning compns. - having amino
PT acid subunits. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 53; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermatase variants of the invention.
CC Thermatase is a protease. These sequences are based on the wild type
CC Bacillus thermatase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermatase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermatase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermatase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
CC
XX Sequence 279 AA;
SQ
Query March 68.04; Score 34; DB 2; Length 279;
Best Local Similarity 80.04; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASIAAARVLD 10
Db 96 ASIILAVRLD 105
RESULT 37
AAM00799 standard; protein; 279 AA.
ID AAM00799;
XX AAM00799;
XX

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DT 20-NOV-1996 (first entry)
 XX Thermiltase A164H, S220E.
 XX
 KW Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 PT Region 66..73
 FT /note= "loop 1"
 PT Region 103..115
 FT /note= "loop 2"
 PT Region 134..141
 FT /note= "loop 3"
 PT Region 162..171
 FT /note= "loop 4"
 PT Misc-difference 164
 FT /note= "A164H"
 FT Region 191..195
 FT /note= "loop 5"
 PT Region 204..224
 FT /note= "loop 6"
 PT Misc-difference 220
 FT /note= "S220E"
 XX
 XX WO9628558-A1.
 PD 19-SEP-1996.
 XX
 PF 06-MAR-1996; 96WO-US003009.
 XX
 XX 09-MAR-1995; 95US-00401573.
 XX
 PA (PROC) PROCTER & GAMBLE CO.
 XX
 PI Brode PF, Barnett BL, Rubingh DN;
 XX
 DR WPI; 1996-433830/43.
 XX
 PT New thermiltase variants, partic. for cleaning compns. - having amino
 PT acid substs. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 XX Example 75; Page ?; 159pp; English.
 PS
 XX
 CC AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 CC
 XX Sequence 279 AA;
 SQ
 Query Match 68.0%; Score 34; DB 2; Length 279;
 Best local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ASIAARVLD 10
 ||| |||
 Db 96 ASIARVLD 105
 RESULT 38
 AAM00803
 ID AAM00803 standard; protein; 279 AA.
 XX
 AC AAM00803;
 XX
 DT 20-NOV-1996 (first entry)
 XX
 DE Thermiltase L221Q.
 XX
 KW Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 PT Region 66..73
 FT /note= "loop 1"
 PT Region 103..115
 FT /note= "loop 2"
 PT Region 134..141
 FT /note= "loop 3"
 PT Region 162..171
 FT /note= "loop 4"
 FT Region 191..195
 FT /note= "loop 5"
 FT Region 204..224
 FT /note= "loop 6"
 PT Misc-difference 221
 FT /note= "L221Q"
 XX
 XX WO9628558-A1.
 EN
 XX
 PD 19-SEP-1996.
 XX
 PF 06-MAR-1996; 96WO-US003009.
 XX
 XX 09-MAR-1995; 95US-00401573.
 XX
 PA (PROC) PROCTER & GAMBLE CO.
 XX
 PI Brode PF, Barnett BL, Rubingh DN;
 XX
 DR WPI; 1996-433830/43.
 XX
 PT New thermiltase variants, partic. for cleaning compns. - having amino
 PT acid substs. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 XX Example 91; Page ?; 159pp; English.
 PS
 XX
 CC AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase

CC variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. CC These sequences have decreased adsorption to insoluble substrates, thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
DB 96 ASIAAARVLD 105

RESULT 39
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AC AAW00767;
XX 20-NOV-1996 (first entry)
DT Thermittase Q66N.
XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermittase; hygiene;
KM subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.
OS
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FH Key Location/Qualifiers
FT 66..73
FT /note= "loop 1"
FT Misc-difference 66
FT /note= "Q66N"
FT 103..115
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FT 134..141
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FT /note= "loop 5"
FT 204..224
FT /note= "loop 6"
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XX WO9628558-A1.
XX 19-SEP-1996.
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XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;
XX
XX WPI; 1996-433830/43.
XX
XX New thermittase variants, partic. for cleaning compns. - having amino
PT acid subunits, to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 7; Page 7; 159pp; English.
XX
XX AAW00766-W00803 represent thermittase variants of the invention.
CC Thermittase is a protease. These sequences are based on the wild type

CC Bacillus thermittase subtilisin sequence, which is specified but not given in the specification (there are no sequences given in their entirety in the specification). The variant sequences have one or more substitutions in one or more of the six loop regions of the thermittase sequence. The CC loop regions play a significant role in the adsorption of the enzyme molecule to a surface-bound peptide. The amino acids of the loop regions, CC make contact with any surface to which the molecule is exposed. The CC proximity of the loop regions to the active site and binding pocket of the thermittase in the catalytically productive adsorption of the enzyme CC to the surface bound molecule. Mutations in the loop regions will CC therefore have a significant effect on this adsorption. The thermittase CC variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. CC These sequences have decreased adsorption to insoluble substrates, thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
DB 96 ASIAAARVLD 105

RESULT 40
AAW00771 standard; protein; 279 AA.
AC AAW00771;
XX 20-NOV-1996 (first entry)
DT Thermittase G139N.
XX
XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermittase; hygiene;
KM subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT Misc-difference 139
FT /note= "G139N"
FT 162..171
FT /note= "loop 4"
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FT 204..224
FT /note= "loop 6"
XX
XX WO9628558-A1.
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;

XX WPI; 1996-433830/43.

DR
XX New thermilase variants, partic. for cleaning compns. - having amino
PT acid suberns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.

XX
PS Example 19; Page ?; 159pp; English.

XX
CC AAW00766-W00803 represent thermilase variants of the invention.
CC Thermilase is a protease. These sequences are based on the wild type
CC Bacillus thermilase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermilase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermilase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermilase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX

SO Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAPARVLD 10
||| |
Db 96 ASILAVRVLD 105

Search completed: March 31, 2005, 12:02:29
Job time : 86.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:44 ; Search time 21.4844 Seconds
(without alignment)
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Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAAKVLVDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	11	US-09-383-667-12	Sequence 12, Appl
2	46	92.0	11	US-09-383-667-19	Sequence 19, Appl
3	36	72.0	755	US-09-342-648-2	Sequence 2, Appl
4	34	68.0	278	US-08-865-203-6	Sequence 6, Appl
5	34	68.0	278	US-07-849-420-6	Sequence 6, Appl
6	34	68.0	278	US-09-253-854-6	Sequence 6, Appl
7	34	68.0	278	US-08-955-424-6	Sequence 6, Appl
8	34	68.0	279	US-09-135-658-4	Sequence 4, Appl
9	34	68.0	279	US-09-512-251A-6	Sequence 6, Appl
10	34	68.0	279	US-09-515-150A-6	Sequence 6, Appl
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28	31	62.0	177	3	US-08-821-324-38	Sequence 38, Appl
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31	31	62.0	177	3	US-09-106-582-38	Sequence 38, Appl
32	31	62.0	177	3	US-09-106-582-55	Sequence 55, Appl
33	31	62.0	177	4	US-09-159-469-38	Sequence 38, Appl
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36	31	62.0	177	4	US-09-693-542-55	Sequence 55, Appl
37	31	62.0	243	4	US-09-270-767-45191	Sequence 45191, A
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ALIGNMENTS

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RESULT 1
US-09-383-667-12
; Sequence 12, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camella W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip B.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 12
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; TYPE: PRT
; ORGANISM: Homo sapiens
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; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Db 1 ASIAAAKVLVDY 11
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; Sequence 19, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camella W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip B.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2

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; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
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; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-19

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Best Local Similarity 90.9%; Pred. No. 0.0013;
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Db      1 ASIAAGRVLDY 11

RESULT 3
US-09-342-648-2
; Sequence 2, Application US/09342648
; Patent No. 6248584
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Ode11, Joan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Transcription Coactivators
; FILE REFERENCE: BB-1169-B
; CURRENT APPLICATION NUMBER: US/09/342,648
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,659
; EARLIER FILING DATE: July 13, 1998
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 755
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (179)
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; LOCATION: (241)
US-09-342-648-2

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Db      240 AXIADTRLVDY 250

RESULT 4
US-08-865-203-6
; Sequence 6, Application US/08865203
; Patent No. 5935815
; GENERAL INFORMATION:
; APPLICANT: van de Ven, Willem Jan Marie
; APPLICANT: van den Ouweland, Anna Maria Wilhelmina
; APPLICANT: Van Duijnhoven, Johannes Lambertus Petrus
; APPLICANT: Robroek, Antonius Johannes Maria
; APPLICANT: Koning, Piet Nico Maria
; TITLE OF INVENTION: Pharmaceutical Composition Having An
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; TITLE OF INVENTION: Endoproteolytic Activity; A Process for
; TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
; TITLE OF INVENTION: Proteins And For The (Micro)Biological
; TITLE OF INVENTION: Production Of Proteins
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOFFMANN & BARON, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; FILING DATE: 29-MAY-1997
; APPLICATION NUMBER: US/08/865,203
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Tran, Jessica H.
; REGISTRATION NUMBER: 40,846
; REFERENCE/DOCKET NUMBER: 294-41 DIV II
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-865-203-6

Query Match      68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ASIAARVLD 10
Db      96 ASILAARVLD 105

RESULT 5
US-07-849-420-6
; Sequence 6, Application US/07849420
; Patent No. 5989856
; GENERAL INFORMATION:
; APPLICANT: van de Ven, Willem Jan Marie
; APPLICANT: van den Ouweland, Anna Maria Wilhelmina
; APPLICANT: Van Duijnhoven, Johannes Lambertus Petrus
; APPLICANT: Robroek, Antonius Johannes Maria
; APPLICANT: Koning, Piet Nico Maria
; TITLE OF INVENTION: Pharmaceutical Composition Having An
; TITLE OF INVENTION: Endoproteolytic Activity; A Process for
; TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
; TITLE OF INVENTION: Proteins And For The (Micro)Biological
; TITLE OF INVENTION: Production Of Proteins
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,420
FILING DATE: 19920624
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Moran, Thomas F.
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 2805/41413
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9550
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-849-420-6

Query Match 68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
Db 96 ASILAVRLD 105

RESULT 6

US-09-253-854-6
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Patent No. 6132717
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: Van Duijnoven, Johannes Lambertus Petrus;
APPLICANT: Robroek, Antonius Johannes Maria; and
APPLICANT: Konig, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity; A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HOPFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,854
FILING DATE: Unassigned
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II/CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
TELEX:
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-253-854-6

Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
Db 96 ASILAVRLD 105

RESULT 7

US-08-955-424-6
Sequence 6, Application US/08955424
Patent No. 6274365
GENERAL INFORMATION:
APPLICANT: Van de Ven, Willem Jan Marie
APPLICANT: Van den Ouweland, Anna Maria Wilhelmina
APPLICANT: Van Duijnoven, Johannes Lambertus Petrus
APPLICANT: Konig, Piet Nico Maria
APPLICANT: Robroek, Antonius Johannes Maria
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION HAVING AN ENDOPEPTOLYTIC
TITLE OF INVENTION: ACTIVITY; A PROCESS FOR ENDOPEPTOLYTICALLY PROCESSING
TITLE OF INVENTION: (PRECURSOR) PROTEINS AND FOR THE (MICRO) BIOLOGICAL
TITLE OF INVENTION: SEQUENCE LISTINGS 1-12 294-41 DIV/FWC
FILE REFERENCE: SEQUENCE LISTINGS 1-12 294-41 DIV/FWC
CURRENT APPLICATION NUMBER: US/08/955,424
CURRENT FILING DATE: 1997-10-22
EARLIER APPLICATION NUMBER: 08/568,152
EARLIER FILING DATE: 1995-06-12
EARLIER APPLICATION NUMBER: 07/849,420
EARLIER FILING DATE: 1992-06-24
EARLIER APPLICATION NUMBER: PCT/NL90/00151
EARLIER FILING DATE: 1990-10-21
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 278
TYPE: PRT
ORGANISM: Thermactinomyces vulgaris
US-08-955-424-6

Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
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Db 96 ASILAVRLD 105

RESULT 8

US-09-135-658-4
Sequence 4, Application US/09135658
Patent No. 5972683
GENERAL INFORMATION:
APPLICANT: Tsai, Ying-Chieh
TITLE OF INVENTION: MUTANT TYPE SUBSTITUTED YAB AND ITS APPLICATION
FILE REFERENCE: 6653-011-999
CURRENT APPLICATION NUMBER: US/09/135,658
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 86112766
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 4
LENGTH: 279

TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-135-658-4

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
Db 96 ASIAPARVLD 105

RESULT 9
US-09-512-251A-6
Sequence 6, Application US/09512251A
Patent No. 655315
GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5349, 204-US
CURRENT APPLICATION NUMBER: US/09/512,251A
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent version 3.1
SEQ ID NO 6
LENGTH: 279
TYPE: PRT
ORGANISM: Bacillus
US-09-512-251A-6

Query Match 68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
Db 96 ASIAPARVLD 105

RESULT 10
US-09-515-150A-6
Sequence 6, Application US/09515150A
Patent No. 6558938
GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5348, 204-US
CURRENT APPLICATION NUMBER: US/09/515,150A
CURRENT FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent version 3.1
SEQ ID NO 6
LENGTH: 279
TYPE: PRT
ORGANISM: Bacillus
US-09-515-150A-6

Query Match 68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
Db 96 ASIAPARVLD 105

RESULT 11
US-09-196-281-9
Sequence 9, Application US/09196281A
Patent No. 6605458
GENERAL INFORMATION:
APPLICANT: Hansen, Peter K.
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
TITLE OF INVENTION: Protease Variants And Compositions
FILE REFERENCE: 5435, 200-US
CURRENT APPLICATION NUMBER: US/09/196,281A
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: 1332/97
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 279
TYPE: PRT
ORGANISM: Bacillus
US-09-196-281-9

Query Match 68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
Db 96 ASIAPARVLD 105

RESULT 12
5472855-6
Patent No. 5472855
APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
FILING DATE: 22-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 90, 902
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: 823, 039
FILING DATE: 14-JAN-1992
APPLICATION NUMBER: 35, 652
FILING DATE: 06-APR-1987
APPLICATION NUMBER: 334, 081
FILING DATE: 04-APR-1989
APPLICATION NUMBER: 127, 134
FILING DATE: 01-DEC-1987
APPLICATION NUMBER: 846, 627
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 858, 594
FILING DATE: 30-APR-1986
APPLICATION NUMBER: 614, 612
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614, 615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614, 617
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614, 491
FILING DATE: 29-MAY-1984
SEQ ID NO: 6
LENGTH: 279
5472855-6

Query Match 68.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10

Db 96 ASILAVRLD 105

RESULT 13

5472855-6
; Patent No. 5472855
; APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
; TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,964
; FILING DATE: 22-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 90,902
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 823,039
; FILING DATE: 14-JAN-1992
; APPLICATION NUMBER: 35,652
; FILING DATE: 06-APR-1987
; APPLICATION NUMBER: 334,081
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: 127,134
; FILING DATE: 01-DEC-1987
; APPLICATION NUMBER: 846,627
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 858,594
; FILING DATE: 30-APR-1986
; APPLICATION NUMBER: 614,612
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,615
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,617
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,491
; FILING DATE: 29-MAY-1984
; SEQ ID NO: 6:
; LENGTH: 279
5472855-6

Query Match 66.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASILAVRLD 10
Db 96 ASILAVRLD 105

RESULT 14

US-09-698-286A-10
; Sequence 10, Application US/09698286A
; Patent No. 6677442
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; TITLE OF INVENTION: Human REV1 Gene and Protein As Diagnostic, Preventive, and Therap
; FILE REFERENCE: 050228-0247
; CURRENT APPLICATION NUMBER: US/09/698,286A
; FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,140
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 85
; TYPE: PRT
; ORGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (17)-(22)
; OTHER INFORMATION: Gap in alignment
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (50)-(60)

; OTHER INFORMATION: Gap in alignment
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (30)-(33)
; OTHER INFORMATION: Gap in alignment
US-09-698-286A-10

Query Match 66.0%; Score 33; DB 4; Length 85;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SIARVLDY 11
Db 71 SIARVLDY 80

RESULT 15

US-09-710-279-622
; Sequence 622, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-622

Query Match 66.0%; Score 33; DB 4; Length 194;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIARVLDY 11
Db 106 NVASASVDY 115

RESULT 16

US-09-134-001C-3417
; Sequence 3417, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3417
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3417

Query Match 66.0%; Score 33; DB 3; Length 223;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIIMARVLDY 11
DB 135 NVASASVLDY 144

RESULT 17

US-09-248-796A-18164
; Sequence 18164, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18164
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18164

Query Match 66.0%; Score 33; DB 4; Length 331;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIIMARVLD 10
DB 262 ASVAIAAKVME 271

RESULT 18

US-09-489-039A-12051
; Sequence 12051, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12051
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12051

Query Match 66.0%; Score 33; DB 4; Length 364;
Best Local Similarity 54.5%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIIMARVLDY 11
DB 220 ASVACPSILDY 230

RESULT 19

US-09-602-787A-508
; Sequence 508, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Mark
; APPLICANT: Krüger, Burkhard

APPLICANT: Sch"der, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberkauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
FILE REFERENCE: BGI-125CD
CURRENT APPLICATION NUMBER: US/09/602,787A
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USN 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932182.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932190.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932191.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932229.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932927.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940830.0
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940833.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941395.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942077.7
PRIOR FILING DATE: 1999-09-03

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; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 508
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-508

Query Match      66.0%; Score 33; DB 4; Length 402;
Best Local Similarity 63.6%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 ASIAARVLDY 11
Db      260 ASIAPAAIADY 270

RESULT 20
US-09-540-236-3193
; Sequence 3193, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3193
; LENGTH: 867
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-3193

Query Match      66.0%; Score 33; DB 4; Length 867;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      2 SIAARVLDY 11
Db      439 SVADARVWDF 448

RESULT 21
US-09-902-540-16309
; Sequence 16309, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902.540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16309
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16309

Query Match      66.0%; Score 33; DB 4; Length 910;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
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```
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      2 SIAARVLDY 11
Db      844 NVAAIRVYDY 853

RESULT 22
US-09-252-991A-17003
; Sequence 17003, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17003
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17003

Query Match      64.0%; Score 32; DB 4; Length 234;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      3 IAAARVLD 10
Db      9 ISAAARVLD 16

RESULT 23
US-09-724-797-34
; Sequence 34, Application US/09724797
; Patent No. 6733998
; GENERAL INFORMATION:
; APPLICANT: Jon S. THORSON
; TITLE OF INVENTION: MICROMONOPORA ECHINOSPORA GENES
; TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
; FILE REFERENCE: 2653-40
; CURRENT APPLICATION NUMBER: US/09/724.797
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/111,325
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Bacteria
US-09-724-797-34

Query Match      64.0%; Score 32; DB 4; Length 280;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      4 AAARVLDY 11
Db      8 AAARVLDY 15

RESULT 24
US-09-252-991A-31470
; Sequence 31470, Application US/09252991A
; Patent No. 6551795
```

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 31142
SEQ ID NO 31470
LENGTH: 480
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31470

Query Match 64.0%; Score 32; DB 4; Length 480;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
||:|||||
Db 236 ASVLDARELDY 246

RESULT 25
US-09-902-540-10906
Sequence 10906, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(115849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10906
LENGTH: 111
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-10906

Query Match 62.0%; Score 31; DB 4; Length 111;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
||:|||||
Db 40 AARLDY 46

RESULT 26
US-08-975-762-38
Sequence 38, Application US/08975762
Patent No. 6207169
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington

TREATMEN

COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,762
FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Entlichia
US-08-975-762-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
||:|||||
Db 23 AGWLAKVLDY 33

RESULT 27
US-08-975-762-55
Sequence 55, Application US/08975762
Patent No. 6207169
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,762
FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:

TREATMEN

LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-762-55

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 28
US-08-821-324-38
; Sequence 38, Application US/08821324
; Patent No. 6231869
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821.324
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31.392
; REFERENCE/DOCKET NUMBER: 210121.439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Ehrlichia

US-08-821-324-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 29
US-09-295-028-38
; Sequence 38, Application US/09295028
; Patent No. 6277381

; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; FILE REFERENCE: 210121.439C4
; CURRENT APPLICATION NUMBER: US/09/295.028
; CURRENT FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; TYPE: PRT
; LENGTH: 177
; ORGANISM: Ehrlichia sp.
US-09-295-028-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 30
US-09-295-028-55
; Sequence 55, Application US/09295028
; Patent No. 6277381
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; FILE REFERENCE: 210121.439C4
; CURRENT APPLICATION NUMBER: US/09/295.028
; CURRENT FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-295-028-55

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 31
US-09-106-582-38
; Sequence 38, Application US/09106582
; Patent No. 6306402
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

THERAPY

COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,582
FILING DATE: 29-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-106-582-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 32
US-09-106-582-55
Sequence 55, Application US/09106582
Patent No. 6306402
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,582
FILING DATE: 29-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:

LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-582-55

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 33
US-09-159-469-38
Sequence 38, Application US/09159469
Patent No. 6607728
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,469
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/106,582
FILING DATE: 29-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-159-469-38

Query Match 62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

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RESULT 34
US-09-159-469-55
; Sequence 55, Application US/09159469
; Patent No. 6607728
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY OF EHRlichia INFECTION
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/159,469
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/106,582
; FILING DATE: 29-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-159-469-55

Query Match      62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy      1 ASIAARVLDY 11
Db      23 AGMLAKVLD 33

RESULT 35
US-09-693-542-38
; Sequence 38, Application US/09693542
; Patent No. 6673356
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF EHRlichia INFECTION
; FILE REFERENCE: 210121.439C6
; CURRENT APPLICATION NUMBER: US/09/693,542
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 177
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; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-693-542-38

Query Match      62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy      1 ASIAARVLDY 11
Db      23 AGMLAKVLD 33

RESULT 36
US-09-693-542-55
; Sequence 55, Application US/09693542
; Patent No. 6673356
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF EHRlichia INFECTION
; FILE REFERENCE: 210121.439C6
; CURRENT APPLICATION NUMBER: US/09/693,542
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-693-542-55

Query Match      62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy      1 ASIAARVLDY 11
Db      23 AGMLAKVLD 33

RESULT 37
US-09-270-767-45191
; Sequence 45191, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45191
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45191

Query Match      62.0%; Score 31; DB 4; Length 243;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      3 IAAARVLDY 11
Db      204 LPAARVLDY 212

RESULT 38
US-09-066-046-22
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; Sequence 22, Application US/09066046A
; Patent No. 6204252
; GENERAL INFORMATION:
; APPLICANT: MURPHY, Cheryl
; STOREY, James
; BELTZ, Gerald A.
; COUGHLIN, Richard T.
; TITLE OF INVENTION: CHARACTERIZATION OF GRANULOCYTIC
; EHRlichIA AND METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,046A
; FILING DATE: 24-Apr-1998
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 106,941.155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-066-046-22
Query Match 62.0%; Score 31; DB 3; Length 264;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASIAARVLDY 11
Db 20 AGMLAAKVLDF 30
RESULT 39
US-09-252-991A-32574
; Sequence 32574, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32574
; LENGTH: 338
; TYPE: PRT
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32574
Query Match 62.0%; Score 31; DB 4; Length 338;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 AARVLDY 11
Db 137 AARVLDY 143
RESULT 40
US-09-252-991A-28830
; Sequence 28830, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28830
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28830
Query Match 62.0%; Score 31; DB 4; Length 374;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASIAAARVL 9
Db 235 AATAAARLL 243
Search completed: March 31, 2005, 12:13:26
Job time : 22.484 secs
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GenCore version 5.1.6
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OM protein - protein search, using 8w model

Run on: March 31, 2005, 12:10:00 ; Search time 61.5312 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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- 19: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	74.0	408	15	US-10-389-566-831
2	37	74.0	573	15	US-10-425-114-45544
3	37	74.0	1203	16	US-10-437-963-120758
4	36	72.0	652	15	US-10-369-493-14688
5	36	72.0	652	15	US-10-369-493-15165
6	36	72.0	655	15	US-10-369-493-14406
7	36	72.0	656	15	US-10-369-493-11635
8	36	72.0	1064	16	US-10-437-963-189048
9	35	70.0	45	16	US-10-437-963-201347
10	35	70.0	107	16	US-10-437-963-175236
11	34	68.0	198	16	US-10-767-701-38882
12	34	68.0	231	15	US-10-369-493-17091
13	34	68.0	279	14	US-10-336-324-6

14	34	68.0	279	14	US-10-403-105-9	Sequence 9, Appl1
15	34	68.0	642	16	US-10-767-701-45651	Sequence 45651, A
16	34	68.0	671	15	US-10-369-493-7093	Sequence 7093, Ap
17	34	68.0	674	15	US-10-369-493-4338	Sequence 4338, Ap
18	34	68.0	691	15	US-10-425-114-70274	Sequence 70274, A
19	34	68.0	827	16	US-10-437-963-146706	Sequence 146706,
20	34	68.0	1000	16	US-10-437-963-122779	Sequence 122779,
21	33	66.0	204	14	US-10-238-075-276	Sequence 276, App
22	33	66.0	274	14	US-10-032-585-7697	Sequence 7697, Ap
23	33	66.0	299	15	US-10-425-114-40808	Sequence 40808, A
24	33	66.0	331	14	US-10-156-761-8701	Sequence 8701, Ap
25	33	66.0	358	15	US-10-282-122A-62045	Sequence 62045, A
26	33	66.0	358	15	US-10-282-122A-63923	Sequence 63923, A
27	33	66.0	367	15	US-10-282-122A-62857	Sequence 62857, A
28	33	66.0	367	15	US-10-282-122A-64830	Sequence 64830, A
29	33	66.0	402	9	US-10-627-476-508	Sequence 508, App
30	33	66.0	449	15	US-09-738-626-6555	Sequence 6555, Ap
31	33	66.0	453	15	US-10-369-493-21054	Sequence 21054, A
32	33	66.0	466	16	US-10-437-963-136788	Sequence 136788,
33	33	66.0	469	15	US-10-417-700A-49	Sequence 49, Appl
34	33	66.0	509	15	US-10-282-122A-77407	Sequence 77407, A
35	33	66.0	670	15	US-10-369-493-11847	Sequence 11847, A
36	33	66.0	867	15	US-10-282-122A-63141	Sequence 63141, A
37	33	66.0	1958	14	US-10-152-886-53	Sequence 53, Appl
38	32	64.0	144	15	US-10-425-114-53118	Sequence 53118, A
39	32	64.0	146	15	US-10-425-114-53613	Sequence 53613, A
40	32	64.0	220	16	US-10-437-963-107871	Sequence 107871,
41	32	64.0	221	16	US-10-437-963-187946	Sequence 187946,
42	32	64.0	342	15	US-10-369-493-21401	Sequence 21401, A
43	32	64.0	343	15	US-10-424-599-172724	Sequence 172724,
44	32	64.0	365	15	US-10-369-493-17087	Sequence 17087, A
45	32	64.0	404	15	US-10-425-114-49539	Sequence 49539, A

ALIGNMENTS

RESULT 1
US-10-389-566-831
Sequence 831, Application US/10389566
Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US/10/389,566
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PatentIn version 3.2
SEQ ID NO 831
LENGTH: 408
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (103)-(106)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-831

Query Match 74.0%; Score 37; DB 15; Length 408;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ASIAAARVLD 10
||:|||||
Db 275 ASIAAARVLD 284

RESULT 2

US-10-425-114-45544
; Sequence 45544, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yinua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45544
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700800359_F11.dep
US-10-425-114-45544

Query Match

Best Local Similarity 74.0%; Score 37; DB 15; Length 573;
Pred. No. 79;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:|||||

DB 58 ANIADTRVLDY 68

RESULT 3

US-10-437-963-120758
; Sequence 120758, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120758
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.dep
US-10-437-963-120758

Query Match

Best Local Similarity 74.0%; Score 37; DB 16; Length 1203;
Pred. No. 1,7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
|:|||||

DB 330 ASVAATRIID 339

RESULT 4

US-10-369-493-14688

US-10-369-493-14688
; Sequence 14688, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369, 493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14688
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14688

Query Match

Best Local Similarity 72.0%; Score 36; DB 15; Length 652;
Pred. No. 1,4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:|||||

DB 255 AATTAARAIDY 265

RESULT 5

US-10-369-493-15165
; Sequence 15165, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369, 493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15165
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-15165

Query Match

Best Local Similarity 72.0%; Score 36; DB 15; Length 652;
Pred. No. 1,4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:|||||

DB 255 AATTAARAIDY 265

RESULT 6

US-10-369-493-14406
; Sequence 14406, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

```

; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14406
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; US-10-369-493-14406

Query Match          72.0%; Score 36; DB 15; Length 655;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
       ||:||||:|
Db      255 AATAAARAIDY 265

RESULT 7
US-10-369-493-11635
; Sequence 11635, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11635
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; US-10-369-493-11635

Query Match          72.0%; Score 36; DB 15; Length 656;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
       ||:||||:|
Db      255 AATAAARAIDY 265

RESULT 8
US-10-437-963-189048
; Sequence 189048, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovallie, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

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; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189048
; LENGTH: 1064
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85594C.1.pep
; US-10-437-963-189048

Query Match          72.0%; Score 36; DB 16; Length 1064;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASIAARVLD 10
       ||:|||||
Db      116 ASIAARVLD 125

RESULT 9
US-10-437-963-201347
; Sequence 201347, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovallie, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201347
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pep
; US-10-437-963-201347

Query Match          70.0%; Score 35; DB 16; Length 45;
Best Local Similarity 88.9%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 SIAARVLD 10
       |||||
Db      16 SIAARVLD 24

RESULT 10
US-10-437-963-175236
; Sequence 175236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovallie, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
```

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 175236
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(107)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73100C.1.pep
US-10-437-963-175236

Query Match      70.0%; Score 35; DB 16; Length 107;
Best Local Similarity 80.0%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASIAAARVLD 10
DB      34 ASIAAARVSD 43

RESULT 11
US-10-767-701-38892
; Sequence 38892, Application US/10767701
; Publication No. US2004017684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38892
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C77436_1.pep
US-10-767-701-38892

Query Match      68.0%; Score 34; DB 16; Length 198;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AARVLDY 11
DB      114 AARVLDY 120

RESULT 12
US-10-369-493-17091
; Sequence 17091, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

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; SEQ ID NO 17091
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-17091

Query Match      68.0%; Score 34; DB 15; Length 231;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASIAAARVLD 10
DB      100 ATIAARKLD 109

RESULT 13
US-10-336-324-6
; Sequence 6, Application US/10336324
; Publication No. US20030176304A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; APPLICANT: Andersen, Kim
; TITLE OF INVENTION: Protease Variants and Compositions
; FILE REFERENCE: 5349,204-US
; CURRENT APPLICATION NUMBER: US/10/336,324
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US/09/512,251A
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-10-336-324-6

Query Match      68.0%; Score 34; DB 14; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ASIAAARVLD 10
DB      96 ASIAAARVLD 105

RESULT 14
US-10-403-105-9
; Sequence 9, Application US/10403105
; Publication No. US20030180933A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter K.
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; TITLE OF INVENTION: Protease Variants And Compositions
; FILE REFERENCE: 5435,200-US
; CURRENT APPLICATION NUMBER: US/10/403,105
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US/09/196,281A
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1332/97
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-10-403-105-9

Query Match      68.0%; Score 34; DB 14; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;

```

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 15
US-10-767-701-45651
; Sequence 45651, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45651
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1583_1.pep
US-10-767-701-45651

Query Match 68.0%; Score 34; DB 16; Length 642;
Best Local Similarity 63.6%; Pred. No. 3.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:| |||
Db 127 ANMADTRVLDY 137

RESULT 16
US-10-369-493-7093
; Sequence 7093, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7093
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7093

Query Match 68.0%; Score 34; DB 15; Length 671;
Best Local Similarity 54.5%; Pred. No. 3.7e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:| |||
Db 255 AAVALARAVNY 265

RESULT 17
US-10-369-493-4338

; Sequence 4338, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4338
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(674)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-4338

Query Match 68.0%; Score 34; DB 15; Length 674;
Best Local Similarity 54.5%; Pred. No. 3.7e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:| |||
Db 255 AAVALARAVNY 265

RESULT 18
US-10-425-114-70274
; Sequence 70274, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70274
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZKROB73050D03_FLI.pep
US-10-425-114-70274

Query Match 68.0%; Score 34; DB 15; Length 691;
Best Local Similarity 63.6%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:| |||
Db 176 ANMADTRVLDY 186

RESULT 19
US-10-437-963-146706
; Sequence 146706, Application US/10437963
; Publication No. US20040123343A1

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146706
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_47304C.1.pep
US-10-437-963-146706
```

```
Query Match          68.0%; Score 34; DB 16; Length 827;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2  SIAAARVLD 10
        |||||
Db       153 SIALRVLD 161
```

```
RESULT 20
US-10-437-963-122779
; Sequence 122779, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122779
; LENGTH: 1000
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25676C.1.pep
US-10-437-963-122779
```

```
Query Match          58.0%; Score 34; DB 16; Length 1000;
Best Local Similarity 77.8%; Pred. No. 5.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3  IAAARVLDY 11
        :|||
Db       870 VAAADVLDY 878
```

```
RESULT 21
US-10-238-075-276
; Sequence 276, Application US/10238075
; Publication No. US20030148324A1
; GENERAL INFORMATION:
```

```
; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolate
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 276
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-276
```

```
Query Match          66.0%; Score 33; DB 14; Length 204;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1  ASIAARVLDY 11
        |||||
Db       151 AQIAARMEY 161
```

```
RESULT 22
US-10-032-585-7697
; Sequence 7697, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7697
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7697
```

```
Query Match          66.0%; Score 33; DB 14; Length 274;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  ASIAARVLD 10
        |||||
Db       205 ASVAAAKVME 214
```

```
RESULT 23
US-10-425-114-40808
; Sequence 40808, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yinhua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40808
```

```
LENGTH: 299
TYPE: PRT
ORGANISM: Schizochytrium aggregatum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3033-037-H2_F1.1.pep
US-10-425-114-40808
```

```
Query Match      66.0%; Score 33; DB 15; Length 299;
Best Local Similarity 70.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 SIAAARVLDY 11
Db      33 SIAATRVLDH 42
```

```
RESULT 24
US-10-156-761-8701
Sequence 8701, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8701
LENGTH: 331
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8701
```

```
Query Match      66.0%; Score 33; DB 14; Length 311;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 SIAAARVLDY 11
Db      306 SVAATRTLDG 315
```

```
RESULT 25
US-10-282-122A-62045
Sequence 62045, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zvekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
```

```
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62045
LENGTH: 358
TYPE: PRT
ORGANISM: Mycobacterium avium
US-10-282-122A-62045
```

```
Query Match      66.0%; Score 33; DB 15; Length 358;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ASIAAARVLD 10
Db      13 SVAARVLD 22
```

```
RESULT 26
US-10-282-122A-63923
Sequence 63923, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zvekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
```

```

; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63923
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-282-122A-63923

Query Match      66.0%; Score 33; DB 15; Length 358;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      13 SSVAAARVMD 22

RESULT 27
US-10-282-122A-62857
; Sequence 62857, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62857
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-282-122A-62857
```

```

Query Match      66.0%; Score 33; DB 15; Length 367;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      13 SSVAAARVMD 22

RESULT 28
US-10-282-122A-64830
; Sequence 64830, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64830
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64830

Query Match      66.0%; Score 33; DB 15; Length 367;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      13 SSVAAARVMD 22

RESULT 29
US-10-627-476-508
; Sequence 508, Application US/10627476
; Publication No. US20040030116A1
```



```

; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroege, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oekar
; APPLICANT: Habertauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-125CPCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 508
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-10-627-476-508

Query Match      66.0%; Score 33; DB 15; Length 402;
Best Local Similarity 63.6%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 ASIAARVLDY 11
Db      260 ASIAPAALDY 270

RESULT 30
US-09-738-626-6555
; Sequence 6555, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
```

```

; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6555
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-6555

Query Match      66.0%; Score 33; DB 9; Length 449;
Best Local Similarity 63.6%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 ASIAARVLDY 11
Db      307 ASIAPAALDY 317

RESULT 31
US-10-369-493-21054
; Sequence 21054, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369, 493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21054
; LENGTH: 453
; TYPE: PRT
; ORGANISM: SYNECHOCOCCUS SP. WH 8102
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(453)
; OTHER INFORMATION: unsure at all Xaa locations
; US-10-369-493-21054

Query Match      66.0%; Score 33; DB 15; Length 453;
Best Local Similarity 54.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY      1 ASIAARVLDY 11
Db      268 AAVALARSINY 278

RESULT 32
US-10-437-963-136788
; Sequence 136788, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
```

```
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 136788
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38332C.1.pcp
US-10-437-963-136788

Query Match      66.0%; Score 33; DB 16; Length 466;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 SIAAARVLDY 11
Db      106 SIAAARGIDY 115

RESULT 33
US-10-417-700A-49
; Sequence 49, Application US/10417700A
; Publication No. US20040033581A1
; GENERAL INFORMATION:
; APPLICANT: ECOPIA BIOSCIENCES INC.
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STRAFA, Alfredo
; APPLICANT: FARNEY, Chris
; TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosom
; FILE REFERENCE: 3002-14US
; CURRENT APPLICATION NUMBER: US/10/417,700A
; CURRENT FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Pseudomonas syringae pv. syringae strain B301D
US-10-417-700A-49

Query Match      66.0%; Score 33; DB 15; Length 469;
Best Local Similarity 63.6%; Pred. No. 4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
Db      396 ASIGAQRUCDY 406

RESULT 34
US-10-282-122A-77407
; Sequence 77407, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
```

```
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77407
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77407

Query Match      66.0%; Score 33; DB 15; Length 509;
Best Local Similarity 70.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 SIAAARVLDY 11
Db      7 SIALTRVLEY 16

RESULT 35
US-10-369-493-11847
; Sequence 11847, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldner, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11847
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-11847

Query Match      66.0%; Score 33; DB 15; Length 670;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 SIAAARVLDY 11
Db      259 SVALARAVDY 268

RESULT 36
US-10-282-122A-63141
; Sequence 63141, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
```

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hasebeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.03A4
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63141
LENGTH: 867
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-10-282-122A-63141

Query Match 66.0%; Score 33; DB 15; Length 867;
Best Local Similarity 60.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIARVLDY 11
Db 439 SVADRWDF 448

RESULT 37
US-10-152-886-53
Sequence 53, Application US/10152886
Publication No. US2003006491A1
GENERAL INFORMATION:
APPLICANT: ECOPIA BIOSCIENCES INC.
APPLICANT: Farnet, Chris
APPLICANT: Stafla, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING
TITLE OF INVENTION: STRUCTURES
FILE REFERENCE: 3011-3US
CURRENT APPLICATION NUMBER: US/10/152.886
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 53
LENGTH: 1958
TYPE: PRT

ORGANISM: Kitasatosporia sp.
US-10-152-886-53

Query Match 66.0%; Score 33; DB 14; Length 1958;
Best Local Similarity 70.0%; Pred. No. 1.8e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
Db 649 ASVAGLRVLD 658

RESULT 38
US-10-425-114-53118
Sequence 53118, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovacic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425.114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53118
LENGTH: 144
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700162177_FLI.pep
US-10-425-114-53118

Query Match 64.0%; Score 32; DB 15; Length 144;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
Db 89 SSTAAALDY 99

RESULT 39
US-10-425-114-53613
Sequence 53613, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovacic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425.114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53613
LENGTH: 146
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLMO17209D08_FLI.pep
US-10-425-114-53613

Query Match 64.0%; Score 32; DB 15; Length 146;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SIAPARYLD 10
 Db 82 SVSAPARYLD 90

RESULT 40

US-10-437-963-107871
 ; Sequence 107871, Application US/10437963
 ; Publication No. US2004012343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ. ID NOS: 204966
 ; SEQ ID NO 107871
 ; LENGTH: 220
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_12180C.1.pep
 ; US-10-437-963-107871

Query Match 64.0%; Score 32; DB 16; Length 220;
 Best Local Similarity 87.5%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAPARY 8
 Db 53 ASVAPARY 60

Search completed: March 31, 2005, 12:46:08
 Job time : 62.5312 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 15.6406 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR-79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	72.0	663	2 AF2984	3-methylcrotonyl-C
2	36	72.0	709	2 A98299	3-methylcrotonyl-C
3	35	70.0	143	2 A33071	hypothetical prote
4	35	70.0	692	2 S56849	probable membrane
5	35	70.0	696	2 AE1210	teichoic acid bios
6	34	68.0	231	2 D87715	carboxymethylendu
7	34	68.0	279	1 SUMYTV	thermiltase (BC 3.4
8	34	68.0	579	2 I40371	methyltransferase
9	34	68.0	649	2 T38883	hypothetical prote
10	34	68.0	956	2 B71468	probable insulinas
11	33	66.0	162	2 AF1059	probable transcript
12	33	66.0	202	2 AF2831	DNA polymerase III
13	33	66.0	202	2 B97609	probable DNA polym
14	33	66.0	220	2 B98878	conserved hypotnet
15	33	66.0	264	2 G69213	hypothetical prote
16	33	66.0	358	2 T45400	hypothetical prote
17	33	66.0	367	2 C70858	hypothetical prote
18	33	66.0	397	2 C84904	hypothetical prote
19	33	66.0	441	2 A75619	cobyrinic acid a,c
20	33	66.0	482	2 H70463	glycine dehydrogen
21	33	66.0	509	2 G62104	glutamate-tRNA synt
22	33	66.0	614	2 S45053	membrane protein B
23	33	66.0	1027	2 T27970	hypothetical prote
24	33	66.0	1232	2 T06165	multidrug resistan
25	32	64.0	305	2 B85437	methionyl aminopep
26	32	64.0	342	2 G69502	histidinol-phospha
27	32	64.0	363	2 D64640	hypothetical prote
28	32	64.0	365	2 C87712	carbohydrate kinas
29	32	64.0	409	2 AG2869	N-cardamoyl-beta-a

30	32	64.0	415	2 A97646	n-cardamoyl-beta-a
31	32	64.0	435	2 T20819	hypothetical prote
32	32	64.0	448	2 T16256	hypothetical prote
33	32	64.0	576	1 B70558	probable ABC trans
34	32	64.0	655	2 G95524	protein T1N15.9 [1
35	32	64.0	777	2 G95940	probable xanthine
36	32	64.0	817	2 T49642	hypothetical prote
37	31	62.0	119	2 T16347	hypothetical prote
38	31	62.0	131	2 AG2388	hypothetical prote
39	31	62.0	144	2 C75376	hypothetical prote
40	31	62.0	172	2 S75615	hypothetical prote
41	31	62.0	177	2 B83036	probable bacteriof
42	31	62.0	230	2 AF3541	glutathione transf
43	31	62.0	249	2 A81001	electron transfer
44	31	62.0	249	2 F82018	electron transfer
45	31	62.0	254	2 AC3018	conserved hypotnet

ALIGNMENTS

RESULT 1
AF2984 3-methylcrotonyl-CoA carboxylase alpha subunit [imported] - Agrobacterium tumefaciens (s
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision.11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2984
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2333, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-663 <KUR>
A:Cross-references: UNIPROT:Q8U955; GB:AE008689; PTDN:AAU44292.1; PTD:gl7741880; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: mcca
A:Map position: linear chromosome
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
Query Match 72.0%; Score 36; DB 2; Length 663;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Or 1 ASIAAARVLDY 11
Db 258 AATAAARVLDY 268

RESULT 2
A98299 3-methylcrotonyl-CoA carboxylase alpha chain (AF310338) [imported] - Agrobacterium tumef
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision.22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A98299
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A98299
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-709 <KUR>
A:Cross-references: UNIPROT:Q8U955; GB:AE007870; PTDN:AAK9915.1; PTD:gl515159866; GSPDB:G
C:Genetics:
A:Gene: AGR_L_2704

A;Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Query Match 72.0%; Score 36; DB 2; Length 709;
Best Local Similarity 63.6%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
|:|:|:|:|:
Db 304 AATTAARADY 314

RESULT 3
S43071
hypothetical protein 5 - human herpesvirus 6
C;Species: human herpesvirus 6
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
R;Thompson, J.; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z.; Frenkel, N.; RC
Oncogene 9, 1167-1173, 1994
A;Title: A transforming fragment within the direct repeat region of human herpesvirus ty
A;Reference number: S43067; MUID:94181269; PMID:8134119
A;Accession: S43071
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-143 <THO>
A;Cross-references: UNIPROT:Q69582; EMBL:X73675; NID:G469952; PIDN:CA452028.1; PID:G4695
A;Note: the nucleotide sequence was submitted to the EMBL Data library, June 1993

Query Match 70.0%; Score 35; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAARVLT 9
|:|:|:|:|:
Db 7 ASIAARVLT 15

RESULT 4
S56849
probable membrane protein YOL073w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRC558; hypothetical protein J1083
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
R;Rose, M.; Koeltter, P.; Entlian, K.D.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
A;Accession: S56849
A;Molecule type: DNA
A;Residues: 1-692 <ROS>
A;Cross-references: UNIPROT:P40358; EMBL:Z49348; NID:G1008228; PID:G1008229; MIPS:YOL073
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56835
A;Accession: S56847
A;Molecule type: DNA
A;Residues: 135-692 <POH>
A;Cross-references: EMBL:Z49348; MIPS:YOL073w
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisia
A;Reference number: S50798; MUID:95282514; PMID:7762302
A;Accession: S50798
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 135-692 <VAN>
A;Cross-references: EMBL:Z34288; NID:G498992; PIDN:CA484049.1; PID:G498993
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data library, June 1994
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchar
A;Reference number: S47117

A;Accession: S47117
A;Molecule type: DNA
A;Residues: 135-692 <VAN>
A;Cross-references: EMBL:Z34288; NID:G498992; PID:G498993
R;Sor, P.J.
submitted to the EMBL Data library, June 1995
A;Reference number: S57731
A;Accession: S57736
A;Molecule type: DNA
A;Residues: 1-692 <SOR>
A;Cross-references: EMBL:X88851; NID:G895892; PID:G895898
C;Genetics:
A;Gene: SCD:JEM1
A;Cross-references: SGD:S0003609; MIPS:YOL073w
A;Map position: 10L
C;Keywords: transmembrane protein
F;585-655/Domain: dnaJ amino-terminal homology <DNV>

Query Match 70.0%; Score 35; DB 2; Length 692;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAARVLDY 11
|:|:|:|:|:
Db 245 SLAARITDY 254

RESULT 5
AE1210
teichoic acid biosynthesis protein B homolog lmo1085 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
R;Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entlian, K.D.; Fahn, H.,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kretz, J.; Kunz, M.; Kunz, F.; Kurpkat, G.; Madeno, E.; Maicouram, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1210
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <GLA>
A;Cross-references: UNIPROT:Q8Y833; GB:NC_003210; PIDN:CAC99163.1; PID:G16410487; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1085

Query Match 70.0%; Score 35; DB 2; Length 696;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 AARVLDY 11
|:|:|:|:|:
Db 685 AARITDY 692

RESULT 6
D87715
carboxymethylglutaminylase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
R;Nieman, W.C.; Feildlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eison, J.; Heidelberg, J.I
B.; Land, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hart, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87715
A;Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-231 <STO>
 A:Cross-references: UNIPROT:Q9A213; GB:AE005673; NID:g31425534; PIDN:AAK5720.1; GSPDB:C
 C:Genetics:
 A:Gene: CCJ3758
 C:Superfamily: carboxymethylenebutenolidase

Query Match 68.0%; Score 34; DB 2; Length 231;
 Best Local Similarity 80.0%; Pred. No. 23;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |||
 |||
 Db 100 ATIAARRLD 109

RESULT 7
 SUMTIV
 thermilase (EC 3.4.21.66) - Thermocactinomycetes vulgaris

C:Species: Thermocactinomycetes vulgaris

C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004

C:Accession: A00973

R:Metoun, B.; Baudys, M.; Koscka, V.; Hausdorf, G.; Frommel, C.; Hohne, W.E.
 FEBS Lett. 183, 195-200, 1985

A:Title: Complete primary structure of thermilase from Thermocactinomycetes vulgaris and its

A:Reference number: A00973

A:Molecule type: protein

A:Residues: 1-279 <MEU>

A:Cross-references: UNIPROT:P04072

C:Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp.

C:Superfamily: subtilisin; subtilisin homology

C:Keywords: hydrolase; serine proteinase

F:29-233/Domain: subtilisin homology <SBT>

F:38,71,225/Active site: Asp, His, Ser #status predicted

Query Match 68.0%; Score 34; DB 1; Length 279;
 Best Local Similarity 80.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |||
 |||
 Db 96 ASIAARVLD 105

RESULT 8
 140371
 methyltransferase - Bacillus stearothermophilus (fragment)

C:Species: Bacillus stearothermophilus

C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

C:Accession: I40371

R:Rina, M.; Markaki, M.; Bouricis, V.

Gene 150, 71-73, 1994

A:Title: Sequence of the cloned bseC gene: M.BseC reveals high homology to M.BanIII.

A:Reference number: I40371; MUID:95047552; PMID:7959066

A:Accession: I40371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-579 <RBS>

A:Cross-references: UNIPROT:P43423; EMBL:X79509; NID:g619638; PIDN:CAA5604.1; PID:g6196

C:Genetics:

A:Gene: bseCIM

C:Superfamily: site-specific methyltransferase (adenine-specific) Paer71

Query Match 68.0%; Score 34; DB 2; Length 579;
 Best Local Similarity 54.5%; Pred. No. 60;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |||
 |||
 Db 26 AEVIAKRILDY 36

RESULT 9
 T38883
 hypothetical protein SPAC4H3.03c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T38883

R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z21807

A:Accession: T38883

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-649 <MDR>

A:Cross-references: UNIPROT:Q10211; EMBL:Z69380; PIDN:CAA93342.1; GSPDB:GN00066; SPDB:SP

A:Experimental source: strain 972h-; cosmid c4H3

A:Gene: SPDB:SPAC4H3.03c

A:Map position: 1

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c

Query Match 68.0%; Score 34; DB 2; Length 649;
 Best Local Similarity 70.0%; Pred. No. 68;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |||
 |||
 Db 631 AIAARHLD 640

RESULT 10
 B71468
 probable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: B71468

R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: B71468

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-956 <ARN>

A:Cross-references: UNIPROT:O84812; GB:AE001353; GB:AE001273; NID:g3329271; PIDN:AA66840

A:Experimental source: serotype D, strain UW-3/Cx

A:Gene: ptx

C:Genetics:

C:Superfamily: insulin-degrading enzyme (IDE)

Query Match 68.0%; Score 34; DB 2; Length 956;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVDY 11
 |||
 |||
 Db 916 IAAARVDY 924

RESULT 11
 AF1059
 probable transcription regulator STY4801 (imported) - Salmonella enterica subsp. enteric

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A>Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AF1059

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AF1059

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06923.1; PID:G16505571; GSPDB:GN00176
C;Genetics:
A;Gene: STRY4801

Query Match 66.0%; Score 33; DB 2; Length 162;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 ASIAARVLDY 11
Db 112 AVARILDY 119

RESULT 12
AF2831
DNA polymerase III, epsilon subunit [imported] - Agrobacterium tumefaciens (strain C58,

C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2831

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743313

A;Accession: AF2831

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-202 <KUR>

A;Cross-references: UNIPROT:Q8UDP4; GB:AE008688; PIDN:AAL43068.1; PID:G17740536; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:

A;Gene: Atuz077

A;Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ASIAARVLDY 9
Db 156 ASIAARVLDY 164

RESULT 13

B97609
probable DNA polymerase III, epsilon chain [imported] - Agrobacterium tumefaciens (strai
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97609

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quicilo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun
A;Reference number: A97359; MUID:21608551; PMID:117433194

A;Accession: B97609

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-202 <KUR>

A;Cross-references: UNIPROT:Q8UDP4; GB:AE007869; PIDN:AAK67827.1; PID:G15157207; GSPDB:G
C;Genetics:

A;Gene: ACR_C_3764

A;Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ASIAARVLDY 9
Db 156 ASIAARVLDY 164

RESULT 14

F89878
conserved hypothetical protein SA0939 [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89878

R;Kuroda, M.; Ohra, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: F89878

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-220 <KUR>

A;Cross-references: UNIPROT:Q99V10; GB:BA000018; PID:G13700889; PIDN:BA842185.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:

A;Gene: SA0939

C;Superfamily: conserved hypothetical protein MG323

Query Match 66.0%; Score 33; DB 2; Length 220;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIARVLDY 11
Db 131 NVASASVLDY 140

RESULT 15

G69213
hypothetical protein MTH852 - Methanobacterium thermoautotrophicum (strain Delta H)

C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69213

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
; Qu, D.; Spadofora, R.; Vicatore, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Ujwand, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A;Reference number: A69000; MUID:98037514; PMID:93711463

A;Accession: G69213

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-264 <MTH>

A;Cross-references: UNIPROT:Q26940; GB:AB000862; GB:AE000666; MUID:G2621943; PIDN:AB85356
C;Genetics:

A;Gene: MTH852

Query Match 66.0%; Score 33; DB 2; Length 264;
Best Local Similarity 54.5%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ASIAARVLDY 11
Db 94 ASIAARVLDY 104

RESULT 16

T45400
hypothetical protein MCB637.07 [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45400

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

RESULT 21

G82104

glutamy1-tRNA synthetase VC2214 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C/Species: Vibrio cholerae
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C/Accession: G82104
 R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Charadson, D.; Ermolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, R.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000

A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A/Reference number: A82035; MUID:20406833; PMID:10952301

A/Accession: G82104

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-509 <HE>

A/Cross-references: UNIPROT:O31153; GB:AE004293; GB:AE003852; NID:93656766; PIDN:AA9535

A/Experimental source: serogroup O1; strain N16961; biotype El Tor

C/Genetics:

A/Map position: 1

C/Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

Query Match 66.0%; Score 33; DB 2; Length 509;

Best Local Similarity 70.0%; Pred. No. 85;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SIAARVLDY 11

Db 7 SIALTRVLEY 16

RESULT 22

S45053

membrane protein EN2 - Yeast (Saccharomyces cerevisiae)

N/Alternate names: protein K2515; protein YLR088w

C/Species: Saccharomyces cerevisiae

C/Date: 03-May-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C/Accession: S45053; S64922

R/Hamburger, D.; Egerton, M.; Riezman, H.

submitted to the EMBL Data Library, May 1994

A/Description: End2p: a membrane protein with a functional ER retention sequence affects

A/Reference number: S45053

A/Accession: S45053

A/Molecule type: DNA

A/Residues: 1-614 <HM>

A/Cross-references: UNIPROT:P39012; EMBL:X79409; NID:6495141; PID:6495142

R/Benes, V.; Rechmann, S.; Neutwich, U.; Schwager, C.; Ansoerge, W.; Voss, H.

submitted to the Protein Sequence Database, May 1996

A/Reference number: S64920

A/Accession: S64922

A/Molecule type: DNA

A/Residues: 1-614 <BM>

A/Cross-references: EMBL:Z73260; NID:91360458; PID:e245542; PID:91360459; MIPS:YLR088w

A/Experimental source: strain S288C

C/Genetics:

A/Map position: 12R

A/Cross-references: MIPS:YLR088w; SGD:S0004078

C/Key words: transmembrane protein

F/26-42/Domain: transmembrane #status predicted <TM1>

F/361-377/Domain: transmembrane #status predicted <TM2>

F/392-408/Domain: transmembrane #status predicted <TM3>

F/419-435/Domain: transmembrane #status predicted <TM4>

F/464-480/Domain: transmembrane #status predicted <TM5>

F/538-554/Domain: transmembrane #status predicted <TM6>

F/582-598/Domain: transmembrane #status predicted <TM7>

Query Match 66.0%; Score 33; DB 2; Length 614;

Best Local Similarity 80.0%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SIAARVLDY 11

Db 202 SIAARVLDY 211

RESULT 23

T27970

hypothetical protein ZK675.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004

C/Accession: T27970

R/Sims, M.

submitted to the EMBL Data Library, November 1994

A/Reference number: Z20448

A/Accession: T27970

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1027 <ML>

A/Cross-references: UNIPROT:Q09615; EMBL:Z46812; PIDN:CAA6844.1; GSPDB:GN00020; CESP:ZK

A/Experimental source: clone ZK675

C/Genetics:

A/Map position: 2

A/Introns: 39/3; 176/3; 226/3; 268/1; 325/2; 471/3; 639/1; 702/3; 835/1; 919/1

C/Superfamily: DNA polymerase, REV1 type

Query Match 66.0%; Score 33; DB 2; Length 1027;

Best Local Similarity 70.0%; Pred. No. 1.8e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SIAARVLDY 11

Db 325 SIAAGKPLDY 334

RESULT 24

T06165

multidrug resistance protein 1 homolog - barley

C/Species: Hordeum vulgare (barley)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C/Accession: T06165

R/Davies, T.G.B.; Theodoulou, F.L.; Hallahan, D.L.; Forde, B.G.

Gene 199, 195-202, 1997

A/Title: Cloning and characterization of a novel P-glycoprotein homologue from barley.

A/Reference number: Z15500; MUID:98019088; PMID:9358056

A/Accession: T06165

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1232 <DAV>

A/Cross-references: UNIPROT:Q23998; EMBL:Y10099; NID:92292906; PIDN:CAA71179.1; PID:92292

A/Experimental source: cv. Maris Mink

C/Superfamily: multidrug resistance protein; ATP-binding cassette homology

F/381-575/Domain: ATP-binding cassette homology <ABC>

Query Match 66.0%; Score 33; DB 2; Length 1232;

Best Local Similarity 60.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10

Db 329 ASVAATRIIE 338

RESULT 25

E85437

methionyl aminopeptidase-like protein [Imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: E85437

R/anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A/Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: E85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <STO>
A:Cross-references: UNIPROT:Q9SW64; GB:NC_001268; NID:97270653; PIDN:CAB80370.1; GSPDB:C
C:Genetics:
A:Gene: AT937040
A:Map position: 4
C:Superfamily: Escherichia coli methionyl aminopeptidase

Query Match 64.0%; Score 32; DB 2; Length 305;
Best Local Similarity 63.6%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
|:|:|:|:|:|
Db 74 SGIARVRDY 84

RESULT 26
G69502
histidinol-phosphate aminotransferase (hisc-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69502
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Cocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69502
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-342 <KLE>
A:Cross-references: UNIPROT:O28255; GB:AE000963; GB:AE000782; NID:92689286; PIDN:AA88922
C:Superfamily: probable histidinol-phosphate transaminase

Query Match 64.0%; Score 32; DB 2; Length 342;
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SIARVLDY 11
|:|:|:|:|:|
Db 245 AIAALRSUDY 254

RESULT 27
D64640
hypothetical protein HP0964 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: D64640
R:Tomb, J.F.; White, O.; Kellavagge, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: D64640
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-363 <TOM>
A:Cross-references: UNIPROT:O25617; GB:AE000605; GB:AE000511; NID:92314103; PIDN:AA0801
C:Genetics:
A:Start codon: GTG

Query Match 64.0%; Score 32; DB 2; Length 363;
Best Local Similarity 63.6%; Pred. No. 96;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
|:|:|:|:|:|
Db 188 AITKGAVIDY 198

RESULT 28
C87712
carbohydrate kinase, PfkB family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87712
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87712
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STO>
A:Cross-references: UNIPROT:Q9A233; GB:AE005673; NID:913425505; PIDN:AAK25695.1; GSPDB:G
C:Genetics:
A:Gene: CC3733

Query Match 64.0%; Score 32; DB 2; Length 365;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIARVLDY 11
|:|:|:|:|:|
Db 338 SIARVIDH 347

RESULT 29
AG2869
N-carbamoyl-beta-alanine amidohydrolase [imported] - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG2869
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
i Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2869
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <KUR>
A:Cross-references: UNIPROT:Q8UCB8; GB:AE008688; PIDN:AAI43373.1; PID:917740869; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: amAB
A:Map position: circular chromosome
C:Superfamily: N-carbamyl-L-amino acid amidohydrolase

Query Match 64.0%; Score 32; DB 2; Length 409;
Best Local Similarity 60.0%; Pred. No. 11e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
|:|:|:|:|:|
Db 235 AGIAARILE 244

RESULT 30
A97646
n-cabamoyl-beta-alanine amidohydrolase (PA0444) [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C/Accession: A97646
 R/Goodner, B.; Hinkle, G.; Gatung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2338, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A/Reference number: A97359; MUID:21608551; PMID:117433194
 A/Accession: A97646
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-415 <KOR>
 A/Cross-references: UNIPROT:Q8UCU8; GB:AE007869; PIDN:AAK88122.1; PID:G15157556; GSPDB:G15157556
 A/Map position: circular chromosome
 C/Superfamily: N-cardanyl-L-amino acid amidohydrolase

Query Match 64.0%; Score 32; DB 2; Length 415;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ASIAAARVLD 10
 |||:|||||:
 Db 241 AGIAAARILE 250

RESULT 31
 T20819
 hypothetical protein F13B12.4 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T20819
 R/Wild, A.
 submitted to the EMBL Data Library, April 1996
 A/Reference number: Z19329
 A/Accession: T20819
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-435 <WIL>
 A/Cross-references: UNIPROT:Q19374; EMBL:Z70683; PTDN:CAA94589.1; GSPDB:GNO0022; CESP:FA19374
 A/Experimental source: clone F13B12
 C/Genetics:
 A/Gene: CESP:F13B12.4
 A/Map position: 4
 A/Insertions: 38/1; 104/1; 161/3; 358/2

Query Match 64.0%; Score 32; DB 2; Length 435;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ASIAAARVLD 10
 |||:|||||:
 Db 324 ASVATWRILD 333

RESULT 32
 T16256
 hypothetical protein F35C8.3 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T16256
 R/Wu, X.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of C. elegans cosmid F35C8.
 A/Reference number: Z18486
 A/Accession: T16256
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-448 <WUX>
 A/Cross-references: UNIPROT:Q9UAH1; EMBL:U40941; NID:G1072184; PID:G1072189; PTDN:AAA817
 C/Genetics:
 A/Gene: CESP:F35C8.3
 A/Insertions: 70/1; 97/1; 134/1; 162/3; 201/3; 253/3; 308/3; 362/3; 393/3; 413/3

C/Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 64.0%; Score 32; DB 2; Length 448;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ASIAAARVLD 11
 |||:|||||:
 Db 45 AAIAAARVLD 55

RESULT 33
 B70558
 Probable ABC transporter cydC - *Mycobacterium tuberculosis* (strain H37RV)
 C/Species: *Mycobacterium tuberculosis*
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: B70558
 R/Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A/Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A/Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A/Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: B70558
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-576 <COL>
 A/Cross-references: UNIPROT:O06137; GB:Z95554; GB:AL123456; NID:G3361771; PTDN:CAB08897.1
 A/Experimental source: strain H37RV
 C/Genetics:
 A/Gene: cydC
 C/Superfamily: *Mycobacterium tuberculosis* probable ABC transporter cydC; ATP-binding cassette; ATP
 F/358-556/Domain: ATP-binding cassette homology <ABC>

Query Match 64.0%; Score 32; DB 1; Length 576;
 Best Local Similarity 87.5%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 IAARVLD 10
 |||:|||||:
 Db 313 IAARVLD 320

RESULT 34
 G96524
 protein T1N15.9 [imported] - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: G96524
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: G96524
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-655 <STO>
 A/Cross-references: UNIPROT:Q9LPT7; GB:AE005173; NID:G8778668; PIDN:AAF79696.1; GSPDB:GNK
 C/Genetics:
 A/Gene: T1N15.9
 A/Map position: 1

Query Match 64.0%; Score 32; DB 2; Length 655;
 Best Local Similarity 70.0%; Pred. No. 1.8e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 SIIPAARVLDY 11
| : ||| |||
Db 475 AIGAAAGLDY 484

RESULT 35
G95940
probable xanthine dehydrogenase (EC 1.1.1.204) [imported] - *Sinorhizobium meliloti* (strain
C:Species: *Sinorhizobium meliloti*
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95940
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chah, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:1141431
A:Accession: G95940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-777 <KUR>
A:Cross-references: UNIPROT:Q92VB7; GB:AU591985; PIDN:GAC49191.1; PID:g15140676; GSPDB:C
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chah, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: xdbB1, SMD21287
A:Genome: plasmid
C:Superfamily: carbon monoxide dehydrogenase molybdoprotein
C:Keywords: oxidoreductase

Query Match 64.0%; Score 32; DB 2; Length 777;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 SIIPAARVLDY 11
| : ||| |||
Db 740 SMAAASVADY 749

RESULT 36
T49642
hypothetical protein B5022.240 [imported] - *Neurospora crassa*
C:Species: *Neurospora crassa*
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49642
R:Schule, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49642
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-817 <SCH>
A:Cross-references: UNIPROT:Q9P5S8; EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.240
C:Genetics:
A:Experimental source: BAC clone B5022; strain CR74A
A:Gene: NCSP:B5022.240
A:Map position: 6
A:introns: 37/1

Query Match 64.0%; Score 32; DB 2; Length 817;
Best Local Similarity 63.6%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ASIAARVLDY 11
| : ||| |||

Db 146 AGLDARVADY 156

RESULT 37
T16347
hypothetical protein F42G9.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16347
R:Rach, A.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid F42G9.
A:Reference number: Z18498
A:Accession: T16347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-119 <TAI>
A:Cross-references: UNIPROT:Q20348; EMBL:U00051; MID:g1216305; PID:g485118; PIDN:AAA9135
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F42G9.4
A:introns: 56/2; 91/3
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F42G9.4

Query Match 62.0%; Score 31; DB 2; Length 119;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 SIIPAARVLDY 11
| : ||| |||
Db 77 SITSAYLDY 86

RESULT 38
AG2388
hypothetical protein all4663 [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. strain PCC 7120
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2388
R:Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2388
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-131 <KUR>
A:Cross-references: UNIPROT:Q8YNA4; GB:BA000019; PIDN:BA876362.1; PID:g17133800; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4663
C:Superfamily: *Neisseria meningitidis* hypothetical protein NMB0979

Query Match 62.0%; Score 31; DB 2; Length 131;
Best Local Similarity 80.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 SIIPAARVLDY 11
| : ||| |||
Db 7 SIIPAARVLDY 16

RESULT 39
C75376
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: C75376
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.D.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: C75376
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-144 <WHI>
 A/Cross-references: UNIPROT:Q9RTZ1; GB:AE002004; GB:AE000513; NID:96459366; PIDD:AAF1117
 A/Experimental source: strain R1
 C/Genetics:
 A/Gene: DR1607
 A/Map position: 1
 C/Superfamily: *Deinococcus radiodurans* hypothetical protein DR1607

Query Match 62.0%; Score 31; DB 2; Length 144;
 Best local Similarity 77.8%; Pred. No. 59;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIARVYLD 10
 :|||
 Db 32 AIAARVLD 40

RESULT 40

S75615
 hypothetical protein sir1956 - *Synechocystis* sp. (strain PCC 6803)
 C/Species: *Synechocystis* sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S75615
 R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 8.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S75615
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-172 <KAN>
 A/Cross-references: UNIPROT:P74092; EMBL:D90912; GB:AB001339; NID:91653228; PIDD:BA1817
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 62.0%; Score 31; DB 2; Length 172;

Best local Similarity 66.7%; Pred. No. 71;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 IAAARVLDY 11
 |||
 Db 93 IARARVLDY 101

Search completed: March 31, 2005, 12:11:15
 Job time : 17.6406 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 73.0469 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	74.0	421	2	Q6H820
2	37	74.0	694	2	Q8EF52
3	37	74.0	1203	2	Q8S2E4
4	37	74.0	1234	2	Q8GU81
5	36	72.0	402	2	Q62CX8
6	36	72.0	402	2	Q63M18
7	36	72.0	663	2	Q8UAY5
8	36	72.0	709	2	Q7CSK5
9	36	72.0	723	2	Q8H034
10	36	72.0	778	2	Q7MA36
11	36	72.0	1072	2	Q69X93
12	35	70.0	143	2	Q69582
13	35	70.0	184	2	Q6A091
14	35	70.0	329	2	Q9RJR7
15	35	70.0	692	1	VJH3_YEAST
16	35	70.0	696	2	Q8Y833
17	35	70.0	1228	2	Q8Y833
18	35	70.0	6977	2	Q7R034
19	34	68.0	153	2	Q6NAA2
20	34	68.0	231	2	Q9A213
21	34	68.0	279	1	THEFT_THEVU
22	34	68.0	322	2	Q6AH23
23	34	68.0	342	2	Q8ZSL1
24	34	68.0	342	2	Q8ZXL8
25	34	68.0	342	2	Q9LS05
26	34	68.0	344	2	Q9FV51
27	34	68.0	568	2	Q8P714
28	34	68.0	568	2	Q8P714
29	34	68.0	579	1	MYC1_BACST
30	34	68.0	579	2	Q9R0K2
31	34	68.0	589	2	Q7F1D1

32	34	68.0	596	2	Q7QH89	Q7QH89 anophelae g
33	34	68.0	649	1	YAY3_SCHPO	Q10211 schizosacch
34	34	68.0	827	2	Q6ZG00	Q6ZG00 oryza sativ
35	34	68.0	866	2	Q6FY30	Q6FY30 candida gla
36	34	68.0	874	2	Q67R60	Q67R60 symbiodacte
37	34	68.0	912	2	Q8ZM19	Q8ZM19 pyrobaculum
38	34	68.0	920	2	Q8A1R0	Q8A1R0 bacteroides
39	34	68.0	945	2	Q7E2J3	Q7E2J3 oryza sativ
40	34	68.0	956	2	Q84812	Q84812 chlamydia t
41	34	68.0	1206	2	Q8ZXP1	Q8ZXP1 pyrobaculum
42	34	68.0	2785	2	Q8ZVB9	Q8ZVB9 pyrobaculum
43	34	68.0	162	2	Q8Z129	Q8Z129 salmoneilla
44	34	68.0	162	2	Q8ZK37	Q8ZK37 salmoneilla
45	33	66.0	162	2	Q83SS1	Q83SS1 salmoneilla

ALIGNMENTS

RESULT 1					
ID	Q6H820	PRELIMINARY;	PRT:	421 AA.	
AC	Q6H820;				
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	GCN5-related N-acetyltransferase-like.				
CN	Name=O1297_C09.4;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Burkholderia, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Euphorbiaceae; Oryzae; Oryza.				
OX	NCHI_TaxID=33947;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Sasaki T., Matsumoto T., Yamamoto K.;				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AP004087; BAD25129.1; -				
DR	GO; GO:0008080; F:N-acetyltransferase activity; IEA.				
DR	GO; GO:0016740; F:transferase activity; IEA.				
DR	InterPro; IPR000182; GCN5acetyl_trans.				
DR	InterPro; IPR000504; RNA_rec_mot.				
DR	Pfam; PF00583; Acetyltransfer_1; 1.				
DR	PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.				
KW	Transferase.				
SEQ	SEQUENCE 421 AA; 44979 MW; 7A966BFFC673920 CRC64;				
Query Match					
Best Local Similarity		74.0%; Score 37; DB 2; Length 421;			
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
Qy	1 ASIAAARVLD 10				
Db	288 ASIAAARVLD 297				
RESULT 2					
ID	Q8EF52	PRELIMINARY;	PRT:	694 AA.	
AC	Q8EF52;				
DT	01-MAR-2003 (TREMBLrel. 23, Created)				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Acetyl-CoA carboxylase, biotin carboxylase, putative.				
GN	OrderedLocusNames=SO1894;				
OS	Shewanella oneidensis.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;				
OC	Shewanellaceae; Shewanella.				
OX	NCHI_TaxID=70863;				
RY	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MR-1;				
RX	MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;				

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Meche B.A.,
 RA Clayton R.A., Meyer T., Tsaplin A., Scott J., Beaman M.J.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Nayam L.A.,
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
 RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
 RA Venter J.C., Neilson K.H., Fraser C.M.,
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT *Shewanella oneidensis*,"
 RL Nat. Biotechnol. 20:1118-1123(2002).
 DR EMBL; AE015632; AAN54946.1; -.
 DR HSSP; P24182; 1DVL.
 DR TIGR; SO1894; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0009374; F:Biotin binding; IEA.
 DR GO; GO:0016874; F:Ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR01882; Biotin_BS.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR005481; Cbase_L_N.
 DR InterPro; IPR005479; Cbp synth_L_D2.
 DR InterPro; IPR011053; Hybrid_motif.
 DR InterPro; IPR011054; Rudmtc_hyd_motif.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; Biotin_lipoyl; 1.
 DR Pfam; PF00289; Cbase_L_chain; 1.
 DR Pfam; PF02786; Cbase_L_D2; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CBASE_1; UNKNOWN_1.
 DR PROSITE; PS00867; CBASE_2; UNKNOWN_1.
 DR Biotin; Complete proteome.
 KW BIOTIN; Complete proteome.
 SQ SEQUENCE 694 AA; 75656 MW; 05C4ECD8F03C998F CRC64;

Query Match 74.0%; Score 37; DB 2; Length 694;
 Best Local Similarity 54.5%; Pred. No. 1.1e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
 Db 268 AAVAAAKAIDY 278

RESULT 3

OS 08S2E4 PRELIMINARY; PRT; 1203 AA.
 AC 08S2E4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative P-glycoprotein.
 GN Name=PO022F10.15;
 OS *Oryza sativa* (japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Erihartoideae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanemori H.,
 RA Hosokawa S., Maenokawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijikita S., Honda M., Ichikawa Y., Igonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Katsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shimura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,

RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Yama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gokobori T.,
 RT "The genome sequence and structure of rice chromosome 1,"
 RL Nature 420:312-316(2002).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AP003229; BAB89499.1; -.
 DR HSSP; P08716; 1MT0.
 DR Gramene; Q8S2E4; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005524; F:ATPase activity; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_membrane_1.
 DR InterPro; IPR001140; ABC_TM_transp.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS50929; ABC_TMFP; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding.
 SQ SEQUENCE 1203 AA; 131506 MW; B7838BDC1B5F19AA CRC64;

Query Match 74.0%; Score 37; DB 2; Length 1203;
 Best Local Similarity 70.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
 Db 330 ASVAATRIID 339

RESULT 4

OS 08G081 PRELIMINARY; PRT; 1234 AA.
 AC 08G081;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MDR-like ABC transporter.
 GN Name=mdr17;
 OS *Oryza sativa* (japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Erihartoideae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jaisneki M., Ducos E., Martincio E., Boutry M.,
 RT "The ATP-binding cassette transporters: structure, function and gene
 RT family comparison between rice and Arabidopsis,"
 RL Plant Physiol. 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ducos E.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AJ535055; CAD59577.1; -.
 DR HSSP; P08716; 1MT0.
 DR Gramene; Q8G081; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_membrane_1.
 DR InterPro; IPR001140; ABC_TM_transp.


```

DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00664; ABC membrane; 2.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA_2.
DR PROSITE; PS50929; ABC_TM1F; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
DR ATP-binding.
SO SEQUENCE 1234 AA; 134571 MW; C5F9E9D75D28AC93 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 1234;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
Db 330 ASVAARILD 339

RESULT 5
ID 062CX8 PRELIMINARY; PRT; 402 AA.
AC 062CX8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Major facilitator superfamily protein.
GN ORFNames=BMA0712;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Niernan W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Debby R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarría S.,
RA Selengut U., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
DR EMBL; CP000011; AAU46877.1; -.
SQ SEQUENCE 402 AA; 41596 MW; 6FCAL6B0F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
Db 106 ATVAARILD 115

RESULT 6
ID 063M18 PRELIMINARY; PRT; 402 AA.
AC 063M18;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Putative transporter protein.
GN ORFNames=BPS50842;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;

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RX PubMed=15377794;
RA Hoiden M.T.G., Tildall R.W., Peacock S.J., Cerdeno-Tarrega A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosser B., Davis P., Deshazer D.,
RA Feltham T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchavee M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH38304.1; -.
SQ SEQUENCE 402 AA; 41596 MW; 6FCAL6B0F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
Db 106 ATVAARILD 115

RESULT 7
ID 08UA95 PRELIMINARY; PRT; 663 AA.
AC 08UA95;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE 3-methylcrotonyl-CoA carboxylase alpha subunit.
GN Name=mcca; OrderedLocNames=Atu3479; / ATCC 33970).
OS Agrobacterium tumefaciens (strain C58 / Agrobacterium
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Woo L.,
RA Chen Y., Paulsen I.T., Eichen J.A., Karp P.D., Bovee D. St.,
RA Kutayavain T., Levy R., Li M.-Y., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Perry M.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Zhai Z.-Y., Dolan M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AE009278; AAU44292.1; -.
DR PIR; A98299; A98299.
DR PIR; AF2984; AF2984.
DR HSSP; P24182; 1BNC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoYL; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW Biotin; Complete proteome.
SQ SEQUENCE 663 AA; 71187 MW; 236201C5F36D292 CRC64;

```

Query Match 72.0%; Score 36; DB 2; Length 663;
 Best Local Similarity 63.6%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |||||
 Db 258 AATMAARADY 268

RESULT 8
 Q7CSK5 PRELIMINARY; PRT; 709 AA.
 AC Q7CSK5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE AGR L. 2704P.
 GN OrderedLocustNames=AGR L. 2704;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 NCBI_TaxID=176299;
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Galtung S., Miller N., Blanchard M.,
 RA Quirillo B., Goldman B.S., Cao Y., Aakenazi M., Halling L.,
 RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wolman C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
 RA Planagan C., Crowell C., Gureson J., Lomo C., Sear C., Strub G.,
 RA Clelo C., Slater S.,
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL: AB008334; AAK69915.1; -.
 DR HSP; P02905; IBD0.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0009374; F:biotin binding; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR001882; Biotin_BS.
 DR InterPro: IPR005482; Biotin_carb_C.
 DR InterPro: IPR000089; Biotin_lipoyl_L.
 DR InterPro: IPR005481; CPase_L_N.
 DR InterPro: IPR005479; Cphp_synch_L_D2.
 DR InterPro: IPR011053; Hybrid_motif.
 DR InterPro: IPR011054; Rudmt_hyb_motif.
 DR Pfam: PF02785; Biotin_carb_C; 1.
 DR Pfam: PF00364; Biotin_lipoyl_L; 1.
 DR Pfam: PF00289; CPase_L_chain; 1.
 DR PROSITE: PS00188; BIOTIN; 1.
 DR PROSITE: PS00866; CPASE_1; UNKNOWN_1.
 DR PROSITE: PS00867; CPASE_2; UNKNOWN_1.
 KW Biotin.
 SQ SEQUENCE 709 AA; 76278 MW; 1F43A1F1919EFD0 CRC64;
 Query Match 72.0%; Score 36; DB 2; Length 709;
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |||||
 Db 304 AATMAARADY 314

RESULT 9
 Q8H034 PRELIMINARY; PRT; 723 AA.
 AC Q8H034;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein OJ1172F09.9.
 GN Name=OJ1172F09.9;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;
 RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
 RA Baar C., Eppinger M., Raddatz G., Simon U., Lanz C., Kimmek O.,
 RA Nandakumar R., Gross R., Krosin A., Keller H., Jagtap P., Linke B.,
 RA Meyer F., Lederer H., Schuster S.C.;
 RT "Complete genome sequence and analysis of *Woljella succinogenes*,"
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
 DR EMBL: BX571658; CAB06628.1; -.
 DR GO: GO:0019861; C:Flagellum; IEA.
 DR InterPro: IPR008940; Prey1_trans.
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR008941; TPR-like.
 DR Pfam: PF00515; TPR_1; 1.
 DR PROSITE: PSS0293; TPR_REGION; 1.
 KW Complete proteome; Flagellum.
 SQ SEQUENCE 778 AA; 89775 MW; 3E2F992CE949C27E CRC64;

Query Match 72.0%; Score 36; DB 2; Length 723;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 10
 |||||
 Db 616 ASIAARVLDY 625

RESULT 10
 Q7MA36 PRELIMINARY; PRT; 778 AA.
 AC Q7MA36;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE FLAGELLAR FUNCTIONAL PROTEIN.
 GN Name=FLA; OrderedLocustNames=MS0490;
 OS *Woljella succinogenes*.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; *Woljella*.
 NCBI_TaxID=844;
 RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
 RA Baar C., Eppinger M., Raddatz G., Simon U., Lanz C., Kimmek O.,
 RA Nandakumar R., Gross R., Krosin A., Keller H., Jagtap P., Linke B.,
 RA Meyer F., Lederer H., Schuster S.C.;
 RT "Complete genome sequence and analysis of *Woljella succinogenes*,"
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
 DR EMBL: BX571658; CAB06628.1; -.
 DR GO: GO:0019861; C:Flagellum; IEA.
 DR InterPro: IPR008940; Prey1_trans.
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR008941; TPR-like.
 DR Pfam: PF00515; TPR_1; 1.
 DR PROSITE: PSS0293; TPR_REGION; 1.
 KW Complete proteome; Flagellum.
 SQ SEQUENCE 778 AA; 89775 MW; 3E2F992CE949C27E CRC64;

Query Match 72.0%; Score 36; DB 2; Length 778;
 Best Local Similarity 63.6%; Pred. No. 2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |||||
 Db 322 ASIAARVLDY 332

RESULT 11
 Q69X93

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ID Q69X93 PRELIMINARY; PRT; 1072 AA.
AC Q69X93;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Putative receptor-like protein kinase 2.
GN Name=P0633E08.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nupponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone:P0633E08."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AP003622; BAD32908.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR003591; LRR_1yp.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR_1; 22.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00369; LRR_Typ; 11.
DR SMART; SM00230; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase
SQ SEQUENCE 1072 AA; 114368 MW; E15B809971B15F78 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 1072;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 116 ASIAARVLD 125

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RT "A transforming fragment within the direct repeat region of human
RT herpesvirus type 6 that transactivates HIV-1."
RL Oncogene 9:1167-1175 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Thompson J.T.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X73675; CA52028.1; -.
DR PIR; S43071; S43071.
SQ SEQUENCE 143 AA; 13317 MW; EDF78898C3D11734 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAARVLD 9
DB 7 ASIAARVLD 15

RESULT 13
ID Q6A091 PRELIMINARY; PRT; 184 AA.
AC Q6A091;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=DP0753;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OC NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LSV54 / DSM 12343;
RC PubMed=15305914;
RX Rabus R., Ruepp A., Frickey T., Ratel T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amani J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amani R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments."
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR52870; CAG35482.1; -.
KW Complete proteome.
SQ SEQUENCE 184 AA; 20792 MW; 8D9DCB5EDFAA60AF CRC64;

Query Match 70.0%; Score 35; DB 2; Length 184;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 99 ASIAARVLD 108

RESULT 14
ID Q9RJR7 PRELIMINARY; PRT; 329 AA.
AC Q9RJR7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative zinc-binding oxidoreductase.
GN ORFNames=SCF51.18;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A3(2) / M145;
RC

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RX MEDLINE=21996410; PubMed=12000953; DOI=10.1036/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kisser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Metozotrek A., Woodward J.R., Bartell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL391105; CAB59716.1; -.
DR HSSP; O8J3C8; 11Y2.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR02085; Adh zn family.
DR InterPro; IPR011032; GroES like.
DR Pfam; PF00107; ADH_zinc_N; 1.
KM Complete proteome.
SQ SEQUENCE 329 AA; 34155 MW; SDCAD4FB174FD042 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 329;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIAAARYLDY 11
Db 189 SLGAAYLDY 198

RESULT 15
YCH3_YEAST STANDARD; PRT; 692 AA.
ID YCH3_YEAST
AC P40358;
DT 01-FEB-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 44, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 80.4 kDa protein in SMC3-MAPL8 intergenic region.
GN OrderedLocustNames=YJL073W; ORFNames=J1083, HRC558;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Ertan K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sor F.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 135-692 FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=95282514; PubMed=7762302;
RA Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;
RT "Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces
RT cerevisiae includes the mitochondrial ribosomal protein L8.";
RL Yeast 11:57-60(1995).
CC -1- SIMILARITY: Contains 1 J domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC EMBL; Z49348; CAA89365.1; -.

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DR EMBL; X88851; CAA61312.1; -.
DR EMBL; Z34288; CAA84049.1; -.
DR PIR; S56849; S56849.
DR HSSP; P08622; 1BQZ.
DR GERMOLINE; 141687; -.
DR SGD; S00003609; JEM1.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0000300; C:periplasmic to membrane of membrane fraction; IDA.
DR GO; GO:0003767; F:co-chaperone activity; IGI.
DR GO; GO:0000742; P:karyogamy during conjugation with cellular . . .; IGI.
DR GO; GO:0006457; P:protein folding; IGI.
DR InterPro; IPR001623; DnaJ_N.
DR Pfam; PF00226; DnaJ; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
DR PROSITE; PSS0076; DnaJ_2; 1.
KM Hypothetical protein.
FT DOMAIN 560 569 Poly-Gln.
FT DOMAIN 585 655 J-domain.
SQ SEQUENCE 692 AA; 80381 MW; 9F612DD16866981B CRC64;

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Query Match 70.0%; Score 35; DB 1; Length 692;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 2 SIAAARYLDY 11
Db 245 SLAAATLDY 254

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RESULT 16
ID 08Y833 PRELIMINARY; PRT; 696 AA.
AC 08Y833;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lmo1085 protein.
GN OrderedLocustNames=lmo1085;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani P., Couve E., de Daruvar A., Denoux F.,
RA Doman E., Dominguez-Bernal G., Duchaud E., Durand L., Dussurgeat O.,
RA Ertan K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkak G.,
RA Medueno E., Maitounan A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstedt G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tietze A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591977; CAC99163.1; -.
DR PIR; AE1210; AE1210.
DR L1stList; LMO1085; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0047355; F:CDP-glycerol glycerophosphotransferase acti. . .; IEA.
DR GO; GO:0019350; P:cell wall acid biosynthesis; IEA.
DR Pfam; PF04464; Glyphos_transf; 1.
KM Complete proteome.
SQ SEQUENCE 696 AA; 81368 MW; 1668A867FB3408D CRC64;

Query Match 70.0%; Score 35; DB 2; Length 696;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 4 AAARVLDY 11
 DB 685 AAARIDY 692

RESULT 17

O6MK31 PRELIMINARY; PRT; 1228 AA.
 ID O6MK31
 AC O6MK31;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE ABC-type multidrug transporter with fused ATPase and permease domain.
 GN OrderedLocustNames=Bq2583;
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OX NCBI_TaxID=959;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164; DOI=10.1126/science.1093027;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sackett R.E., Schuster S.C.;
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
 genomic perspective";
 RL Science 303:689-692(2004).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; BX842653; CAB80378.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
 DR GO; GO:000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_membrane_1.
 DR InterPro; IPR001140; ABC_TM_transp.
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR008949; Terpenoid_synth.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS0929; ABC_TMIF; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 DR ATP-binding; Complete proteome.
 KW KMW
 SQ SEQUENCE 1228 AA; 136602 MW; CFP9468FE20A1800 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 1228;
 Best Local Similarity 54.5%; Pred. No. 5e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 18

O7R034 PRELIMINARY; PRT; 6977 AA.
 ID O7R034
 AC O7R034;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE GLP 456 20463 41396.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome";
 RL Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AACB0100038; EAA40653.1; -.
 DR InterPro; IPR000408; Reg_chr condens.
 DR PROSITE; PS00626; RCCL2; UNKNOWN 1.
 SO SEQUENCE 6977 AA; 782914 MW; C5C1DEB7211452A3 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 6977;
 Best Local Similarity 72.7%; Pred. No. 2.7e+03;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLDY 11
 DB 4408 ASIAARILAY 4418

RESULT 19

O6NA42 PRELIMINARY; PRT; 153 AA.
 ID O6NA42
 AC O6NA42;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Hypothetical protein precursor.
 OS OrderedLocustNames=RP11344;
 OS Rhodospseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Latimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peters C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodospseudomonas palustris";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572597; CAB26787.1; -.
 DR Complete proteome; Hypothetical protein; signal.
 KW KMW
 FT SIGNAL
 SQ SEQUENCE 153 AA; 16944 MW; DA305CD9BD7B7B47 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 153;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 20

O9A213 PRELIMINARY; PRT; 231 AA.
 ID O9A213
 AC O9A213;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Carboxymethylenebutenolidase.
 GN OrderedLocustNames=CC3758;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;

```

RN [1]
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nielsen W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eissen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Halt D.H.,
RA Kotonay J.F., Sait J., Craven M.B., Knorr H.M., Shetty J.,
RA Bery K.J., Uteirback T.R., Tran K., Wolf A.M., Yamachyan J.J.,
RA Ermoaleva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE006033; AKK25720.1; -.
DR PIR; D87145; D87715.
DR HSSP; P11453; 1GCV.
DR TIGR; CC3758; -.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR002925; Dlenelactn_Hydro.
DR Pfam; PF01738; DLH; 1.
KM Complete proteome.
SQ SEQUENCE 231 AA; 24787 MW; 23E078162327869C CRC64;

Query March 68.0%; Score 34; DB 2; Length 231;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ASINARVLD 10
Db 100 ATINARKLD 109

RESULT 21
ID THEV THEVU STANDARD; PRT; 279 AA.
AC P04072;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thermolase (EC 3.4.21.66).
OS Thermactinomycetes vulgaris.
OC Bacteria; Firmicutes; Bacillales; Thermactinomycetaceae;
OC Thermactinomycetes.
OX NCBI_TaxID=2026;
RN [1]
RP SEQUENCE.
RA Meloun B., Baudys M., Kostka V., Hausdorf G., Frommel C., Hohn W.E.;
RT "Complete primary structure of thermolase from Thermactinomycetes
RT vulgaris and its structural features related to the subtilisin-type
RT proteases.";
RL FEBS Lett. 183:195-200(1985).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=89171261; PubMed=2647518; DOI=10.1016/0014-5793(89)81194-9;
RA Teplyakov A.V., Kuranova I.P., Harutyunyan E.H., Frommel C.,
RA Hohn W.E.;
RT "Crystal structure of thermolase from Thermactinomycetes vulgaris at
RT 2.2-A resolution.";
RL FEBS Lett. 244:208-212(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=90096158; PubMed=2689655;
RA Gros P., Betzel C., Dauter Z., Wilson K.S., Hoi W.G.J.;
RT "Molecular dynamics refinement of a thermolase-egg-lin complex at
RT 1.98-A resolution and comparison of two crystal forms that differ in
RT calcium content.";
RL J. Mol. Biol. 210:347-367(1989).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
RX MEDLINE=90317828; PubMed=2196375;
RA Teplyakov A.V., Kuranova I.P., Harutyunyan E.H., Vainshtein B.K.,
RA Frommel C., Hohn W.E., Wilson K.S.;
RT "Crystal structure of thermolase at 1.4-A resolution.";
RL J. Mol. Biol. 214:261-279(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=91131592; PubMed=1993669;
RA Gros P., Kalk K.H., Hoi W.G.J.;
RT "Calcium binding to thermolase. Crystallographic studies of thermolase
RT at 0.5, and 100 mM calcium.";
RL J. Biol. Chem. 266:12953-12961(1991).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins, including collagen.
CC -1- COFACTOR: Binds 3 calcium ions or 2 calcium ions and 1 sodium ion
CC per subunit. The sodium ion is bound at calcium concentrations up
CC to 5 mM. At 100 mM calcium 3 calcium ions are bound.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the peptidase S8 family.
DR PIR; A00973; SUBTYV.
DR PDB; 1TEC; X-ray; E=1-279.
DR PDB; 1THM; X-ray; @=1-279.
DR PDB; 2TEC; X-ray; E=1-279.
DR PDB; 3TEC; X-ray; E=1-279.
DR MEROPS; S08.007; -.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KM 3D-structure; Calcium-binding; Direct protein sequencing; Hydrolase;
KM Metal-binding; Serine protease.
FT ACT_SITE 38 38
FT ACT_SITE 71 71
FT ACT_SITE 225 225
FT METAL 5 5
FT METAL 47 47
FT METAL 57 57
FT METAL 60 60
FT METAL 62 62
FT METAL 64 64
FT METAL 66 66
FT METAL 82 82
FT METAL 85 85
FT METAL 87 87
FT METAL 89 89
FT TURN 6 7
FT HELIX 8 11
FT HELIX 14 17
FT TURN 18 19
FT HELIX 20 24
FT TURN 25 26
FT TURN 30 31
FT STRAND 33 38
FT TURN 43 44
FT TURN 46 51
FT TURN 52 57
FT STRAND 58 61
FT STRAND 62 62
FT HELIX 71 80
FT TURN 94 95
FT STRAND 97 102
FT STRAND 106 107
FT HELIX 112 124
FT TURN 125 126
FT STRAND 129 132
FT STRAND 136 136
FT HELIX 141 152
FT TURN 153 154
FT STRAND 156 160
FT STRAND 171 171
FT TURN 172 174
FT TURN 176 177
FT STRAND 178 184
FT TURN 186 187
FT STRAND 190 190

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FT TURN 192 193
FT TURN 198 199
FT STRAND 202 205
FT STRAND 209 213
FT TURN 214 216
FT STRAND 217 221
FT HELIX 224 239
FT TURN 240 242
FT HELIX 245 254
FT TURN 255 255
FT STRAND 257 257
FT TURN 260 261
FT STRAND 262 262
FT TURN 263 265
FT STRAND 266 266
FT STRAND 269 270
FT HELIX 273 279
SQ SEQUENCE 279 AA; 28366 MW; 8065049BC8277AC0 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10
Db 96 ASIAARVLD 105

RESULT 22

Q6AH23 PRELIMINARY; PRT; 322 AA.
AC Q6AH23;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zinc-binding oxidoreductase.
GN OrderedLocustNames=Lxc02950;
OS Leifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CTCB07;
RX PubMed=15305603;

RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Trufi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F., Jr., Carter H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.R., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Teal S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Secubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyli subsp. xyli."
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AB016822; AAT8832.1;
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002085; Aah_zn_family.
DR InterPro; IPR002110; ANK_
DR InterPro; IPR01032; GroES_like.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR PRINTS; PRO1415; ANKYRIN.
KW Complete proteome.
SQ SEQUENCE 322 AA; 33244 MW; 9DB928BF3B868BD CRC64;

Query Match 68.0%; Score 34; DB 2; Length 322;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIARVLDY 11
Db 191 SIARVLDY 200

RESULT 23

Q8ZSL1 PRELIMINARY; PRT; 342 AA.
AC Q8ZSL1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE PAREP2b.
GN OrderedLocustNames=PAE1657, PAE2128;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AB009858; AAL63965.1;
DR EMBL; AB009833; AAL63635.1;
KW Complete proteome.
SQ SEQUENCE 342 AA; 37164 MW; E85758D06FEA4343 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 342;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 AARVLDY 11
Db 95 AARVLDY 102

RESULT 24

Q8ZXL8 PRELIMINARY; PRT; 342 AA.
AC Q8ZXL8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PAREP2b.
GN OrderedLocustNames=PAE1214;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AB009809; AAL63329.1;
KW Complete proteome.
SQ SEQUENCE 342 AA; 37134 MW; F42758D0739A4A33 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 342;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 AARVLDY 11

Db 95 AAVRLDY 102

RESULT 25

Q9LS05 PRELIMINARY; PRT; 342 AA.

AC Q9LS05

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Methionine aminopeptidase-like protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_Taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones."

RL DNA Res. 7:131-135(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Removes the amino-terminal methionine from nascent proteins (By similarity).

CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides.

CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).

CC -1- SIMILARITY: Belongs to peptidase family M24A.

DR EMBL; AB028607; BAA95761.1; -.

DR HSSP; P07906; IC24.

DR GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.

DR GO; GO:0008223; F:peptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000994; Peptidase_M24.

DR InterPro; IPR002467; Pept_M24A_MAP1.

DR InterPro; IPR001714; Pept_M24_MAP.

DR Pfam; PF00557; Peptidase_M24_1.

DR PRINTS; PR00599; MAPPEPTIDASE.

DR TIGRFAMs; TIGR00500; met_pdae_1; 1.

KW Aminopeptidase; Cobalt; Hydrolase; Protease.

QX SEQUENCE 342 AA; 37429 MW; 6850AF0B7F9A73B CRC64;

Query Match 68.0%; Score 34; DB 2; Length 342;

Best Local Similarity 100.0%; Pred. No. 2,4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AAVRLDY 11

Db 115 AAVRLDY 121

RESULT 26

Q9FV51 PRELIMINARY; PRT; 344 AA.

AC Q9FV51

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Methionine aminopeptidase-like protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_Taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20514156; PubMed=11060042; DOI=10.1093/emboj/19.21.5916;

RA Giglione C., Serero A., Pierre M., Bolason B., Meinel T.;

RT "Identification of eukaryotic peptide deformylases reveals universality of N-terminal protein processing mechanisms."

RL EMBO J. 19:5916-5929(2000).

CC -1- FUNCTION: Removes the amino-terminal methionine from nascent proteins (By similarity).

CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides.

CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).

CC -1- SIMILARITY: Belongs to peptidase family M24A.

DR EMBL; AF250962; AAC33976.1; -.

DR HSSP; P07906; IC24.

DR GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.

DR GO; GO:0008223; F:peptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000994; Peptidase_M24.

DR InterPro; IPR002467; Pept_M24A_MAP1.

DR InterPro; IPR001714; Pept_M24_MAP.

DR Pfam; PF00557; Peptidase_M24_1.

DR PRINTS; PR00599; MAPPEPTIDASE.

DR TIGRFAMs; TIGR00500; met_pdae_1; 1.

KW Aminopeptidase; Cobalt; Hydrolase; Protease.

QX SEQUENCE 344 AA; 37693 MW; BB12F00F3CF710BA CRC64;

Query Match 68.0%; Score 34; DB 2; Length 344;

Best Local Similarity 100.0%; Pred. No. 2,4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AAVRLDY 11

Db 115 AAVRLDY 121

RESULT 27

Q8P7L4 PRELIMINARY; PRT; 568 AA.

AC Q8P7L4

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Alkaline phosphatase.

GN Name=phoA; OrderedlocusNames=XCC2597;

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_Taxid=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RA da Silva A.C.R., Fairo J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.B., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Canargo L.E.A.,

RA Camarotte G., Camavan F., Cardozo J., Chambergro F., Clapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinoia L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."

RL Nature 417:459-463(2002).

CC -1- SIMILARITY: Belongs to the alkaline phosphatase family.

DR EMBL; AB012371; AAM41869.1; -.

DR HSSP; P05187; 1EW2.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR001952; Alk_phosphatase.


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DR Pfam; PF00245; Alk_phosphatase; 1.
DR PRINTS; PR00113; ALKPHPTASE.
DR SMART; SM00098; alkPpc; 1.
KW Complete proteome.
SQ SEQUENCE 568 AA; 59946 MW; 94CA413CB2942DEC CRC64;

Query Match
Best Local Similarity 66.0%; Score 34; DB 2; Length 568;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SIAARVLD 10
Db 86 TVAAARILD 94

RESULT 28
Q9P1Y6 PRELIMINARY; PRT; 568 AA.
AC Q9P1Y6;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Alkaline phosphatase.
GN Name=PhoA; OrderedLocNames=XAC2759;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=20202145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farach C.S., Purlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Camarotte G., Canavarro F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Curcio-Santos J.R., El-Dorri H.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezsa R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
CC -1- SIMILARITY: Belongs to the alkaline phosphatase family.
DR EMBL; AB011916; AAM37604.1; -.
DR HSSP; P05187; 1EM2.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001952; Alk_phosphatase.
DR Pfam; PF00245; Alk_phosphatase; 1.
DR PRINTS; PR00113; ALKPHPTASE.
DR SMART; SM00098; alkPpc; 1.
KW Complete proteome.
SQ SEQUENCE 568 AA; 60087 MW; E7514C0AF2BEF199 CRC64;

Query Match
Best Local Similarity 66.0%; Score 34; DB 2; Length 568;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SIAARVLD 10
Db 86 TVAAARILD 94

RESULT 29
MTCL_BACST STANDARD; PRT; 579 AA.
ID MTCL_BACST

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AC P43423;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Modification methylase BseCI (EC 2.1.1.72) (Adenine-specific
DE methyltransferase BseCI) (M.BseCI).
GN Name=BseCI;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95047552; PubMed=7959066; DOI=10.1016/0378-1119(94)90860-5;
RA Rina M., Markaki M., Bouriotis V.;
RT "Sequence of the cloned bseCI gene: M. BseCI reveals high homology to
RT M. Bantii";
RL Gene 150:71-73(1994).
CC -1- FUNCTION: This methylase recognizes the double-stranded sequence
CC ATCGAT, causes specific methylation on A-5 on both strands, and
CC protects the DNA from cleavage by the BantII endonuclease.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-
CC adenosyl-L-homocysteine + DNA 6-methylaminopurine.
CC -1- SIMILARITY: Belongs to the M4/M6-methyltransferase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL; X79509; CA56041.1; -.
DR PIR; I40371; I40371.
DR HSSP; P14385; 2ADM.
DR REBASE; 3536; M.BseCI.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR000051; SAM_bind.
DR InterPro; IPR000051; SAM_bind.
DR PRINTS; PR00507; N12N6MTFRASE.
DR PROSITE; PS00092; N6_MTFASE; 1.
KW Methyltransferase; Restriction system; Transferase.
SQ SEQUENCE 579 AA; 66774 MW; A4805FBEBA01835C CRC64;

Query Match
Best Local Similarity 54.5%; Score 34; DB 1; Length 579;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
Db 26 AEVIAKRILDY 36

RESULT 30
Q9ROK2 PRELIMINARY; PRT; 579 AA.
ID Q9ROK2
AC Q9ROK2;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE DNA methyltransferase.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=IV.
RX MEDLINE=20062459; PubMed=10594225;
RA Vasquez C.C., Saavedra C.P., Pichantes S.E.;
RT "Nucleotide sequence of the gene encoding the BseI VI DNA
RT methyltransferase: comparison with other amino-DNA
RT methyltransferases.";

```

RL Curr. Microbiol. 40:114-118(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LV;
 RA Vaquez C.C., Pichantes S.E., Saavedra C.P.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF098974; AA04626.1; -
 DR HSP; P14385; 2ADM.
 DR REBASE; 3547; M.BetLVI.
 DR REBASE; 4520; C.BetLVI.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
 DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransferase; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006306; P:DNA methylation; IEA.
 DR InterPro; IPR011038; Calycin.
 DR InterPro; IPR02296; N12N6_mifrase.
 DR InterPro; IPR02052; N6_Mfase.
 DR InterPro; IPR000051; SAM bind.
 DR PRINTS; PR00507; N12N6MTRFAS.
 DR PROSITE; PS00092; N6_MTRASE; UNKNOWN_1.
 KW Methyltransferase; Transferase.
 SQ SEQUENCE 579 AA; 66820 MW; 4226B9CD43DD0E42 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 579;
 Best Local Similarity 54.5%; Pred. No. 3.9e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 Db 26 AEVIARILDY 36

RESULT 31
 Q7FID1 PRELIMINARY; PRT; 589 AA.
 ID Q7FID1
 AC Q7FID1
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative nucleolar protein.
 GN Name=OJ1484 G09.128;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Euphorbia; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003913; BAD03090.1; -
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR001678; Fmu_NOL1NOP2p.
 DR InterPro; IPR002478; PUA.
 DR Pfam; PF01189; NOL1NOP2_Fmu; 3.
 DR Pfam; PF01472; PUA; 1.
 DR PROSITE; PS01153; NOL1NOP2_SUN; 1.
 DR PROSITE; PS50890; PUA; 1.
 SQ SEQUENCE 589 AA; 64129 MW; E55B6B5A8EB1D95A CRC64;

Query Match 68.0%; Score 34; DB 2; Length 589;
 Best Local Similarity 77.8%; Pred. No. 4e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIARVLD 10
 Db 272 SVARVLD 280

RESULT 32
 Q7OH89 PRELIMINARY; PRT; 596 AA.
 ID Q7OH89

AC Q7OH89;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE EBP1954 (Fragment).
 GN Name=eb1954; ORFNames=ENSGANG00000003144;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAB0100816; EAA05237.1; -
 DR HSP; P06983; 1AH5.
 DR GO; GO:0004418; F:hydroxymethylbilane synthase activity; IEA.
 DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
 DR InterPro; IPR000860; Porphobil deam.
 DR Pfam; PR01379; Porphobil deam; 1.
 DR Pfam; PR03900; Porphobil deam; 1.
 DR PRINTS; PR00151; PORPHBDMASE.
 DR PRODOM; PD002745; Porphobil deam; 1.
 DR TIGRFAMs; TIGR00212; hmc; 1.
 DR PROSITE; PS00533; PORPHOBILINOGEN_DEAM; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 596 AA; 65217 MW; 9F575CED931FA1AE CRC64;

Query Match 68.0%; Score 34; DB 2; Length 596;
 Best Local Similarity 66.7%; Pred. No. 4e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
 Db 518 IASAKVLDY 526

RESULT 33
 YAY3_SCHPO STANDARD; PRT; 649 AA.
 ID YAY3_SCHPO
 AC Q10211;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical protein C4H3.03c in chromosome 1.
 GN ORFNames=SPAC4H3.03c;
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RX STRAIN=972;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jags K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grynolprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Beer P., Zimmermann W., Medler H., Wambutt R., Punnett B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shipkova G.V., Usery D., Bartell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
 CC EMBL; Z69380; CA93342.1; -.
 CC PIR; T38883; T38883.
 CC GeneDB Spombe; SPAC4H3.03c; -.
 DR InterPro: IPR000165; Glyco_hydro_15.
 DR InterPro: IPR008928; Glyco_trans_6hp.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 265 285 Potential.
 FT TRANSMEM 564 584 Potential.
 FT TRANSMEM 626 646 Potential.
 SQ SEQUENCE 649 AA; 74488 MW; 0C97C10E603EB33D CRC64;

Query Match 68.0%; Score 34; DB 1; Length 649;
 Best Local Similarity 70.0%; Pred. No. 4.4e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
 Db 631 AAIAMAHLD 640

RESULT 34
 Q6ZG00 PRELIMINARY; PRT; 827 AA.
 AC Q6ZG00;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Putative brassinosteroid insensitive 1.
 GN Name=OJ118_F05.16;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004158; BAC9489.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR007090; LRR plant.
 DR InterPro: IPR003591; LRR typ.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.

DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam; PF00560; LRR_1; 7.
 DR PRINTS; PR00019; LEURICRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00369; LRR_TYF; 6.
 DR SMART; SM00220; S_TIC; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 SQ SEQUENCE 827 AA; 88805 MW; 10959C22D8A95A9F CRC64;

Query Match 68.0%; Score 34; DB 2; Length 827;
 Best Local Similarity 88.9%; Pred. No. 5.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIARVLD 10
 Db 153 SIARVLD 161

RESULT 35
 Q6FY30 PRELIMINARY; PRT; 866 AA.
 AC Q6FY30;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Similarities with sp|P42223 Saccharomyces cerevisiae YDR351w SBE2 bud
 DE growth protein.
 GN ORFNames=CAGJ0A02486g;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=284593;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolavures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissarie A., Boyer J., Caticolico L., Confiantollet F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreave F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolaki M., Ozcas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straud M.L., Suleau A.,
 RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL; CR380947; CAG57765.1; -.
 SQ SEQUENCE 866 AA; 97660 MW; 42E49D2196D1874F CRC64;

Query Match 68.0%; Score 34; DB 2; Length 866;
 Best Local Similarity 63.6%; Pred. No. 5.8e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
 Db 810 ASIAARVLDY 820

RESULT 36
 Q67R60 PRELIMINARY; PRT; 874 AA.
 AC Q67R60;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE DNA polymerase I.

GN ORFNames=STH848;
 OS Symbiobacterium thermophilum.
 OC Bacteria; Actinobacteria; Symbiobacterium.
 OX NCBI_TaxID=2734;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM14863;
 RA Ueda K., Yamashita A., Ishikawa J., Shinada M., Watsuji T.,
 Motomura K., Ikeda H., Hattori M., Beppu T.;
 RT "Complete genome sequence of an uncultured bacterium Symbiobacterium thermophilum.";
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP006840; BAD39833.1; -
 DR InterPro; IPR002562; 3_5_exonuclease.
 DR InterPro; IPR002421; 5_3_exonuclease.
 DR InterPro; IPR008918; 5_3_exo_C.
 DR InterPro; IPR001098; DNA_pol.
 DR InterPro; IPR002298; DNA_pol.
 DR InterPro; IPR000513; Exo_N_I.
 DR Pfam; PF01612; 3_5_exonuc; 1.
 DR Pfam; PF01367; 5_3_exonuc; 1.
 DR Pfam; PF02739; 5_3_exonuc; 1.
 DR Pfam; PF00476; DNA_pol_A; 1.
 DR PRINTS; PR00868; DNAPOLI.
 DR SMART; SM00475; 53EXOC; 1.
 DR SMART; SM00279; HhH2; 1.
 DR SMART; SM00482; POLAC; 1.
 DR TIGRFAMs; TIGR00593; pola; 1.
 SQ SEQUENCE 874 AA; 96743 MW; B5D7DFCCD225EAC CRC64;

Query Match 68.0%; Score 34; DB 2; Length 874;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
 |||||
 Db 563 AARVLDY 569

RESULT 37
 Q82W19 PRELIMINARY; PRT; 912 AA.
 AC Q82W19;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE ParEP2b.
 GN OrderedLocusNames=PAE1770;
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX MEDLINE=21664397; PubMed=11792863; DOI=10.1073/pnas.241636498;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-C., Stetter K.O., Simon M.T.,
 Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
 DR EMBL; AB009838; AAL63713.1; -
 KW Complete proteome.
 SQ SEQUENCE 912 AA; 102319 MW; 8C988BEF7DA3300E CRC64;

Query Match 68.0%; Score 34; DB 2; Length 912;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AARVLDY 11
 |||||
 Db 95 AARVLDY 102

RESULT 38
 Q8A1R0 PRELIMINARY; PRT; 920 AA.
 AC Q8A1R0;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Beta-mannosidase.
 GN OrderedLocusNames=B73599;
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=2250858; PubMed=12663928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076 (2003).
 DR EMBL; AE016941; AAC78704.1; -
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR006102; Glyco_hydro_21g.
 DR InterPro; IPR006104; Glyco_hydro_25b.
 DR Pfam; PF00703; Glyco_hydro_2; 1.
 DR Pfam; PF02837; Glyco_hydro_2_N; 1.
 KW Complete proteome.
 SQ SEQUENCE 920 AA; 106822 MW; 4DF439A6D7648666 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 920;
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IAAARVLDY 11
 |||||
 Db 756 IAAARVLDY 764

RESULT 39
 Q7EZJ3 PRELIMINARY; PRT; 945 AA.
 AC Q7EZJ3;
 DT 05-JUN-2004 (TREMBlrel. 27, Created)
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative valyl-tRNA synthetase.
 GN Name=P0428D12.115;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC clone:P0428D12.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004664; BAC83606.1; -
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004632; F:valine-tRNA ligase activity; IEA.
 DR GO; GO:0006438; P:valyl-tRNA aminoacylation; IEA.
 DR InterPro; IPR002300; tRNA-synt_1a.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002303; tRNA-synt_val.
 DR InterPro; IPR009080; tRNA-synt_val.
 DR InterPro; IPR010978; tRNA binding arm.
 DR InterPro; IPR009008; ValRS_tIers_edit.
 DR Pfam; PF00133; tRNA-synt_1; 1.

DR PRINTS; PR00986; TRNASYNTHVAL.
 DR TIGRFAMs; TIGR00422; va1s; 1.
 DR PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase.
 SQ SEQUENCE 945 AA; 107631 MW; 418F8306AFB4FDAC CRC64;

Query Match 68.0%; Score 34; DB 2; Length 945;
 Best Local Similarity 77.8%; Pred. No. 6.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
 :|||:|
 Db 815 VAAADVLDY 823

RESULT 40

ID 084812 PRELIMINARY; PRT; 956 AA.
 AC 084812;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
 DE Insulinase family/Protease III.
 GN Name=Ptr; OrderedLocustNames=CT806;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D / UM-3 / Cx;
 RX MEDLINE=9900809; PubMed=9784136; DOI=10.1126/science.282.5389.754;
 RA Stephens R.S., Kalman S., Lammell C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 DR EMBL; AE001353; AAC68402.1; -.
 DR PIR; B71468; B71468.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR01431; Insulinase like.
 DR InterPro; IPR07863; Peptidase M16_C.
 DR Pfam; PF00675; Peptidase_M16_I.
 DR Pfam; PF05193; Peptidase_M16_C; 2.
 DR Complete proteome; Protease.
 KW SEQUENCE 956 AA; 108366 MW; B0930E59D4FA486E CRC64;

Query Match 68.0%; Score 34; DB 2; Length 956;
 Best Local Similarity 77.8%; Pred. No. 6.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
 :|||:|
 Db 916 IAAARSMYD 924

Search completed: March 31, 2005, 12:09:41
 Job time : 76.2135 secs

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CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/FIXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

XX Sequence 13 AA;
SQ

Query Match 100.0%; Score 66; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DQ 1 SGSTSNIGNNYVS 13
|||
I SGSTSNIGNNYVS 13

Db 1 SGSTSNIGNNYVS 13

RESULT 2
AAU02544 ID AAU02544 standard; protein; 109 AA.
XX AC AAU02544;
DT 29-AUG-2001 (first entry)
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 31.
XX MM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX KM heart disease; complementarity determining region; CDR.
XX OS Homo sapiens.

PX WO200127279-A1.
PN 19-APR-2001.
XX PF 11-OCT-2000; 2000WO-GB003900.
XX PR 12-OCT-1999; 99US-0158612P.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Edwards BM, Main SH, Vaughan TJ;
XX DR WPI, 2001-282031/29.
XX N-PSDB; AAS03444.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

Claim 1; Page 120; 182pp; English.

AUU02501-AAU02635, and AUU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies

CC for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

XX Sequence 109 AA;

Dy Query Match 100.0%; Score 66; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNNVYS 13

Db 23 SGSTSNIGNNNVVS 35

RESULT 3
AAU02558 standard; protein; 110 AA.

XX AAU02558;
AC
XX AAU02558;
DT 29-AUG-2001 (first entry)
DE Anti-adipocyte monoclonal antibody light chain, FAT 44.
XX
XX Antibody: adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
PN MOZ00127279-Al.
FN 19-APR-2001.
PD
PE 11-OCT-2000; 200OWO-GB003900.
PR 12-OCT-1999; 99US-0158612P.
PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Edwards BM, Main SH, Vaughan TV;
XN WPI: 2001-282031/29.
DR N-PADB; AAS03458.
PP
PT Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
PF
PS Claim 1, Page 128-129; 182pp; English.

XX ANU02501-AAU02635, and ANU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarily determining regions (CDRs) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

SQ Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||
Db 23 SGSTSNIGNNYVS 35

RESULT 4

ID AAU02612 standard; protein; 110 AA.

AC AAU02612;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 99.

KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

PN MO200127279-A1.

PD 19-APR-2001.

PF 11-OCT-2000; 2000WO-GB003900.

PR 12-OCT-1999; 99US-0158812P.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Edwards BM, Main SH, Vaughan TJ;

DR WPI; 2001-282031/29.

DR N-PSDB; AAS03512.

PT Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

PS Claim 1; Page 163; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. CC The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

CC Sequence 110 AA;

Qy Query Match 100.0%; Score 66; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||
Db 23 SGSTSNIGNNYVS 35

RESULT 5
AAU02627

ID AAU02627 standard; protein; 110 AA.

AC AAU02627;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 112.

KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

PN MO200127279-A1.

PD 19-APR-2001.

PF 11-OCT-2000; 2000WO-GB003900.

PR 12-OCT-1999; 99US-0158812P.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Edwards BM, Main SH, Vaughan TJ;

DR WPI; 2001-282031/29.

DR N-PSDB; AAS03527.

PT Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

PS Claim 1; Page 172; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. CC The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

XX Sequence 110 AA;

Qy Query Match 100.0%; Score 66; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||
Db 23 SGSTSNIGNNYVS 35

RESULT 6

ID AAU02629 standard; protein; 110 AA.

AC AAU02629;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 113.

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 XX MO200127279-A1.
 XX
 PD 19-APR-2001.
 XX
 PD 11-OCT-2000; 2000MO-GB003900.
 XX
 PF 12-OCT-1999; 99US-0158812P.
 XX
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PT Edwards BM, Main SH, Vaughan TJ;
 XX
 DR WP; 2001-282031/29.
 DR N-PSDB; AAS03529.
 XX
 PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX
 PS Claim 1; Page 173; 182pp; English.
 XX
 CC AAU023501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC
 XX
 SQ Sequence 110 AA;
 XX
 Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 1 SGGSTSNIGNNTVS 13
 Db |||||||||
 |||||||||
 23 SGGSTSNIGNNTVS 35
 RESULT 7
 AAU02542
 ID AAU02542 standard; protein; 111 AA.
 XX
 XX AAU02542;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 XX Anti-adipocyte monoclonal antibody light chain, FAT 30.
 DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200127279-A1.
 XX
 PD 19-APR-2001.
 XX

[illegible]

XX WPI; 2001-282031/29.
 DR N-PSDB; AAS03451.
 XX
 PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX
 PS Claim 1; Page 124; 182pp; English.
 XX
 CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 XX
 SQ Sequence 111 AA;
 XX
 Query Match 100.0%; Score 66; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 |||||
 Db 24 SGSTSNIGNNYVS 36
 |||||
 RESULT 9
 ABP45887
 ID ABP45887 standard; protein; 240 AA.
 XX
 AC ABP45887;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1898.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 PT
 PS Claim 1; Page 2666-2667; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 240 AA;
 XX
 Query Match 100.0%; Score 66; DB 5; Length 240;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 |||||
 Db 153 SGSTSNIGNNYVS 165
 |||||
 RESULT 10
 ADG96714
 ID ADG96714 standard; protein; 240 AA.
 XX
 AC ADG96714;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds Blys Segid 1898.
 XX
 KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antirheumatic; neuroprotective;
 KW antiinflammatory; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 PN WO2003055979-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2003-505530/47.
 DR
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.

XX ABP45916 standard; protein; 243 AA.
XX
XX ABP45916;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Bly5 binding scFv SEQ ID 1927.
XX
XX Bly5; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX W0200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2700-2701; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Bly5) polypeptides. Bly5 is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antineoplastic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Bly5. The antibodies bind to Bly5
XX and so may be used to detect and quantitate the presence of Bly5 in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Bly5. They may also be
XX administered to treat diseases associated with aberrant Bly5 expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX Sequence 243 AA;
XX
XX Query Match 100.0%; Score 66; DB 5; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 0.006;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
AAO31147
ID AAO31147 standard; protein; 243 AA.

OY 1 SGSTSNIGNNYVS 13
|||
Db 155 SGSTSNIGNNYVS 167

XX AAO31147;
XX
XX 06-OCT-2003 (first entry)
XX
XX Human CM085C11 scFv protein that specifically binds TR7.
XX
XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;
XX complementarity determining region; CDR; light chain variable domain; VL;
XX TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
XX DR3; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
XX Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
XX glioblastoma; graft versus host disease; antibody therapy; neotropic;
XX AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
XX immunosuppressive; neuroprotective; antibody therapy; antibody.
XX
XX Homo sapiens.
XX
XX W02003054216-A2.
XX
XX 03-JUL-2003.
XX
XX 19-DEC-2002; 2002WO-US040597.
XX
XX 20-DEC-2001; 2001US-0341237P.
XX 05-APR-2002; 2002US-0369877P.
XX 04-JUN-2002; 2002US-0384828P.
XX 18-JUL-2002; 2002US-0396591P.
XX 15-AUG-2002; 2002US-0403370P.
XX 13-NOV-2002; 2002US-0425737P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
XX WPI; 2003-569250/53.
XX DR N-PSDB; PAL62844.
XX
XX New antibody or its fragment, useful for treating, preventing or
XX ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
XX gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
XX disease, AIDS.
XX
XX Claim 2; Page 288; 301pp; English.
XX
XX The invention relates to an isolated antibody or its fragments such as
XX VHCDR1 (heavy chain variable domain complementarity determining region),
XX VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
XX determining region), VLCDR2 or VLCDR3. The antibody or its fragment
XX immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
XX apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
XX TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
XX antibody or its fragment is useful for treating, preventing or
XX ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
XX gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
XX nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
XX graft versus host disease, AIDS (acquired immune deficiency syndrome) or
XX a neurodegenerative disorder. The invention is useful in antibody
XX therapy. The present sequence is human scFv protein that specifically
XX binds TR7
XX
XX Sequence 243 AA;
XX
XX Query Match 100.0%; Score 66; DB 6; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 0.006;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

OY 1 SGSTSNIGNNYVS 13
|||
Db 155 SGSTSNIGNNYVS 167

ADG96743
ID ADG96743 standard; protein; 243 AA.
XX
AC ADG96743;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys Segid 1927.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antineumatic; antiarthritic; neuroprotective;
KM antiinflammatory; antiallergic; cyostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1927; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineumatic, antiallergic, neuroprotective,
CC antiinflammatory, antiallergic, antiallergic, and cyostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 66; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. NO. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNSIGNNYVS 13
|||
Db 155 SGGSTNSIGNNYVS 167
|||
RESULT 16

ADG34310
ID ADG34310 standard; protein; 243 AA.
XX
AC ADG34310;
XX
DT 26-FEB-2004 (first entry)
XX
DE Neurokinin B antibody SEQ ID NO:33.
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
XX
PR 30-MAY-2002; 2002US-0383802P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben CA, Ruben SM;
XX
DR WPI; 2004-053456/05.
DR N-PSDB; ADG34291.
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preclampsia.
XX
PS Claim 2; SEQ ID NO 33; 127pp; English.
XX
CC The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 66; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. NO. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNSIGNNYVS 13
|||
Db 155 SGGSTNSIGNNYVS 167
|||
RESULT 17
ADG34306
ID ADG34306 standard; protein; 243 AA.
XX
AC ADG34306;
XX
DT 26-FEB-2004 (first entry)
XX
DE Neurokinin B antibody SEQ ID NO:29.
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
XX

PR 30-MAY-2002; 2002US-0383802P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM,
XX
XX WPI; 2004-053456/05.
DR N-PSDB; ADG34287.
XX
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
composition for treating or preventing hypertension or preeclampsia.
XX
XX
PS Claim 2; SEQ ID NO 29; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
XX Sequence 243 AA:
SQ
Query Match 100.0%; Score 66; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNVYS 13
DB 155 SGGSTSNIGNNVYS 167
RESULT 18
ADG34303
ID ADG34303 standard; protein; 244 AA.
XX
XX ADG34303;
AC
XX 26-FEB-2004 (first entry)
DT
XX
XX Neurokinin B antibody SEQ ID NO:26.
DE
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
XX Synthetic.
OS
XX
XX WO2003102136-A2.
PN
XX
XX 11-DEC-2003.
PD
XX
XX 29-MAY-2003; 2003WO-US016802.
PF
XX
XX 30-MAY-2002; 2002US-0383802P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM,
PI
XX
XX WPI; 2004-053456/05.
DR N-PSDB; ADG34284.
XX
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
composition for treating or preventing hypertension or preeclampsia.
XX
XX
PS Claim 2; SEQ ID NO 26; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.

XX
SQ Sequence 244 AA;
Query Match 100.0%; Score 66; DB 8; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNVYS 13
DB 156 SGGSTSNIGNNVYS 168
RESULT 19
ABP45915
ID ABP45915 standard; protein; 245 AA.
XX
XX ABP45915;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human Blys binding scFv SEQ ID 1926.
DE
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX
XX WO200202641-A1.
PN
XX
XX 10-JAN-2002.
PD
XX
XX 15-JUN-2001; 2001WO-US019110.
PE
XX
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI
XX
XX WPI; 2002-114799/15.
DR
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX
PS Claim 1; Page 2699-2700; 3148bp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX

SO Sequence 245 AA;
Query Match 100.0%; Score 66; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
| | | | | | | | | | | | | | |
DB 157 SGSTSNIGNNYVS 169

RESULT 20
ADG96742
ID ADG96742 standard; protein; 245 AA.
XX
AC ADG96742;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SegID 1926.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scfv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antineumatic; antiarthritic; neuroprotective;
KM antiinflammatory; antiaesthetic; antiallergic; cyostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1926; 394pp; English.
XX
PS This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scfvs) derived, preferably, from the variable
XX heavy CD3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antineumatic, antiallergic, neuroprotective,
XX antiinflammatory, antiaesthetic, antiallergic and cyostatic. This
XX polypeptide sequence is a single chain antibody that binds Blys of the
XX invention. NOTE: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 245 AA;
Query Match 100.0%; Score 66; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
| | | | | | | | | | | | | | |
DB 157 SGSTSNIGNNYVS 169

RESULT 21
ADG98057
ID ADG98057 standard; protein; 245 AA.
XX
AC ADG98057;
XX
DT 11-MAR-2004 (first entry)
XX
DE TNF proliferation inducing protein ligand (APRIL) SegID 3241.
XX
KW human; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antineumatic; antiallergic; neuroprotective;
KM antiinflammatory; antiaesthetic; antiallergic; cyostatic; APRIL; TNF;
KM ligand.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Claim 1; SEQ ID NO 3241; 394pp; English.
XX
PS This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scfvs) derived, preferably, from the variable
XX heavy CD3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antineumatic, antiallergic, neuroprotective,
XX antiinflammatory, antiaesthetic, antiallergic and cyostatic. This
XX polypeptide sequence is an APRIL protein, a TNF proliferation inducing
XX ligand that can form a fusion protein with a Blys protein of the
XX invention.

SQ Sequence 245 AA;
Query Match 100.0%; Score 66; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
|||
Db 157 SGSTSNIGNNYVS 169
|||
RESULT 22
ADE83862
ID ADE83862 standard; protein; 245 AA.
AC ADE83862;
XX
XX 29-JAN-2004 (first entry)
DE Chemokine beta-4 binding antibody F081C09 protein SEQ ID NO:21.
XX
XX antibody; chemokine beta-4; CK-B4; single chain Fv; scFvs;
KM antiapoptotic; dermatological; antiinflammatory; immunosuppressive;
KM antineumatic; antiarthritic; cerebroprotective; cytostatic; anti-HIV;
KM vulnery; dermatitis; autoimmune disease; rheumatoid arthritis;
KM systemic lupus erythematosus; autoimmune encephalitis; cancer;
KM HIV infection; wound; inflammatory disorder; human; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003092597-A2.
XX
XX 13-NOV-2003.
XX
XX 30-APR-2003; 2003WO-US013414.
XX
XX 01-MAY-2002; 2002US-0376561P.
XX
XX (HUMA-) HUMAN GENOME SCL INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI: 2004-022614/02.
XX
XX N-PSDB; ADE83845.
XX
XX
XX New antibody that specifically binds to a chemokine beta-4 polypeptide,
XX useful for diagnosing, treating, preventing or ameliorating psoriasis,
XX rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
XX and wounds.
XX
XX
XX Claim 1; SEQ ID NO 21; 181bp; English.
XX
XX The present invention describes an antibody (I) that specifically binds
XX to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
XX amino acid sequence at least 95% identical to a second amino acid
XX sequence comprising a VH complementarity determining region (CDR) or VL
XX CDR of any of the single chain Fv (scFvs) from any of 17 fully defined
XX sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
XX (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
XX (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
XX cell comprising the vector of (3); (5) a cell line engineered to express
XX (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
XX that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
XX method for detecting aberrant expression of CK-B4 polypeptide, comprising
XX assaying the level of CK-B4 polypeptide expression in a first biological
XX sample of an individual using at least one of (1), and comparing the
XX level of CK-B4 polypeptide assayed in the biological sample with a
XX standard level of CK-B4 polypeptide expression or level of CK-B4
XX polypeptide in a second, normal biological sample, where an increase or
XX decrease in the assayed level of CK-B4 polypeptide in the first
XX biological sample compared to the standard level is indicative of
XX aberrant expression; and (9) a method of treating, preventing or

CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
CC administering (1) to the animal. (I) has antipsoriatic, dermatological,
CC antiinflammatory, immunosuppressive, antirheumatic, antiarthritic,
CC cerebroprotective, cytostatic, anti-HIV and vulnery activities. The
CC methods and compositions of the present invention are useful for
CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
CC erythematosus and autoimmune encephalitis. They can also be used in
CC cancer, HIV infection, wounds and inflammatory disorders. The present
CC sequence is used in the exemplification of the present invention.
XX
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 66; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
|||
Db 157 SGSTSNIGNNYVS 169
|||
RESULT 23
ADG34308
ID ADG34308 standard; protein; 245 AA.
XX
XX ADG34308;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Neurokinin B antibody SEQ ID NO:31.
DE
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
XX Synthetic.
OS
XX
XX WO2003102136-A2.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US016802.
XX
XX 30-MAY-2002; 2002US-0383802P.
XX
XX (HUMA-) HUMAN GENOME SCL INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI: 2004-053456/05.
XX
XX N-PSDB; ADG34289.
XX
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.
XX
XX
XX Claim 2; SEQ ID NO 31; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
XX B. An antibody of the invention has hypotensive, and gynaecological
XX activity, and may have a use in gene therapy. The antibody is useful for
XX preparing a composition for treating or preventing hypertension or pre-
XX eclampsia. The present sequence is used in the exemplification of the
XX invention.
XX
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 66; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
|||
Db 157 SGSTSNIGNNYVS 169
|||

RESULT 24
ADG34313
ID ADG34313 standard; protein; 245 AA.
XX
AC ADG34313;
XX
DT 26-FEB-2004 (first entry)
XX
DE Neurokinin B antibody SEQ ID NO:36.
XX
KM antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PE 29-MAY-2003; 2003WO-US016802.
XX
PR 30-MAY-2002; 2002US-0383802P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM,
XX
PI WPI; 2004-053456/05.
XX
DR N-PSDB; ADG34294.
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
XX
PS Claim 2; SEQ ID NO 36; 127bp; English.
XX
CC The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 245 AA;
XX
Query Match 100.0%; Score 66; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SGGSTNIGNNVYS 13
DB 157 SGGSTNIGNNVYS 169

RESULT 25
ABP45902
ID ABP45902 standard; protein; 246 AA.
XX
AC ABP45902;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1913.
XX
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.

XX
FN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
PI WPI; 2002-114799/15.
XX
DR Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PT Claim 1; Page 2683-2684; 3148pp; English.
XX
PS This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX antineumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
SQ Sequence 246 AA;
XX
Query Match 100.0%; Score 66; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SGGSTNIGNNVYS 13
DB 158 SGGSTNIGNNVYS 170

RESULT 26
ABP45906
ID ABP45906 standard; protein; 246 AA.
XX
AC ABP45906;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1917.
XX
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.

PN WO200202641-A1.
 XX 10-JAN-2002.
 PD
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 XX 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Baraeh SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 2688-2689; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytototoxic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineoplastic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 XX
 SQ Sequence 246 AA;
 XX
 Query Match 100.0%; Score 66; DB 5; Length 246;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 |||||
 |||||
 Db 158 SGSTSNIGNNYVS 170
 RESULT 27
 ADG96733
 ID ADG96733 standard; protein: 246 AA.
 XX
 AC ADG96733;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds BLyS SegID 1917.
 XX
 KW antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antineoplastic; antiallergic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 XX WO2003055979-A2.
 XX

PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 XX 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Ruben SM, Baraeh SC, Choi GH, Vaughan TV, Hilbert D;
 DR WPI; 2003-505530/47.
 XX
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BLyS), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Example 1; SEQ ID NO 1917; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scfvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey BLyS. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of BLyS or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antineoplastic, antiallergic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds BLyS of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIP0 at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 246 AA;
 XX
 Query Match 100.0%; Score 66; DB 7; Length 246;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 |||||
 |||||
 Db 158 SGSTSNIGNNYVS 170
 RESULT 28
 ADG96729
 ID ADG96729 standard; protein: 246 AA.
 XX
 AC ADG96729;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds BLyS SegID 1913.
 XX
 KW antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antineoplastic; antiallergic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 XX WO2003055979-A2.
 XX

PD 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0311469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Baraash SC, Choi GH, Vaughan TV, Hilbert D,
PI WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1913; 394dp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CD3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including warts, multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antirheumatic, neuroprotective,
CC antiinflammatory, antiallergic, antiallergic and cyclostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 66; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNYVS 13
DB 158 SGGSTNIGNNYVS 170
RESULT 29
ADEB3872
ID ADEB3872 standard; protein; 246 AA.
XX
XX ADEB3872;
XX
XX 29-JAN-2004 (first entry)
XX
XX Chemokine beta-4 binding antibody F002C08 protein SEQ ID NO:31.
XX
XX antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
XX antiapoptotic; dermatological; antiinflammatory; immunosuppressive;
XX antiinflammatory; antiallergic; cerebroprotective; cyclostatic; anti-HIV;
XX vulnary; dermatitis; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; autoimmune encephalitis; cancer;
XX HIV infection; wound; inflammatory disorder; human; psoriasis.
XX
XX Synthetic.
OS Homo sapiens.
XX

PN NO2003092597-A2.
XX
XX 13-NOV-2003.
XX
XX 30-APR-2003; 2003WO-US013414.
XX
XX 01-MAY-2002; 2002US-0376561P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM,
PI WPI; 2004-022614/02.
XX
XX N-PSDS; ADEB3855.
XX
XX New antibody that specifically binds to a chemokine beta-4 polypeptide,
PT useful for diagnosing, treating, preventing or ameliorating psoriasis,
PT rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
PT and wounds.
XX
XX Claim 1; SEQ ID NO 31; 181dp; English.
XX
XX The present invention describes an antibody (I) that specifically binds
CC to a chemokine beta-4 (CK-B4) polypeptide, where (I) comprises a first
CC amino acid sequence at least 95% identical to a second amino acid
CC sequence comprising a VH complementarily determining region (CDR) or VL
CC CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
CC sequences of 245-253 amino acids (ADEB3861 to ADEB3877). Also described:
CC (1) a kit comprising (I); (2) an isolated nucleic acid molecule encoding
CC (I); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
CC cell comprising the vector of (3); (5) a cell line engineered to express
CC (I); (6) an antibody that binds the same epitope as (I); (7) an antibody
CC that competitively inhibits the binding (I) to a CK-B4 polypeptide; (8) a
CC method for detecting aberrant expression of CK-B4 polypeptide, comprising
CC assaying the level of CK-B4 polypeptide expression in a first biological
CC sample of an individual using at least one of (1), and comparing the
CC level of CK-B4 polypeptide assayed in the biological sample with a
CC standard level of CK-B4 polypeptide expression or level of CK-B4
CC polypeptide in a second, normal biological sample, where an increase or
CC decrease in the assayed level of CK-B4 polypeptide in the first
CC biological sample compared to the standard level is indicative of
CC aberrant expression; and (9) a method of treating, preventing or
CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
CC administering (I) to the animal. (I) has antiapoptotic, dermatological,
CC antiinflammatory, immunosuppressive, antirheumatic, antiallergic,
CC cerebroprotective, cyclostatic, anti-HIV and vulnary activities. The
CC methods and compositions of the present invention are useful for
CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
CC erythematosus and autoimmune encephalitis. They can also be used in
CC cancer, HIV infection, wounds and inflammatory disorders. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 66; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNYVS 13
DB 158 SGGSTNIGNNYVS 170
RESULT 30
ABP45671
ID ABP45671 standard; protein; 247 AA.
XX
XX ABP45671;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1682.
DE

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XX KM Bly/s; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX KM tumour necrosis factor; B cell proliferation; B cell differentiation;
XX KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX DR WPI; 2002-114799/15.
XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2409-2410; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
XX CC B lymphocyte stimulator (Bly/s) polypeptides. Bly/s is a member of the
XX CC tumour necrosis factor (TNF) super family and induces B cell
XX CC proliferation and differentiation. The antibodies of the invention have
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
XX CC inhibit the expression and activity of Bly/s. The antibodies bind to Bly/s
XX CC and so may be used to detect and quantitate the presence of Bly/s in
XX CC biological samples and may be used in this way to diagnose disease
XX CC associated with aberrant expression of Bly/s. They may also be
XX CC administered to treat diseases associated with aberrant Bly/s expression
XX CC and activity such as cancer, immune, and autoimmune disorders and
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX CC the antibodies and fragments of the antibodies described in the method of
XX CC the invention
XX SQ Sequence 247 AA;
XX
XX Query Match 100.0%; Score 66; DB 5; Length 247;
XX Best Local Similarity 100.0%; Pred. No. 0.0061;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SGSTSNIGNNYVS 13
Db 159 SGSTSNIGNNYVS 171

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XX KM Bly/s; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX KM tumour necrosis factor; B cell proliferation; B cell differentiation;
XX KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX DR WPI; 2002-114799/15.
XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2124-2125; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
XX CC B lymphocyte stimulator (Bly/s) polypeptides. Bly/s is a member of the
XX CC tumour necrosis factor (TNF) super family and induces B cell
XX CC proliferation and differentiation. The antibodies of the invention have
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
XX CC inhibit the expression and activity of Bly/s. The antibodies bind to Bly/s
XX CC and so may be used to detect and quantitate the presence of Bly/s in
XX CC biological samples and may be used in this way to diagnose disease
XX CC associated with aberrant expression of Bly/s. They may also be
XX CC administered to treat diseases associated with aberrant Bly/s expression
XX CC and activity such as cancer, immune, and autoimmune disorders and
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX CC the antibodies and fragments of the antibodies described in the method of
XX CC the invention
XX SQ Sequence 247 AA;
XX
XX Query Match 100.0%; Score 66; DB 5; Length 247;
XX Best Local Similarity 100.0%; Pred. No. 0.0061;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SGSTSNIGNNYVS 13
Db 159 SGSTSNIGNNYVS 171

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RESULT 31
ABP45432
ID ABP45432 standard; protein; 247 AA.
XX AC ABP45432;
XX DT 19-AUG-2002 (first entry)
XX DE Human Bly/s binding scFv SEQ ID 1443.
XX

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RESULT 32
ABP45923
ID ABP45923 standard; protein; 247 AA.
XX AC ABP45923;
XX DT 19-AUG-2002 (first entry)
XX DE Human Bly/s binding scFv SEQ ID 1934.
XX
XX KM Bly/s; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

```

XX	OS	Homo sapiens.
XX	XX	
XX	PD	WO200202641-A1.
XX	XX	
XX	PD	10-JAN-2002.
XX	XX	
XX	PF	15-JUN-2001; 2001WO-US019110.
XX	XX	
PR	PR	16-JUN-2000; 2000US-0212210P.
PR	PR	17-OCT-2000; 2000US-0240816P.
PR	PR	16-MAR-2001; 2001US-0276248P.
PR	PR	21-MAR-2001; 2001US-0277379P.
PR	PR	25-MAY-2001; 2001US-02993499P.
XX	XX	
PA	PA	(HUMA-) HUMAN GENOME SCI INC.
PA	PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	XX	
XX	PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	XX	WPI; 2002-114799/15.
XX	XX	
PT	PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT	PT	diagnosis and treatment of cancers and immune disorders.
XX	XX	
PS	PS	Claim 1; Page 2708-2709; 3148pp; English.
XX	XX	
CC	CC	This invention describes novel antibodies that immunospecifically bind to
CC	CC	B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC	CC	tumour necrosis factor (TNF) super family and induces B cell
CC	CC	proliferation and differentiation. The antibodies of the invention have
CC	CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	CC	inhibit the expression and activity of Blys. The antibodies bind to Blys
CC	CC	and so may be used to detect and quantitate the presence of Blys in
CC	CC	biological samples and may be used in this way to diagnose disease
CC	CC	associated with aberrant expression of Blys. They may also be
CC	CC	administered to treat diseases associated with aberrant Blys expression
CC	CC	and activity such as cancer, immune, and autoimmune disorders and
CC	CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and
CC	CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	CC	the antibodies and fragments of the antibodies described in the method of
CC	CC	the invention
SO	SO	
SO	SO	Sequence 247 AA;
XX	XX	
QY	QY	Query Match 100.0%; Score 66; DB 5; Length 247;
QY	QY	Best Local Similarity 100.0%; Pred. No. 0.0061;
QY	QY	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DB	DB	
DB	DB	1 SGGTSNIGNNYVS 13
DB	DB	159 SGGTSNIGNNYVS 171
XX	XX	
XX	XX	RESULT 33
XX	XX	ABP45917
XX	XX	ID ABP45917 standard; protein; 247 AA.
XX	XX	
XX	XX	ABP45917;
XX	XX	
XX	XX	19-AUG-2002 (first entry)
XX	XX	
XX	XX	Human Blys binding scfv SEQ ID 1928.
XX	XX	
XX	XX	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX	XX	tumour necrosis factor; B cell proliferation; B cell differentiation;

KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.
OS	Homo sapiens.
XX	
PM	WO200202641-A1.
XX	
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US019110.
XX	
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-024081EP.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	
DR	WPI, 2002-114799/15.
XX	
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT	diagnosis and treatment of cancers and immune disorders.
XX	
PS	Claim 1; Page 2701-2702; 3148pp; English.
XX	
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of Blys. The antibodies bind to Blys
CC	and so may be used to detect and quantitate the presence of Blys in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of Blys. They may also be
CC	administered to treat diseases associated with aberrant Blys expression
CC	and activity such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method of
CC	the invention
XX	
SO	Sequence 247 AA:
XX	
Query Match	100.0%; Score 66; DB 5; Length 247;
Best Local Similarity	100.0%; Pred. No. 0.0061;
Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 SGSTSNIGNNTYS 13
DB	159 SGSTSNIGNNTYS 171
XX	
RESULT 34	
ABP45696	
ID	ABP45696 standard; protein; 247 AA.
XX	
AC	ABP45696;
XX	
DT	19-AUG-2002 (first entry)
XX	
DE	Human Blys binding scFv SEQ ID 1707.
XX	
KW	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;
KW	immunopressive; immunostimulant; immunomodulatory; antirheumatic;

aberrant expression or inappropriate function of Blys or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds Blys of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 247 AA;

Query Match 100.0%; Score 66; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. NO. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||
Db 159 SGSTSNIGNNYVS 171

RESULT 39
ADG96498
ID ADG96498 standard; protein; 247 AA.

AC ADG96498;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds Blys SegID 1682.

KM antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KM antiinflammatory; antiasthmatic; antiallergic; cytostatic.

OS Unidentified.

PN WO2003055979-A2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-0311469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;

XX WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator (Blys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1682; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (Blys). The Blys gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CD33 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey Blys. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the

aberrant expression or inappropriate function of Blys or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds Blys of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 247 AA;

Query Match 100.0%; Score 66; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. NO. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||
Db 159 SGSTSNIGNNYVS 171

RESULT 40
ADG96744
ID ADG96744 standard; protein; 247 AA.

AC ADG96744;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds Blys SegID 1928.

KM antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KM antiinflammatory; antiasthmatic; antiallergic; cytostatic.

OS Unidentified.

PN WO2003055979-A2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-0311469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;

XX WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator (Blys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1928; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (Blys). The Blys gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CD33 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey Blys. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the

CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiaesthetic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

SO Sequence 247 AA;

Query Match 100.0%; Score 66; DB 7; Length 247;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNVYS 13
 |||||
 Db 159 SGSTSNIGNNVYS 171

Search completed: March 31, 2005, 12:02:30
 Job time : 101.75 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:44 ; Search time 25.3906 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUG COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	13	4	US-09-383-667-13
2	62	93.9	98	2	US-08-665-202-37
3	62	93.9	98	4	US-09-315-574-37
4	62	93.9	111	2	US-08-665-202-36
5	62	93.9	111	2	US-08-665-202-42
6	62	93.9	111	2	US-08-665-202-43
7	62	93.9	111	3	US-08-983-607-35
8	62	93.9	111	4	US-09-315-574-36
9	62	93.9	111	4	US-09-315-574-42
10	62	93.9	111	4	US-09-315-574-43
11	62	93.9	112	2	US-08-665-202-39
12	62	93.9	112	3	US-08-983-607-31
13	62	93.9	112	3	US-09-025-769B-18
14	62	93.9	112	4	US-09-315-574-39
15	62	93.9	112	4	US-09-490-070A-18
16	62	93.9	112	4	US-09-490-153-18
17	62	93.9	112	4	US-09-490-324-18
18	62	93.9	114	3	US-09-240-274-62
19	62	93.9	234	4	US-09-372-425A-4
20	62	93.9	258	4	US-08-665-202-5
21	62	93.9	258	4	US-09-315-574-5
22	62	93.9	262	3	US-09-069-821-4
23	62	93.9	262	4	US-09-956-086-4
24	62	93.9	262	4	US-09-956-087-4
25	62	93.9	282	3	US-09-420-592A-7
26	62	93.9	282	4	US-09-985-442-7
27	62	93.9	282	4	US-09-983-580-7

28	61	92.4	111	2	US-08-652-816A-15	Sequence 15, Appl
29	58	87.9	111	2	US-08-665-202-40	Sequence 40, Appl
30	58	87.9	111	4	US-09-315-574-40	Sequence 40, Appl
31	58	87.9	113	1	US-08-211-202-112	Sequence 112, App
32	57	86.4	109	3	US-09-240-274-55	Sequence 55, Appl
33	57	86.4	109	3	US-09-025-769B-32	Sequence 32, Appl
34	57	86.4	109	3	US-09-025-769B-51	Sequence 51, Appl
35	57	86.4	109	4	US-09-490-070A-32	Sequence 32, Appl
36	57	86.4	109	4	US-09-490-070A-51	Sequence 51, Appl
37	57	86.4	109	4	US-09-490-153-32	Sequence 32, Appl
38	57	86.4	109	4	US-09-490-153-51	Sequence 51, Appl
39	57	86.4	109	4	US-09-490-324-32	Sequence 32, Appl
40	57	86.4	109	4	US-09-490-324-51	Sequence 51, Appl
41	55	83.3	110	1	US-08-199-911-2	Sequence 2, Appl1
42	53	80.3	98	1	US-08-211-202-111	Sequence 111, App
43	53	80.3	98	2	US-08-665-202-38	Sequence 38, Appl
44	53	80.3	98	4	US-09-315-574-38	Sequence 38, Appl
45	53	80.3	109	3	US-09-240-274-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-383-667-13
Sequence 13, Application US/09383667
Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Devaux, Brigitte
APPLICANT: Eaton, Dan L.
APPLICANT: Haas, Philip E.
APPLICANT: Judice, J. Kevin
APPLICANT: Kirchhofer, Daniel
APPLICANT: Suggest, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 13
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-13
Query Match 100.0%; Score 66; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.000; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;
Cy 1 SGSTSNIGNYVS 13
Db 1 SGSTSNIGNYVS 13
RESULT 2
US-08-665-202-37
Sequence 37, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-37

Query Match 93.3%; Score 62; DB 2; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 3
US-09-315-574-37
Sequence 37, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-37

Query Match 93.3%; Score 62; DB 4; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 4
US-08-665-202-36
Sequence 36, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-36

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
DB 23 SGSSSNIGNNYVS 35

RESULT 5
US-08-665-202-42
Sequence 42, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-42

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
DB 23 SGSSSNIGNNYVS 35

RESULT 6
US-08-665-202-43

Sequence 43, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-43

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
DB 23 SGSSSNIGNNYVS 35

RESULT 7
US-08-983-607-35
Sequence 35, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Xiahong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
AND Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kimeky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: V373
FEATURE:
NAME/KEY: light chain
US-08-983-607-35

Query Match 93.9%; Score 62; DB 3; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 8
US-09-315-574-36
Sequence 36, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574

FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-36

Query Match 93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 9
US-09-315-574-42
Sequence 42, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-42

Query Match 93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 10
US-09-315-574-43
Sequence 43, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-43

Query Match 93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 11
US-08-665-202-39
Sequence 39, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-39

Query Match 93.9%; Score 62; DB 2; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 12
US-08-983-607-31
Sequence 31, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen

APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
NUMBER OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kinney
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: V73
FEATURE:
NAME/KEY: light chain
US-08-983-607-31

Query Match 93.9%; Score 62; DB 3; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
||:|||||||
Db 24 SGGSSNIGNNYVS 36

RESULT 13
US-09-025-769B-18
Sequence 18, Application US/09025769B
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-18

Query Match 93.9%; Score 62; DB 3; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
||:|||||||
Db 23 SGGSSNIGNNYVS 35

RESULT 14
US-09-315-574-39
Sequence 39, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-39

Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSSNIGNNYVS 35

RESULT 15

US-09-490-070A-18

Sequence 18, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSES: Colin G. Sandercock, Esq. c/o Heller Ehtman

White & McAuillie

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-070A-18

Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSSNIGNNYVS 35

RESULT 16

US-09-490-153-18

Sequence 18, Application US/09490153

Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-490-153-18

Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSSNIGNNYVS 35

RESULT 17
US-09-490-324-18
Sequence 18, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vito
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-324-18
Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
|||:|||||||
Db 23 SGGSSNIGNNVYS 35
RESULT 18
US-09-240-274-62
Sequence 62, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 62
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain N02
US-09-240-274-62
Query Match 93.9%; Score 62; DB 3; Length 114;
Best Local Similarity 92.3%; Pred. No. 0.0082;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
|||:|||||||
Db 22 SGGSSNIGNNVYS 34
RESULT 19
US-09-372-425A-4
Sequence 4, Application US/09372425A
Patent No. 6475749
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 788-5100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Light chain - AA
US-09-372-425A-4
Query Match 93.9%; Score 62; DB 4; Length 234;
Best Local Similarity 92.3%; Pred. No. 0.017;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
|||:|||||||
Db 41 SGGSSNIGNNVYS 53

RESULT 20
US-08-665-202-5
Sequence 5, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-202-5

Query Match 93.9%; Score 62; DB 2; Length 258;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 167 SGSSSNIGNNYVS 179

RESULT 21
US-09-315-574-5
Sequence 5, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-315-574-5

Query Match 93.9%; Score 62; DB 4; Length 258;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 167 SGSSSNIGNNYVS 179

RESULT 22
US-09-069-821-4
Sequence 4, Application US/09069821
Patent No. 6323322
GENERAL INFORMATION:
APPLICANT: FILPULA, DAVID
APPLICANT: WANG, MAOLANG
APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821
FILING DATE: 30-APR-1998
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977, 2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-069-821-4

Query Match 93.9%; Score 62; DB 3; Length 262;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 23
US-09-956-086-4
Sequence 4, Application US/09956086
Patent No. 6743696
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LISHYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNF, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977, 2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. 6743896 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-086-4

Query Match 93.9%; Score 62; DB 4; Length 262;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 24
US-09-956-087-4
Sequence 4, Application US/09956087
Patent No. 6743908
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LISHYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNF, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977, 2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 262 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-087-4

Query Match 93.9%; Score 62; DB 4; Length 262;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:|||||
DB 23 SGSSSNIGNNVYS 35

RESULT 25
US-09-420-592A-7
; Sequence 7, Application US/09420592A
; Patent No. 633396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-420-592A-7

Query Match 93.9%; Score 62; DB 3; Length 282;
Best Local Similarity 92.3%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:|||||
DB 23 SGSSSNIGNNVYS 35

RESULT 26
US-09-985-442-7
; Sequence 7, Application US/09985442
; Patent No. 6692942
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6692942el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-985-442-7;

Query Match 93.9%; Score 62; DB 4; Length 282;
Best Local Similarity 92.3%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:|||||
DB 23 SGSSSNIGNNVYS 35

RESULT 27
US-09-983-580-7
; Sequence 7, Application US/09983580
; Patent No. 6764853
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6764853el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-983-580-7

Query Match 93.9%; Score 62; DB 4; Length 282;
Best Local Similarity 92.3%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:|||||
DB 23 SGSSSNIGNNVYS 35

RESULT 28
US-08-652-816A-15
; Sequence 15, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Oebourm, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A

;; FILING DATE: 23-MAY-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9125579.4
;; FILING DATE: 02-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9125579.8
;; FILING DATE: 02-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9206318.9
;; FILING DATE: 24-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9206372.6
;; FILING DATE: 23-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9525004.9
;; FILING DATE: 07-DEC-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9610824.6
;; FILING DATE: 23-MAY-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB92/02240
;; FILING DATE: 02-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/244,597
;; FILING DATE: 01-JUN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: David W. Clough
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 28111/33308
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
US-08-652-816A-15

Query Match 92.4%; Score 61; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 SGTSTNIGNNYVS 13
Db 23 SGTSTNIGNNYVS 35

RESULT 29
US-08-665-202-40
Sequence 40, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,238
;; FILING DATE: 14-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,250
;; FILING DATE: 15-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hunter, Tom
;; REGISTRATION NUMBER: 38,498
;; REFERENCE/DOCKET NUMBER: 02307E-061410
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-665-202-40

Query Match 87.9%; Score 58; DB 2; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.035;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 SGTSTNIGNNYVS 13
Db 23 SGTSTNIGNNYVS 35

RESULT 30
US-09-315-574-40
Sequence 40, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-40

Query Match 87.9%; Score 58; DB 4; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.035;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
||:|||||
Db 23 SGSTSNIGNNYVS 35

RESULT 31
US-08-211-202-112
Sequence 112, Application US/08211202
Patent No. 5565332

GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESS: Boston
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211.202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-112

Query Match 87.9%; Score 58; DB 1; Length 113;
Best Local Similarity 91.7%; Pred. No. 0.035;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
||:|||||
Db 23 SGSSSNIGNNTV 34

RESULT 32
US-09-240-274-55
Sequence 55, Application US/09240274
Patent No. 6253455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THERMOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240.274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081.380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028.550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I03
US-09-240-274-55

Query Match 86.4%; Score 57; DB 3; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
||:|||||
Db 22 SGSSSNIGNNTVS 34

RESULT 33
US-09-025-769B-32
Sequence 32, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Hiding
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-32

Query Match 86.4%; Score 57; DB 3; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:||||:||||
Db 23 SGSSSNIGNNYVS 35

RESULT 34
US-09-025-769B-51
Sequence 51, Application US/09025769B
GENERAL INFORMATION:
PATENT No. 6300064
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, VIC
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-51

Query Match 86.4%; Score 57; DB 3; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:||||:||||
Db 23 SGSSSNIGNNYVS 35

RESULT 35
US-09-490-070A-32
Sequence 32, Application US/09490070A
PATENT No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, VIC
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2000
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-490-070A-32

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:||||:||||
Db 23 SGSSSNIGNNYVS 35

RESULT 36
US-09-490-070A-51

Sequence 51, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McLaughlin
1666 K Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2000
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-490-070A-51

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
DB 23 SSSSSNIGNNVYS 35

RESULT 37
US-09-490-153-32
Sequence 32, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
City: New York
STATE: New York

COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-490-153-32

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
DB 23 SSSSSNIGNNVYS 35

RESULT 38
US-09-490-153-51
Sequence 51, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
City: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-490-153-51

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 39
US-09-490-324-32
Sequence 32, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-490-324-32

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 40
US-09-490-324-51
Sequence 51, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-490-324-51

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

Search completed: March 31, 2005, 12:13:27
Job time : 26.3906 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 12:10:00 ; Search time 72.7188 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNVYS 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	66	100.0	240 10 US-09-880-748-1898	Sequence 1898, Ap
2	66	100.0	240 15 US-10-293-418-1898	Sequence 1898, Ap
3	66	100.0	243 10 US-09-880-748-1927	Sequence 1927, Ap
4	66	100.0	243 14 US-10-322-673-53	Sequence 53, Appl
5	66	100.0	243 15 US-10-293-418-1927	Sequence 1927, Ap
6	66	100.0	245 10 US-09-880-748-1926	Sequence 1926, Ap
7	66	100.0	245 15 US-10-293-418-1926	Sequence 1926, Ap
8	66	100.0	245 15 US-10-293-418-1926	Sequence 1926, Ap
9	66	100.0	246 10 US-09-880-748-1913	Sequence 1913, Ap
10	66	100.0	246 10 US-09-880-748-1917	Sequence 1917, Ap
11	66	100.0	246 15 US-10-293-418-1913	Sequence 1913, Ap
12	66	100.0	246 15 US-10-293-418-1917	Sequence 1917, Ap
13	66	100.0	247 10 US-09-880-748-1443	Sequence 1443, Ap

14	66	100.0	247 10 US-09-880-748-1682	Sequence 1682, Ap
15	66	100.0	247 10 US-09-880-748-1707	Sequence 1707, Ap
16	66	100.0	247 10 US-09-880-748-1899	Sequence 1899, Ap
17	66	100.0	247 10 US-09-880-748-1928	Sequence 1928, Ap
18	66	100.0	247 10 US-09-880-748-1934	Sequence 1934, Ap
19	66	100.0	247 15 US-10-293-418-1443	Sequence 1443, Ap
20	66	100.0	247 15 US-10-293-418-1682	Sequence 1682, Ap
21	66	100.0	247 15 US-10-293-418-1707	Sequence 1707, Ap
22	66	100.0	247 15 US-10-293-418-1899	Sequence 1899, Ap
23	66	100.0	247 15 US-10-293-418-1928	Sequence 1928, Ap
24	66	100.0	247 15 US-10-293-418-1934	Sequence 1934, Ap
25	66	100.0	249 10 US-09-880-748-1419	Sequence 1419, Ap
26	66	100.0	249 10 US-09-880-748-1618	Sequence 1618, Ap
27	66	100.0	249 10 US-09-880-748-1698	Sequence 1698, Ap
28	66	100.0	249 15 US-10-293-418-1419	Sequence 1419, Ap
29	66	100.0	249 15 US-10-293-418-1618	Sequence 1618, Ap
30	66	100.0	249 15 US-10-293-418-1698	Sequence 1698, Ap
31	66	100.0	251 10 US-09-880-748-1309	Sequence 1309, Ap
32	66	100.0	251 10 US-09-880-748-1671	Sequence 1671, Ap
33	66	100.0	251 10 US-09-880-748-1809	Sequence 1809, Ap
34	66	100.0	251 15 US-10-293-418-1309	Sequence 1309, Ap
35	66	100.0	251 15 US-10-293-418-1671	Sequence 1671, Ap
36	66	100.0	251 15 US-10-293-418-1809	Sequence 1809, Ap
37	66	100.0	252 10 US-09-880-748-988	Sequence 988, Ap
38	66	100.0	252 10 US-09-880-748-1698	Sequence 1698, Ap
39	66	100.0	252 15 US-10-293-418-988	Sequence 988, Ap
40	66	100.0	252 15 US-10-293-418-1698	Sequence 1698, Ap
41	66	100.0	253 10 US-09-880-748-935	Sequence 935, Ap
42	66	100.0	253 10 US-09-880-748-935	Sequence 935, Ap
43	66	100.0	253 10 US-09-880-748-939	Sequence 939, Ap
44	66	100.0	253 10 US-09-880-748-1611	Sequence 1611, Ap
45	66	100.0	253 10 US-09-880-748-1936	Sequence 1936, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1898
; Sequence 1898, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match 100.0%; Score 66; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
DB 153 SGSTSNIGNNVYS 165

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RESULT 2
US-10-293-418-1898
; Sequence 1898, Application US/10293418
; Publication No. US200302396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1898

Query Match          100.0%; Score 66; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGTSTNIGNNYVS 13
Db      153 SGTSTNIGNNYVS 165

RESULT 3
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

Query Match          100.0%; Score 66; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGTSTNIGNNYVS 13
Db      153 SGTSTNIGNNYVS 165
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGTSTNIGNNYVS 13
Db      155 SGTSTNIGNNYVS 167

RESULT 4
US-10-322-673-53
; Sequence 53, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PFS85
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-322-673-53

Query Match          100.0%; Score 66; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGTSTNIGNNYVS 13
Db      155 SGTSTNIGNNYVS 167

RESULT 5
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US200302396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
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; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match 100.0%; Score 66; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 155 SGSTSNIGNNYVS 167

RESULT 6
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; Sequence 1926, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926

Query Match 100.0%; Score 66; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 157 SGSTSNIGNNYVS 169

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; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926

Query Match 100.0%; Score 66; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 157 SGSTSNIGNNYVS 169

RESULT 8
US-10-293-418-3241
; Sequence 3241, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3241
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3241

Query Match 100.0%; Score 66; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 157 SGSTSNIGNNYVS 169

RESULT 9
US-09-880-748-1913
; Sequence 1913, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523

;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1913

Query Match 100.0%; Score 66; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 158 SGSTSNIGNNYVS 170

RESULT 10
US-09-880-748-1917
;; Sequence 1917, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1917
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1917

Query Match 100.0%; Score 66; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 158 SGSTSNIGNNYVS 170

RESULT 11
US-10-293-418-1913
;; Sequence 1913, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

;; FILE REFERENCE: P523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1913

Query Match 100.0%; Score 66; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 158 SGSTSNIGNNYVS 170

RESULT 12
US-10-293-418-1917
;; Sequence 1917, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1917
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1917

Query Match 100.0%; Score 66; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13

Db 158 SGSTSNIGNNVYS 170

RESULT 13
US-09-880-748-1443
; Sequence 1443, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1443

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 14
US-09-880-748-1682
; Sequence 1682, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1682

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 15
US-09-880-748-1707
; Sequence 1707, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1707
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1707

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 16
US-09-880-748-1899
; Sequence 1899, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1899

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 17

US-09-880-748-1928
; Sequence 1928, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1928

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 18
US-09-880-748-1934
; Sequence 1934, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1934

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 19

US-10-293-418-1443
; Sequence 1443, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1443

Query Match 100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 20
US-10-293-418-1682
; Sequence 1682, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17

Query Match 100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;


```

; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1682

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  SGSTSNIGNNVYS 13
        |||||
Db      159  SGSTSNIGNNVYS 171

RESULT 21
US-10-293-418-1707
; Sequence 1707, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1707
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1707

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  SGSTSNIGNNVYS 13
        |||||
Db      159  SGSTSNIGNNVYS 171

RESULT 22
US-10-293-418-1899
; Sequence 1899, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817

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; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1899

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  SGSTSNIGNNVYS 13
        |||||
Db      159  SGSTSNIGNNVYS 171

RESULT 23
US-10-293-418-1928
; Sequence 1928, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1928

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  SGSTSNIGNNVYS 13
        |||||
Db      159  SGSTSNIGNNVYS 171

RESULT 24
US-10-293-418-1934

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; Sequence 1934, Application US/10293418
; Publication No. US200302239641
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1934
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Query Match
Best Local Similarity 100.0%; Score 66; DB 15; Length 247;
Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 159 SGSTSNIGNNYVS 171
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RESULT 25
US-09-880-748-1419
; Sequence 1419, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1419
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1419
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Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 249;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
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```
Db 161 SGSTSNIGNNYVS 173
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RESULT 26
US-09-880-748-1618
; Sequence 1618, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1618
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```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 249;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 161 SGSTSNIGNNYVS 173
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```
RESULT 27
US-09-880-748-2049
; Sequence 2049, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2049
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2049
```

```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 249;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 2000
 ; PRIOR APPLICATION NUMBER:

```

; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1309
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1309

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 251;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTSNIGNNYVS 13
Db      163 SGSTSNIGNNYVS 175

RESULT 32
US-09-880-748-1671
; Sequence 1671, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1671
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1671

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 251;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTSNIGNNYVS 13
Db      163 SGSTSNIGNNYVS 175

RESULT 33
US-09-880-748-1809
; Sequence 1809, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1809
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1809

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 251;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTSNIGNNYVS 13
Db      163 SGSTSNIGNNYVS 175
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```

; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1809
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1809

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 251;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTSNIGNNYVS 13
Db      163 SGSTSNIGNNYVS 175

RESULT 34
US-10-293-418-1309
; Sequence 1309, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1309
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1309

Query Match
Best Local Similarity 100.0%; Score 66; DB 15; Length 251;
Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTSNIGNNYVS 13
Db      163 SGSTSNIGNNYVS 175

RESULT 35
US-10-293-418-1671
; Sequence 1671, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
```

;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1671
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1671

Query Match 100.0%; Score 66; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||||
Db 163 SGSTSNIGNNVYS 175

RESULT 36
US-10-293-418-1809
;; Sequence 1809, Application US/10293418
;; Publication No. US2003022396A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1809
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1809

Query Match 100.0%; Score 66; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||||

Db 163 SGSTSNIGNNVYS 175
RESULT 37
US-09-880-748-988
;; Sequence 988, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 988
;; LENGTH: 252
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-988

Query Match 100.0%; Score 66; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||||
Db 163 SGSTSNIGNNVYS 175

RESULT 38
US-09-880-748-1698
;; Sequence 1698, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1698
;; LENGTH: 252
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1698

Query Match 100.0%; Score 66; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||||

Db 164 SGSTSNIGNNYVS 176

RESULT 39

US-10-293-418-988
 ; Sequence 988, Application US/10293418
 ; Publication No. US2003023996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: p5523p2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 988
 ; LENGTH: 252
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-988

Query Match 100.0%; Score 66; DB 15; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
 Db 163 SGSTSNIGNNYVS 175

RESULT 40

US-10-293-418-1698
 ; Sequence 1698, Application US/10293418
 ; Publication No. US2003023996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: p5523p2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1698
 ; LENGTH: 252
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-1698

Query Match 100.0%; Score 66; DB 15; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
 Db 164 SGSTSNIGNNYVS 176

Search completed: March 31, 2005, 12:46:09
 Job time : 73.7188 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:19 ; Search time 18.4844 Seconds
(without alignments)
67.666 Million cell updates/sec

Title: US-10-614-959-13

Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	93.9	98	2 S36050	Ig lambda chain -
2	62	93.9	111	2 S47009	Ig lambda chain V1
3	62	93.9	111	2 S19664	Ig lambda chain V
4	62	93.9	113	2 A29700	Ig lambda chain V
5	62	93.9	232	2 S25742	Ig lambda chain -
6	62	93.9	235	2 S05270	Ig lambda chain pr
7	59	89.4	130	2 S09712	Ig lambda chain V
8	57	86.4	130	1 LIHUBL	Ig lambda chain pr
9	56	84.8	111	2 S47185	Ig lambda chain pr
10	55	84.8	111	2 S24321	Ig lambda chain -
11	55	83.3	111	1 LIHUNW	Ig lambda chain pr
12	53	80.3	98	2 S36048	Ig lambda chain V-
13	53	80.3	111	1 LIHUNG	Ig lambda chain -
14	53	80.3	129	2 S78058	Ig lambda chain pr
15	53	80.3	130	2 S78057	Ig lambda chain pr
16	52	78.8	109	1 LIHUEP	Ig lambda chain V-
17	50	75.8	98	2 S36046	Ig lambda chain -
18	49	74.2	234	2 S25757	Ig lambda chain -
19	48	72.7	112	2 C44151	Ig lambda chain V
20	46	69.7	216	2 A42193	Ig lambda chain (B
21	45	68.2	98	2 S36047	Ig lambda chain -
22	45	68.2	110	2 S36258	Ig lambda chain V
23	45	68.2	112	2 D44151	Ig lambda chain pr
24	45	68.2	117	2 S23627	Ig lambda chain pr
25	45	68.2	233	2 S25752	Ig lambda chain -
26	44	66.7	112	2 A44151	Ig lambda chain V
27	44	66.7	112	2 B44151	Ig lambda chain V
28	44	66.7	235	2 S25754	Ig lambda chain -
29	43.5	65.9	235	2 S14675	Ig lambda chain -

30	43	65.2	95	2 S49571	Ig lambda chain pr
31	43	65.2	149	2 S23626	Ig lambda chain V
32	43	65.2	2272	2 T18572	gag, pol and env p
33	43	65.2	2500	2 G71609	hypothetical prote
34	42	63.6	110	2 S57428	Ig light chain V-J
35	42	63.6	110	2 S57408	Ig lambda chain V-
36	42	63.6	233	2 S25744	Ig lambda chain -
37	42	63.6	348	2 F96997	uncharacterized co
38	41	62.1	99	2 S36054	Ig lambda chain -
39	41	62.1	107	2 B46516	Ig lambda chain V
40	41	62.1	111	1 L6HUT4	Ig lambda chain V-
41	41	62.1	112	1 LIHUM4	Ig lambda chain V-
42	41	62.1	414	2 A71646	5-aminolevulinat
43	40	60.6	109	1 LIHUMA	Ig lambda chain V-
44	40	60.6	112	1 LIHUMA	Ig lambda chain V-
45	40	60.6	217	2 JB0246	Ig lambda chain NI

ALIGNMENTS

RESULT 1

S36050
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36050
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36050
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <M1>
A:Cross-references: EMBL:Z22191; NID:G312298; PIDN:CAA80201.1; PTD:G312299
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:15-91/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 93.9%; Score 62; DB 2; Length 98;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SSSSSNIGNNYVS 35

RESULT 2

S47009
Ig lambda chain V1-J3 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47009
R:Mamoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
Submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A:Reference number: S47009
A:Accession: S47009
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <MAH>
A:Cross-references: EMBL:Z35495; NID:G517346; PIDN:CAA84629.1; PTD:G517347
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:15-91/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 92.3%; Score 62; DB 2; Length 111;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SSSSSNIGNNYVS 35

Db 23 SGSSSNIGNNVYS 35

RESULT 3

S19664

Ig lambda chain V region (clone alpha-phox15) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19664; S24444

R/Marker: J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19664

A/Molecule type: mRNA

A/Residues: 1-111 <MAR>

A/Cross-references: EMBL:X61641

R/Jones, P.T.

Submitted to the EMBL Data Library, October 1991

A/Reference number: S24442

A/Accession: S24444

A/Molecule type: mRNA

A/Residues: 1-110, 'W' <DON>

A/Cross-references: EMBL:X61641; NID:G35458; PIDN:CAA43822.1; PID:G1335271

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111;

Best Local Similarity 92.3%; Pred. No. 0.0011;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 23 SGSSSNIGNNVYS 35

RESULT 4

A29700

Ig lambda chain V region (zim) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000

C/Accession: A29700

R/Bulter, M.; Brenner, M.; Linke, R.P.

Biol. Chem. Hoppe-Seyler 368, 863-870, 1987

A/Title: Is the formation of AL-type amyloid promoted by structural peculiarities of immunoglobulin

A/Reference number: A29700; MUID:87299022; PMID:3620114

A/Accession: A29700

A/Molecule type: protein

A/Residues: 1-113 <EUL>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/14-90/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 113;

Best Local Similarity 92.3%; Pred. No. 0.0012;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 SGSSSNIGNNVYS 34

RESULT 5

S25742

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S25742

R/Combracio, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A/Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lambda

A/Reference number: S16439; MUID:91257162; PMID:11904362

A/Accession: S25742

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-232 <COM>

A/Cross-references: EMBL:X57806; NID:G33709; PIDN:CAA40944.1; PID:G33710

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/147-215/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 232;

Best Local Similarity 92.3%; Pred. No. 0.0025;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 39 SGSSSNIGNNVYS 51

RESULT 6

S05270

Ig lambda chain precursor - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C/Accession: S05270; S04601

R/Kishimoto, T.

Submitted to the EMBL Data Library, March 1989

A/Reference number: S05270

A/Accession: S05270

A/Molecule type: mRNA

A/Residues: 1-235 <KIS1>

A/Cross-references: EMBL:X14583; NID:G33394; PIDN:CAA32725.1; PID:G33395

R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A/Reference number: S04601; MUID:89206497; PMID:2500644

A/Accession: S04601

A/Molecule type: mRNA

A/Residues: 1-130 <KIS2>

A/Cross-references: EMBL:X14583

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/1-20/Domain: signal sequence #status predicted <SIG>

F/21-235/Product: Ig lambda chain #status predicted <MAT>

F/150-218/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 235;

Best Local Similarity 92.3%; Pred. No. 0.0025;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 42 SGSSSNIGNNVYS 54

RESULT 7

S09712

Ig lambda chain V region - human

C/Species: Homo sapiens (man)

C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S09712

R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.

Biochem. J. 268, 135-140, 1990

A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of

A/Reference number: S09710; MUID:90262535; PMID:2111699

A/Accession: S09712

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-130 <HUG>

A/Cross-references: GB:X52109; NID:G31454; PIDN:CAA36343.1; PID:G31455

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/34-110/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 59; DB 2; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.0045;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 42 SGTSSNIGNNYVS 54

RESULT 8
L1HNB
Ig lambda chain precursor V-I region (BL2) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A01966
R/Tsuji moto, Y.; Croce, C.M.
Nucleic Acids Res. 12, 8407-8414, 1984
A/Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.
A/Reference number: A01966; MUID:85062823; PMID:6095199
A/Accession: A01966
A/Molecule type: mRNA
A/Residues: 1-130 <TSU>
A/Cross-references: UNIPROT:P06316; GB:X01147; NID:G33335; PIDN:CAA5598.1; PID:G758087
C/Genetics:
A/Gene: GDB:IGLV@
A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-115/Region: V segment
F/34-110/Domain: immunoglobulin homology <IMM>
F/116-130/Region: J segment
F/41-108/Disulfide bonds: #status predicted

Query Match 86.4%; Score 57; DB 1; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 42 SGTSSNIGNNYVS 54

RESULT 9
S47185
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Westman, A.P.
submitted to the EMBL Data Library, June 1994
A/Description: Cloning and analysis of Igm anti-chryoglobulin autoantibodies from patien
A/Reference number: S47181
A/Accession: S47185
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-111 <MC>
A/Cross-references: EMBL:X79782; NID:G506428; PIDN:CAA56178.1; PID:G506429
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/14-90/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 56; DB 2; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.013; 1; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 22 SGTSSNIGNNYVS 34

RESULT 10
S24321
Ig lambda chain precursor - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S24321
R/Aucouturier, P.; Khamilchi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne,
Biochem. J. 285, 149-152, 1992
A/Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr
A/Reference number: S24319; MUID:92344562; PMID:1379039
A/Accession: S24321
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-131 <AUC>
A/Cross-references: EMBL:X64134; NID:932808; PIDN:CAA5495.1; PID:G32809
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-110/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 56; DB 2; Length 131;
Best Local Similarity 84.6%; Pred. No. 0.015; 1; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 42 SGTSSNIGNNYVS 54

RESULT 11
L1HNB
Ig lambda chain V-I region (New) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C/Accession: A01964
R/Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A/Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg
A/Reference number: A01964; MUID:65060892; PMID:4177823
A/Accession: A01964
A/Molecule type: protein
A/Residues: 1-111 <LAN>
A/Cross-references: UNIPROT:P01701
C/Comment: This is a Bence Jones protein.
C/Genetics:
A/Gene: GDB:IGLV@
A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: blocked amino end; heterotetramer
F/15-91/Domain: immunoglobulin homology <IMM>
F/11/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F/22-89/Disulfide bonds: #status predicted

Query Match 83.3%; Score 55; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.019; 1; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 23 SGTSSNIGNNYVS 35

RESULT 12
S36048
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36048; S36049
R/Williams, S.C.

submitted to the EMBL Data Library, April 1993

A:Reference number: S36046
A:Accession: S36046
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <HW>
A:Cross-references: EMBL:Z22189; NID:9312294; PIDN:CAA80199.1; PID:9312295; EMBL:Z22190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 0.037;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
|||:||||:|
Db 23 SGSSSNIGNNVY 34

RESULT 13

L1HUNG

Ig lambda chain V-I region (Nig-64) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01965
R:Kamezani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
A:Title: Comparative studies on the structure of the light chains of human immunoglobulin
A:Reference number: A91970; MUID:83186114; PMID:6404900
A:Accession: A01965
A:Molecule type: protein
A:Residues: 1-111 <KM>
A:Cross-references: UNIPROT:P01702
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer
F:15-91/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status
F:22-89/Disulfide bonds: #status predicted

Query Match 80.3%; Score 53; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.042;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 13
|||:||||:|
Db 23 SGSSSNIGNNVY 35

RESULT 14

S78058

Ig lambda chain precursor V-J region (clone MAB 67VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78058; S23723
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78058
A:Accession: S78058
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: EMBL:X5446; NID:937923; PIDN:CAA8313.1; PID:9330121
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockings
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1178404

A:Accession: S23723

A:Molecule type: mRNA
A:Residues: 19-129 <HAR>
A:Cross-references: EMBL:X5446
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:33-109/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 129;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
|||:||||:|
Db 41 SGSSSNIGNNVY 52

RESULT 15

S78057

Ig lambda chain precursor V-J region (Epos) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78057; S23722
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78057
A:Molecule type: mRNA
A:Residues: 1-130 <HAR>
A:Cross-references: EMBL:X54438; NID:937920; PIDN:CAA8307.1; PID:937921
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockings,
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1178404
A:Accession: S23722
A:Molecule type: mRNA
A:Residues: 20-130 <HAR>
A:Cross-references: EMBL:X54438
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:1-19/Domain: signal sequence (fragment) #status predicted <MAT>
F:20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 130;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
|||:||||:|
Db 42 SGSSSNIGNNVY 53

RESULT 16

L1HTEP

Ig lambda chain V-I region (Epos) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A24656
R:Toft, K.G.; Sletten, K.; Huseby, G.
Biol. Chem. Hoppe-Seyler 366, 617-625, 1985
A:Title: The amino-acid sequence of the variable region of a carbohydrate-containing anti
A:Reference number: A24656; MUID:86000126; PMID:3529803
A:Accession: A24656
A:Molecule type: protein
A:Residues: 1-109 <TOF>
A:Cross-references: UNIPROT:P06888
A:Note: residues 1-2, 56-62, and 74-78 and the sequenced peptides were positioned by hom
C:Genetics:
A:Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 12 C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: amyloid; blocked amino end; glycoprotein; heterotetramer; immunoglobulin F/11-91/Domain: immunoglobulin homology <IMM>
F/11/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status F/12-89/Disulfide bonds: #status predicted
F/14/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 78.8%; Score 52; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.061;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
DB 23 SGSSSNIGNNV 34

RESULT 17
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S36046
R/Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36046
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <WILL>
A/Cross-references: EMBL:Z22187; NID:G312312; PIDN:CAA80197.1; PID:G312313
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 75.8%; Score 50; DB 2; Length 98;
Best Local Similarity 76.9%; Pred. No. 0.12;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 13
DB 23 SGSSSNIGNNV 35

RESULT 18
Ig lambda chain - human (fragment)
S25757
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25757
R/Combario, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda)-C(lambda) gene sequences of the human immunoglobulin lambda F/149-217/Domain: immunoglobulin homology <IMM>
A/Accession: S25757
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-234 <COM>
A/Cross-references: EMBL:X57822; NID:G33743; PIDN:CAA40959.1; PID:G33744
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 74.2%; Score 49; DB 2; Length 234;
Best Local Similarity 76.9%; Pred. No. 0.46;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 13
DB 41 SGSTSNIGNNV 53

RESULT 19
C44151
Ig lambda chain V region (BO-10) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C/Accession: C44151
R/Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotlien, R.H.; Graff, R.; Degraw, J.; Fyfe, J.; Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A/Reference number: A44151; MUID:9228746; PMID:1373487
A/Accession: C44151
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-112 <ZEB>
A/Note: nucleotide translation not given
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/14-90/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 48; DB 2; Length 112;
Best Local Similarity 76.9%; Pred. No. 0.31;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 13
DB 22 SGSTSNIGNNV 34

RESULT 20
A42193
Ig lambda chain (BJP-DIA) - human
N/Alternate names: amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda chain (C)Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jan-2000
C/Accession: A42193; S18297
R/Klaflki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N.
Biochemistry 31, 3265-3272, 1992
A/Title: Complete amino acid sequence determination demonstrate identity of the urinary A/Reference number: A42193; MUID:92207944; PMID:1554711
A/Accession: A42193
A/Molecule type: protein
A/Residues: 1-216 <KLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F/131-199/Domain: immunoglobulin homology <IMM>
F/11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 69.7%; Score 46; DB 2; Length 216;
Best Local Similarity 69.2%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 13
DB 23 SGSSSNIGNNV 35

RESULT 21
S36047
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36047
R/Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36047
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <WILL>
A/Cross-references: EMBL:Z22186; NID:G312291; PIDN:CAA80198.1; PID:G312292
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

F;15-91/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 98;
Best Local Similarity 69.2%; Pred. No. 0.9;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 23 SGSSSNIGSNTVN 35

RESULT 22

S36258

Ig lambda chain V region (clone alpha-CD4-74) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C;Accession: S36258

R;Gifflth, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage display libraries.

A;Reference number: S36256; MUID:93178446; PMID:7679990

A;Accession: S36258

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-110 <GRI>

A;Cross-references: EMBL:Z18849

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-91/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 110;
Best Local Similarity 76.9%; Pred. No. 1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 23 SGSSSNIGSNTVN 35

RESULT 23

D44151

Ig lambda chain V region (BO-12) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C;Accession: D44151

R;Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotien, R.H.; Graff, R.; Degraw, J.; Pyat

Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992

A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.

A;Reference number: A44151; MUID:9228746; PMID:1373487

A;Accession: D44151

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-112 <ZEB>

A;Note: nucleotide translation is not given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-90/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 112;
Best Local Similarity 69.2%; Pred. No. 1;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 22 SGSSSNIGSNTVN 34

RESULT 24

S23627

Ig lambda chain precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S23627

R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Dettos, M.; Kozin, F.; Carson, D.A.; C

J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv

A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23627

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-117 <OLE>

A;Cross-references: EMBL:X59707; NID:G34426; PIDN:CAA42228.1; PID:G34427

C;Genetics:

A;Intons: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-110/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 117;
Best Local Similarity 69.2%; Pred. No. 1.1;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 42 SGSSSNIGSNTVN 54

RESULT 25

S25752

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S25752

R;Comitato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A;Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lamt

A;Reference number: S16439; MUID:91257162; PMID:1904362

A;Accession: S25752

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-233 <COM>

A;Cross-references: EMBL:X57817; NID:G33733; PIDN:CAA40954.1; PID:G33734

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 233;
Best Local Similarity 69.2%; Pred. No. 2.3;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 40 SGSSSNIGSNTVN 52

RESULT 26

A44151

Ig lambda chain V region (BO-08) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C;Accession: A44151

R;Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotien, R.H.; Graff, R.; Degraw, J.; Pyat

Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992

A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.

A;Reference number: A44151; MUID:9228746; PMID:1373487

A;Accession: A44151

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-112 <ZEB>

A;Note: nucleotide translation not given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-90/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 112;
Best Local Similarity 69.2%; Pred. No. 1.6;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 22 SGTSSNIGNTVNV 34

RESULT 27

Ig Lambda chain V region (BO-09) - human (fragment)
 B44151
 C:Species: Homo sapiens (man)
 C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
 C:Accession: B44151
 R:Zabedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; Degraw, J.; Pya
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
 A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
 A:Reference number: A44151; MUID:92228746; PMID:1373487
 A:Accession: B44151
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-112 <ZEB>
 A:Cross-references: GB:M88310; NID:g183954; PIDN:AAA5968.1; PID:g183955
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 112;
 Best Local Similarity 69.2%; Pred. No. 1.6;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 22 SGTSSNIGNTVNV 34

RESULT 28

Ig Lambda chain - human (fragment)
 S25754
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S25754
 R:Combratio, G.; Klobeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A:Title: V(lambda) and V(lambda) gene segments of the human immunoglobulin lan
 A:Reference number: S16439; MUID:91257162; PMID:1904362
 A:Accession: S25754
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-235 <COM>
 A:Cross-references: EMBL:X57819; NID:g33737; PIDN:CAA40956.1; PID:g33738
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 235;
 Best Local Similarity 69.2%; Pred. No. 3.4;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 41 SGTSSNIGNTVNV 53

RESULT 29

Ig Lambda chain - human
 S14675
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
 C:Accession: S14675; S12445
 R:Vasilek, T.J.
 submitted to the EMBL Data Library, February 1990
 A:Reference number: S14675
 A:Accession: S14675

A:Molecule type: DNA
 A:Residues: 1-235 <VAS1>
 A:Cross-references: UNIPROT:Q8WUK4; EMBL:X51754
 R:Vasilek, T.J.; Leder, P.
 J. Exp. Med. 172, 609-620, 1990
 A:Title: Structure and expression of the human immunoglobulin lambda genes.
 A:Reference number: S12440; MUID:90324881; PMID:2115572
 A:Accession: S12445
 A:Molecule type: DNA
 A:Residues: 1-129 <VAS2>
 A:Cross-references: EMBL:X51754
 C:Genetics:
 A:Introns: 16/1; 130/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 65.9%; Score 43.5; DB 2; Length 235;
 Best Local Similarity 71.4%; Pred. No. 4.2;
 Matches 10; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 42 SGTSSDIGNNYVS 55

RESULT 30

Ig lambda chain precursor V region - human (fragment)
 S49571
 C:Species: Homo sapiens (man)
 C>Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C:Accession: S49571
 R:Giachino, C.; Padovan, E.; Lanzavecchia, A.
 submitted to the EMBL Data Library, November 1994
 A:Description: K+1+ dual receptor B cells are present in the human peripheral repertoire
 A:Reference number: S49571
 A:Accession: S49571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-95 <G1A>
 A:Cross-references: EMBL:Z46625; NID:g575259; PIDN:CAA86595.1; PID:g575260
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 65.2%; Score 43; DB 2; Length 95;
 Best Local Similarity 75.0%; Pred. No. 1.9;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGTSTNIGNNYV 12
 |||:|||||:
 Db 9 SGTSSNIGSNDV 20

RESULT 31

Ig lambda chain V region - human (fragment)
 S23626
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S23626
 R:Olse, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deflos, M.; Kozin, F.; Carson, D.A.;
 J. Exp. Med. 175, 831-842, 1992
 A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
 A:Reference number: S23623; MUID:92156804; PMID:1740665
 A:Accession: S23626
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-149 <OLE>
 A:Cross-references: EMBL:X59706; NID:g34204; PIDN:CAA42227.1; PID:g34205
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:134-110/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 43; DB 2; Length 149;

A;Accession: S57428
A;Status: preliminary

RESULT 37

RESULT 37
F96997

uncharacterized conserved protein of probably eukaryotic origin CAC0793 [Imported] - C1d
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: F96997
R/Molling, J.; Berton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1d
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: F96997
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-348 <KIR>
A/Cross-references: UNIPROT:Q97KX3; GB:AE001437; P1DN:AAK78769.1; P1D:g15023680; GSPDB:C
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC0793

Query Match 63.6%; Score 42; DB 2; Length 348;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 SGSTSNIGNNV 11
|||
Db 158 TGSSNIGACTV 166

RESULT 38
S36054
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36054
R/Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36054
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-99 <MTL>
A/Cross-references: EMBL:Z22195; NID:G312310; P1DN:CAA80205.1; P1D:g312311
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 99;
Best Local Similarity 66.7%; Pred. No. 4.5;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNV 12
|||
Db 23 TGSSNIGACTV 34

RESULT 39
B46516
Ig lambda chain V region - horse (fragment)
C/Species: Equus caballus (domestic horse)
C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: B46516
R/Home, W.A.; Ford, J.E.; Gibson, D.M.
J. Immunol. 149, 3927-3936, 1992
A/Title: L chain isotype regulation in horse. I. Characterization of Ig lambda genes.
A/Reference number: A46516; MUID:93094587; PMID:1460283
A/Accession: B46516
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-107 <HOM>
A/Experimental source: spleen
A/Note: sequence extracted from NCBI backbone (NCBI:120369)
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
F;23-101/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 4.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNV 11
|||
Db 31 TGSSNIGACTV 41

RESULT 40
L6HUT1
Ig lambda chain V-VI region (WLT) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A01989
R/Dwulet, F.E.; Strako, K.; Benson, M.D.
Scand. J. Immunol. 22, 653-660, 1985
A/Title: Amino acid sequence of a lambda VI primary (VL) amyloid protein (WLT).
A/Reference number: A01989; MUID:86122667; PMID:4089539
A/Accession: A01989
A/Molecule type: protein
A/Residues: 1-111 <DMU>
A/Cross-references: UNIPROT:P06318
C/Genetics:
A/Gene: GDB:IGLV6
A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-22/Region: framework 1
F;15-93/Domain: immunoglobulin homology <IMM>
F;23-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-57/Region: complementarity-determining 2
F;58-91/Region: framework 3
F;92-101/Region: complementarity-determining 3
F;102-111/Region: framework 4
F;122-91/Disulfide bonds: #status predicted

Query Match 62.1%; Score 41; DB 1; Length 111;
Best Local Similarity 58.3%; Pred. No. 5.1;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNV 12
|||
Db 23 TGSSNIGACTV 34

Search completed: March 31, 2005, 12:11:15
Job time : 18.4844 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 86.3281 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGTSTNIGNNYVS 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	86.4	130	1 LV1G_HUMAN	P06316 homo sapien
2	56	84.8	101	2 O81ZD8	O81ZD8 homo sapien
3	55	83.3	110	2 O8TE63	O8TE63 homo sapien
4	55	83.3	111	1 LV1C_HUMAN	P01701 homo sapien
5	53	80.3	108	2 O96S80	O96S80 homo sapien
6	53	80.3	111	1 LV1D_HUMAN	P01702 homo sapien
7	52	78.8	109	1 LV1D_HUMAN	P06888 homo sapien
8	52	78.8	235	2 O6IN99	O6IN99 homo sapien
9	51	77.3	236	2 O8NEJ1	O8NEJ1 homo sapien
10	49	74.2	237	2 O6DHM4	O6DHM4 homo sapien
11	45	68.2	221	2 O6GMW6	O6GMW6 homo sapien
12	44	66.7	221	2 O87LH3	O87LH3 vrbrio para
13	44	66.7	326	2 O7SCJ5	O7SCJ5 neurospora
14	44	66.7	441	2 O8JRX2	O8JRX2 phorioranea
15	43	65.2	1170	2 O7WZM9	O7WZM9 pseudomonas
16	43	65.2	1357	2 O9W4M4	O9W4M4 drosophila
17	43	65.2	2186	1 YU52_CAEEL	P34431 caenorhabdi
18	43	65.2	2270	2 O17329	O17329 plasmodium
19	43	65.2	2962	2 O96223	O96223 plasmodium
20	42	63.6	236	2 O6GMV7	O6GMV7 homo sapien
21	42	63.6	348	2 O97KX3	O97KX3 clostridium
22	42	63.6	633	1 ACES_ELEEL	O42275 electrophor
23	41	62.1	111	1 LV6D_HUMAN	P06318 homo sapien
24	41	62.1	112	1 LV1H_HUMAN	O9V7W7 drosophila
25	41	62.1	388	2 O9V7W7	O9V7W7 rickettsia
26	41	62.1	414	1 HEM1_RICPR	O9ACB8 rickettsia
27	41	62.1	414	2 O6BVS3	O6BVS3 debaromyce
28	41	62.1	847	2 O6BVS9	O6BVS9 plasmodium
29	41	62.1	958	2 O7RRT8	O7RRT8 drosophila
30	41	62.1	1272	2 O95SG4	O95SG4 drosophila
31	41	62.1	1272	2 O9W117	O9W117 drosophila

32	41	62.1	1298	2 O81IE2	O81IE2 drosophila
33	41	62.1	1336	2 O81IA0	O81IA0 drosophila
34	41	62.1	1701	2 O81IS0	O81IS0 plasmodium
35	40	60.6	109	1 LV1F_HUMAN	P04208 homo sapien
36	40	60.6	112	1 LV1F_HUMAN	P01700 homo sapien
37	40	60.6	159	2 O8GFE2	O8GFE2 photorhabdu
38	40	60.6	314	2 O76611	O76611 caenorhabdi
39	40	60.6	315	2 O8W1R8	O8W1R8 lycopersico
40	40	60.6	410	2 O8FIZ5	O8FIZ5 escherichia
41	40	60.6	415	2 O9FJF2	O9FJF2 arabidopsis
42	40	60.6	514	2 O47936	O47936 francisella
43	40	60.6	561	2 O7R259	O7R259 neurospora
44	40	60.6	569	2 O7Q967	O7Q967 anopheles g
45	40	60.6	715	1 CLPB_MYCPN	P75247 mycoplasma

ALIGNMENTS

RESULT 1

LV1G_HUMAN STANDARD, PRT: 130 AA.

AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;

RT "Molecular cloning of a human immunoglobulin lambda chain variable
sequence.";

RL Nucleic Acids Res. 12:8407-8414(1984).

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DR EMBL: X01147; CAA25598.1; -.

DR PIR: A01966; L1HUBL.

DR HSSP: P01703; 7FAB.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; IG; 1.

DR SMART: SMO0406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.

DR Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 130 Ig lambda chain V-I region BL2.

FT DOMAIN 20 115 V segment.

FT DOMAIN 116 130 V segment.

FT DISULFID 41 108 By similarity.

FT NON_TER 130 130

SQ SEQUENCE 130 AA; 13564 MW; FA44BBI7D3A55EBF CRC64;

Query Match 86.4%; Score 57; DB 1; Length 130;

Best Local Similarity 84.6%; Pred. No. 0.069;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 SGTSTNIGNNYVS 13

|||||

Db 42 SGGSSNIGNDYVS 54

RESULT 2

Q81ZD8 PRELIMINARY; PRT; 101 AA.
AC Q81ZD8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-chyotoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145444; AAN64328.1; -.
DR HSP; P01703; 7PAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;

Query Match 84.8%; Score 56; DB 2; Length 101;
Best Local Similarity 84.6%; Pred. No. 0.079; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGSTNIGNNYVS 13
Db 13 SGGSSNIGNNYVS 25

RESULT 3

Q8TE63 PRELIMINARY; PRT; 110 AA.
AC Q8TE63;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95007525; PubMed=7923137;
RA Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
RT "Establishment, molecular rescue, and expression of 123AV16-1, a
RT tumor-reactive human monoclonal antibody.";
RL Cancer Res. 54:5178-5185 (1994).
DR EMBL; L33985; AAL68704.1; -.
DR HSP; P01703; 7PAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT CHAIN <1 >110 Immunoglobulin light chain variable
FT region.
FT SEQUENCE 110 AA; 11479 MW; 599D1628F8F5437C CRC64;

Query Match 83.3%; Score 55; DB 2; Length 110;
Best Local Similarity 76.9%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTNIGNNYVS 13
Db 23 SGGSTNIGNNYVS 35

RESULT 4

ID LVIC_HUMAN STANDARD; PRT; 111 AA.
AC P01701;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=69060892; PubMed=4177823;
RA Langer B., Steimetz-Kayne M., Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein New (lambda-
RT type). Subgroups in the variable part of immunoglobulin L-chains of
RT the lambda-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951 (1968).
CC -1 MISCELLANEOUS: This is a Bence-Jones protein.
CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01964; L1HUNW.
DR HSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 105 Ig-like.
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT DISULFID 22 89 By similarity.
FT NON_TER 111 111
FT SEQUENCE 111 AA; 11453 MW; AABCBCA3C49F2AD3 CRC64;

Query Match 83.3%; Score 55; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGSTNIGNNYVS 13
Db 23 SGGSTNIGNNYVS 35

RESULT 5

Q96SBO PRELIMINARY; PRT; 108 AA.
AC Q96SBO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin lambda light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin

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RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AAB68783.1; -.
DR PDB; 1KU4; Model; L=1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
FT NON TER 1
SO SEQUENCE 108 AA; 11594 MW; FAB5DC478A043F48 CRC64;

Query Match 80.3%; Score 53; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 0.28;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGKNVY 12
Db 23 SSSSNIGSNV 34

RESULT 6
LYVID HUMAN STANDARD; PRT; 111 AA.
ID LYVID_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kamezaki F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup."
RL J. Biochem. 93:421-429(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01965; LIHONG.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT MOD_RS 1
FT DISULFID 22 89 By similarity.
FT NON TER 111
SO SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 80.3%; Score 53; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.29;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGKNVY 13
Db 23 SSSSNIGDNFVS 35

RESULT 7
LYVID HUMAN STANDARD; PRT; 109 AA.
ID LYVID_HUMAN STANDARD; PRT; 109 AA.
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86000126; PubMed=3929803;
RA Toft K.G., Stetten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
RT containing amyloid fibril protein EPS (immunoglobulin light chain,
RT type lambda)."
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC -1- MISCELLANEOUS: Residues 1-2, 56-62, and 74-78 and the sequenced
CC peptides were positioned by homology.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A24656; LIHUP.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KM Amyloid; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin V region.
FT DOMAIN 1 105 Ig-like.
FT CARBOHYD 104 104 N-linked (GlcNAc...).
FT DISULFID 22 89 By similarity.
FT NON TER 109 109
SO SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;

Query Match 78.8%; Score 52; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.42;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGKNVY 12
Db 23 SSSSNIGKNVY 34

RESULT 8
O6IN99 PRELIMINARY; PRT; 235 AA.
ID O6IN99 PRELIMINARY; PRT; 235 AA.
AC O6IN99;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE IGLC2 protein.
GN Name=IGLC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sec; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein; 237 AA; 25108 MW; 6814170F7E784825 CRC64;
SQ SEQUENCE

Query Match 74.2%; Score 49; DB 2; Length 237;
Best Local Similarity 83.3%; Pred. No. 3;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTNIGNNVY 12
DB 42 SGSSNIGNNVY 53

RESULT 11
Q6GMW6 PRELIMINARY; PRT; 235 AA.
AC Q6GMW6;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausberg R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlycki S., Carrincci P., Prange C.J.,
RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallajon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Krausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073784; AAH73784.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sec; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.

DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein; 235 AA; 24803 MW; 058B05F6118F1B8 CRC64;
SQ SEQUENCE
Query Match 68.2%; Score 45; DB 2; Length 235;
Best Local Similarity 69.2%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTNIGNNVY 13
DB 42 SGSSNIGNNVY 54

RESULT 12
Q87LH3 PRELIMINARY; PRT; 221 AA.
AC Q87LH3;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Putative short-chain dehydrogenase.
GN OrderedLocustNames=VP2639;
OS Vibrrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 221063 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
RT distinct from that of *V. cholerae*";
RL Lancet 361:743-749(2003).
DR EMBL; AP005082; BAC69092.1; -
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; ADH_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDBRHH.
KM Complete proteome.
SQ SEQUENCE 221 AA; 23803 MW; D545E953C9AB3A2P CRC64;

Query Match 66.7%; Score 44; DB 2; Length 221;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSSTNIGNNVY 13
DB 203 GALANIGNYVS 214

RESULT 13
Q7SCU5 PRELIMINARY; PRT; 326 AA.
AC Q7SCU5;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU00836.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endtizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Seitzemikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Guerre S.,
 RA Kamal M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
 RA Kryscofova S., Kasumseen C., Metzendorf R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Sessler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.,
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
 RL Nature 0:0-0(2003).
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 -1- CAUTION: The sequence shown here is derived from an
 preliminary data.
 CC EMBL: AABX0100101; EAA34466.1; -
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . ; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR000254; CMB fungal.
 DR InterPro: IPR005103; Glyco_hydro_61.
 DR Pfam: PF00734; CBM_1; 1.
 DR Pfam: PF03443; Glyco_hydro_61; 1.
 DR PROSITE: PS00562; CBD_FUNGAL; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 326 AA; 33269 MW; 61BC539A292B59F CRC64;

Query Match 66.7%; Score 44; DB 2; Length 326;
 Best Local Similarity 61.5%; Pred. No. 30;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 SGSTNIGNNVVS 13
 Db 311 SGSTCKVNDYVS 323

RESULT 14
 ID Q9W4M4 PRELIMINARY; PRT; 441 AA.
 AC Q9W4M4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Late expression factor 4.
 GN Name=PhogV087;
 OS Phthorimea operculella granulovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OC NCBI_TaxID=192584;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Croizier L., Taha A., Croizier G., Lopez Ferber M.,
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: A9499596; AAM70285.1; -
 DR GO: GO:0030528; F:transcription regulator activity; IEA.
 DR GO: GO:0045449; P:regulation of transcription; IEA.
 DR InterPro: IPR007790; LEF-4.
 DR Pfam: PF05098; LEF-4; 1.
 SQ SEQUENCE 441 AA; 51639 MW; DC7B3982232B3550 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 441;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SGSTNIGNNV 12
 Db 264 SGNTFNIGNNYL 275

RESULT 15
 Q7WZNS

ID Q7WZNS PRELIMINARY; PRT; 1170 AA.
 AC Q7WZNS;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE PiliY1.
 GN Name=piliY1;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 CC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA14;
 RC PubMed=14983043; DOI=10.1073/pnas.0304622101;
 RA He J., Baldini R.L., Dezell E., Saucier M., Zhang Q., Liberati N.T.,
 RA Lee D., Urbach J., Goodman H.M., Rahne L.G.,
 RA "The broad host range pathogen Pseudomonas aeruginosa strain PA14
 carries two pathogenicity islands harboring plant and animal virulence
 genes.",
 RT Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
 RL EMBL: AY273871; AAP81276.1; -
 DR InterPro: IPR008707; Nucleoside_P1C.
 DR Pfam: PF05557; Nucleoside_P1C; 1.
 DR Pfam: PF05557; Nucleoside_P1C; 1.
 SQ SEQUENCE 1170 AA; 128118 MW; 9F4CDF6D81B62F3 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1170;
 Best Local Similarity 70.0%; Pred. No. 1.ee+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GSSTNIGNNV 11
 Db 139 GSSTNLSNNY 148

RESULT 16
 ID Q9W4M4 PRELIMINARY; PRT; 1357 AA.
 AC Q9W4M4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CG1570-PA.
 GN ORFNames=CG1570;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fostel C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Idaghi M., Kalish F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,

RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., Moleod M.P., Moberg D.,
 RA Merkulov G., Mishina N.V., Moberg D., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
 RA Palazolo M., Peltman G.S., Fan S., Pollard J., Port V., Reese M.G.,
 RA Rinehart K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Strickas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodger, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe W., Dugan S.P., Friese E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Strickas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Strickas R.,
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003430; AAF45927.1; -;
 DR FLYBASE; FBgn0029697; CG15570.
 SQ SEQUENCE 1357 AA; 13690 MW; C282DC6F34A61A CRC64;

YL52 CAEBL STANDARD; PRT; 2166 AA.
 ID YL52 CAEBL
 AC P34431; P34432;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 26-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Hypothetical protein P44E2.2 in chromosome III.
 GN ORFNames=F44E2.2/F44E2.1;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Bristol N2;
 RL MEDLINE=94150718; PubMed=7906398; DOI=10.1038/368032a0;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kersey J., Kirov J., Laisner N.,
 RA Latreille P., Lighthouse J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkeen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer B., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,
 RA Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Bristol N2;
 RL MEDLINE=99069613; PubMed=9851916;
 RA The C. elegans sequencing consortium;
 RT "The genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [3]
 RP REVISIONS AND ALTERNATIVE SPLICING.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=b;
 CC IsoId=P34431-1; Sequence=displayed;
 CC Name=a;
 CC IsoId=P34431-2; Sequence=VSP_005225;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Contains 1 CCHC-type zinc finger.
 CC -1- SIMILARITY: Contains 1 peptidase A1 domain.
 CC -1- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC -----
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 CC -----
 DR EMBL; L23646; AAA28035.2; -;
 DR EMBL; L23646; AAL02516.1; -;
 DR HSP; P03366; 1HMV.
 DR WormBase; WBGene00018416; F44E2.2.
 DR WormBase; F44E2.2a; CE07254.
 DR WormBase; F44E2.2b; CE29321.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR001584; Rye.
 DR InterPro; IPR004477; RVTse.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00665; tve; 1.
 DR Pfam; PF00078; RVT; 1.

RESULT 17

DR Pfam: PF00098; zfc-CCHC; 1.
 DR PRINTS: PR0039; C2HCZNFINGER.
 DR SMART: SM00343; Znf_C2HC; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; 1.
 DR PROSITE: PS50878; RT_POL; 1.
 DR PROSITE: PS50158; ZF_CCHC; 1.
 KM Alternative splicing: Aspartyl protease; Hydrolyase;
 KM Hypothetical protein; RNA-directed DNA polymerase; Transferase;
 KM Zinc-finger.
 FT ZN_FING 589 606 CCHC-type.
 FT DOMAIN 966 1145 Reverse transcriptase.
 FT ACT_SITE 664 664 Processase (By similarity).
 FT VARSPIC 91 101 Missing (in isoform a).
 FT /Ftrd-VSP 005225
 SQ SEQUENCE 2186 AA; 249691 MW; 29C5A10F81FB3D6 CRC64;
 Query Match 65.2%; Score 43; DB 1; Length 2186;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 STSNIGNNV 12
 Db 219 STSNVGNVV 228
 RESULT 18
 Q17329 PRELIMINARY; PRT; 2272 AA.
 ID Q17329
 AC Q17329
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 25, Last annotation update)
 DE Gag, pol and env protein.
 OS Caenothaditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peleodermidae; Caenothaditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Cer1 retrotransposon;
 RX MEDLINE=94150718; PubMed=7906398; DOI=10.1038/368032a0;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kireten J., Laister N., Lattelle P.,
 RA Litching J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Spratt J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Cer1 retrotransposon;
 RX MEDLINE=92168156; PubMed=1538779; DOI=10.1038/356037a0;
 RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
 RA Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Coulson A.,
 RA Craxton M., Durbin R., Berks M., Metzstein M., Hawkins T.,
 RA Ainscough R., Waterston R.,
 RT "The C. elegans genome sequencing project: a beginning (see
 RT comments)";
 RL Nature 356:37-41(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Cer1 retrotransposon;
 RA Britten R.J.;
 RT "Active gypsy/Ty3 retrotransposons or retroviruses in Caenorhabditis
 RT elegans";
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1994).
 RN [4]

RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Cer1 retrotransposon;
 RA Britten R.J.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U15406; AA50456.1; -
 DR PIR: S44816; S44816.
 DR PIR: T18572; T18572.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0003723; F:RNA binding; IEA.
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006310; P:DNA recombination; IEA.
 DR GO: GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR InterPro: IPR001969; Pept_Asp_AS.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR001878; Znf_CCHC.
 DR InterPro: IPR00477; RVase.
 DR Pfam: PF00078; RVT_1; 1.
 DR Pfam: PF00098; ZF_CCHC; 1.
 DR PRINTS: PR0039; C2HCZNFINGER.
 DR SMART: SM00343; Znf_C2HC; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
 DR PROSITE: PS50158; ZF_CCHC; 1.
 KM RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 2272 AA; 259695 MW; 47034F67AC3DA2B0 CRC64;
 Query Match 65.2%; Score 43; DB 2; Length 2272;
 Best Local Similarity 80.0%; Pred. No. 3.2e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 STSNIGNNV 12
 Db 305 STSNVGNVV 314
 RESULT 19
 Q06223 PRELIMINARY; PRT; 2500 AA.
 ID Q06223
 AC Q06223
 DT 01-MAY-1999 (TRENBLREL. 10, Created)
 DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
 DE Hypothetical protein PFB0650w.
 GN Name=PFB0650w;
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99021743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
 RA Gardner M.J., Tettein H., Carucci D.J., Cummings L.M., Aravind L.,
 RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Pederson J.,
 RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perea M.,
 RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
 RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
 RT falciparum";
 RL Science 282:1126-1132(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=2225705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angioli S.,
 RA Berteau M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrett B.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum";

RL Nature 419:498-511(2002).
 DR EMBL; AB001408; AAC71919.1; -.
 DR PIR; G71609; G71609.
 KM Hypothetical protein.
 SQ SEQUENCE 2500 AA; 293886 MW; B91DB801ED521221 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 2500;
 Best Local Similarity 70.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 STSNIGNNV 12
 Db 594 STNNMNNM 603

RESULT 20

06GMV7 PRELIMINARY; PRT; 236 AA.
 AC 06GMV7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carrinell P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.U., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strauberg R.;
 RT Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC073795; AAH73795.1; -.
 DR InterPro; IPR003599; IG 1-like.
 DR InterPro; IPR007110; IG 1-like.
 DR InterPro; IPR003597; IG 1.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR003596; IG V.
 DR Pfam; PF07654; CI-set; 1.
 DR Pfam; PF00047; IG 2.
 DR SMART; SM00409; IG 2.
 DR SMART; SM00407; IG 1.
 DR SMART; SM00406; IG 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KM Hypothetical protein_
 SQ SEQUENCE 236 AA; 24950 MW; 3B0477247847B930 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 236;

Best Local Similarity 69.2%; Pred. No. 48;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SGSTNIGNNV 13
 Db 42 SGSSNIGNNV 54

RESULT 21

097KX3 PRELIMINARY; PRT; 348 AA.
 AC 097KX3;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Uncharacterized conserved protein of probably eukaryotic origin.
 GN Ordered locus names=CAC0793;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 NC NCBI_TaxID=1486;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=1146286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng O.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Taturov R.L., Sabatne F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AB007594; AAU78769.1; -.
 DR PIR; P96997; P96997.
 DR InterPro; IPR001220; Lectin legB.
 DR PROSITE; PS00307; LECTIN_LEGUE_BETA; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 348 AA; 39594 MW; 592731AED6573DF9 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 348;
 Best Local Similarity 88.9%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 STSNIGNNV 11
 Db 158 STSNIGNNV 166

RESULT 22

ACES_ELEBL STANDARD; PRT; 633 AA.
 AC 042275;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
 OS Electrophorus electricus (Electric eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
 OC Electrophoridae; Electrophorus.
 NC NCBI_TaxID=8005;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96070504; PubMed=9407087; DOI=10.1074/jbc.272.52.33045;
 RA Simon S., Massoulié J.;
 RT "Cloning and expression of acetylcholinesterase from Electrophorus."
 RT Splicing pattern of the 3' exons in vivo and in transfected mammalian
 cells.";
 RL J. Biol. Chem. 272:33045-33055(1997).
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.

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DR EMBL, AF030422; AAB86606.1; -
DR HSSP, P04058; 1H23.
DR InterPro, IPR002018; CarboxylesteraseB.
DR InterPro, IPR000997; Cholinesterase.
DR InterPro, IPR000379; Ser esterase.
DR Pfam, PF00135; Coesterase; 1.
DR PRINTS, PR00878; CHOLINESTERASE.
DR PROSITE, PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE, PS00941; CARBOXYLESTERASE_B_2; 1.
KM Glycoprotein; Hydrolyase; Membrane; Neurotransmitter degradation;
KM Serine esterase; Signal; Synapse.
FT SIGNAL 1 23 Potential.
FT CHAIN 1 23 Acetylcholinesterase.
FT ACT_SITE 225 633 Acyl-ester intermediate (By similarity).
FT ACT_SITE 352 352 Charge relay system (By similarity).
FT ACT_SITE 494 494 Charge relay system (By similarity).
FT DISULFID 91 118 By similarity.
FT DISULFID 279 290 By similarity.
FT DISULFID 427 579 By similarity.
FT DISULFID 630 630 Interchain (By similarity).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 633 AA; 71814 MW; FC92FE7E4ADB84C3 CRC64;

Query Match 63.6%; Score 42; DB 1; Length 633;
Best Local Similarity 69.2%; Pred. No. 1.3e+00;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 13
DB 459 SGSSSNVGSN 471

RESULT 23
LV6D HUMAN STANDARD; PRT; 111 AA.
AC P06318;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-VI region WLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=66122667; PubMed=4089539;
RA Dvulet F.E., Strako K., Benson M.D.;
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein
RT (WLT).";
RL Scand. J. Immunol. 22:653-660(1985).
DR HSSP, P06318; 1GDUU.
DR HSSP, P06319; 1GDUU.
DR GO, GO:0005576; C:extracellular; NAS.
DR GO, GO:0003823; F:antigen binding; NAS.
DR GO, GO:0006955; P:immune response; NAS.
DR InterPro, IPR007110; Ig-like.
DR InterPro, IPR003596; Ig_v.
DR Pfam, PF00047; Ig_1.

```

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DR SMART, SM00406; IGV; 1.
DR PROSITE, PSS0835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 22 Framework-1.
FT DOMAIN 23 35 Complementarity-determining-1.
FT DOMAIN 36 50 Framework-2.
FT DOMAIN 51 57 Complementarity-determining-2.
FT DOMAIN 58 91 Framework-3.
FT DOMAIN 92 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 22 91 By similarity.
FT NON_TER 111
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37CE24F CRC64;

Query Match 62.1%; Score 41; DB 1; Length 111;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
DB 23 TGSSSGISNVY 34

RESULT 24
LV1H HUMAN STANDARD; PRT; 112 AA.
AC P06867;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Minaseo E., Roy U.P., Congy N., Perran-Rivat L., Minaseo C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features.";
RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
CC were positioned by homology.
CC -1- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
CC markers.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR, A25479; L1HMM.
DR HSSP, P01703; 7FAB.
DR GO, GO:0005576; C:extracellular; NAS.
DR GO, GO:0003823; F:antigen binding; NAS.
DR GO, GO:0006955; P:immune response; NAS.
DR InterPro, IPR007110; Ig-like.
DR InterPro, IPR003596; Ig_v.
DR Pfam, PF00047; Ig_1.
DR SMART, SM00406; IGV; 1.
DR PROSITE, PSS0835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region;
KM Monoclonal antibody; Pyrolydione carboxylic acid.
FT DOMAIN 1 106 Ig-like.
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON_TER 112
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFEBE4 CRC64;

```

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Query Match 62.1%; Score 41; DB 1; Length 112;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNN 10
DB 23 SGSSSNVGSN 32

```

RESULT 25
 Q9VRW7 PRELIMINARY; PRT; 388 AA.
 AC Q9VRW7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE CG13300-PA.
 GN ORFNames=CG13300;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Ashby A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Boutin J., Brockstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foelel C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei E., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheefer F., Shen H.,
 RA Shue B.C., Sinden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weisscock G.M., Weissbach J.,
 RA Williams S.M., Woodger, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RT Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537572;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Friese B., Hodgeson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weisscock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*.
 RT melanogaster euchromatic genome sequence."
 RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminier J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Friese B., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective."
 RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminier J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Dysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review."
 RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYbase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYbase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003563; AAF50665.1; -;
 DR InFrac; Q9VRW7; -;
 DR FLYbase; FBgn0035699; CG13300.
 SO SEQUENCE 388 AA; 41664 MW; 2F8F5E96584B1F38 CRC64;
 Qy 1 SGGTSNIGNNV 12
 Db 224 NGSSNNNNHML 235
 Query Match 62.1%; Score 41; DB 2; Length 388;
 Best Local Similarity 58.3%; Pred. No. 1.2e+02;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 RESULT 26
 ID1 HEMI RICPR STANDARD; PRT; 414 AA.
 AC Q9ZCB8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE 5-aminolevulinic acid synthase (EC 2.3.1.37) (5-aminolevulinic acid synthase) (delta-aminolevulinic synthase) (Delta-ALA synthetase).
 GN Name=hema; OrderedLocNames=RP841;
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_Taxid=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
 RA Anderson S.G.E., Zomrodipour A., Anderson J.O.,
 RA Scharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of *Rickettsia prowazekii* and the origin of
 RT mitochondria."
 RT Nature 396:133-140(1998).
 CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + glycine = 5-aminolevulinic acid + COA + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Heme biosynthesis; first (rate-limiting) step.
 CC -1- SIMILARITY: Belongs to the class-II pyridoxal-phosphate-dependent
 CC aminotransferase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@idb-sib.ch).

DR EMBL; AJ235273; CAA15265.1; -
DR PIR; A71646; A71646.
DR InterPro; IPR010961; Saminolev_synth.
DR InterPro; IPR003408; Ala_synthase.
DR InterPro; IPR004839; Aminotrans_1/IT.
DR InterPro; IPR01917; Aminotrans_1I.
DR Pfam; PF02490; Ala_synthase; 1.
DR Pfam; PF00155; Aminotran_1.2; 1.
DR TIGRfams; TIGR01822; 2am3keto_CoA; 1.
DR TIGRfams; TIGR01821; Saminolev_synth; 1.
DR TIGRfams; TIGR01825; Gly_Cac_Trel; 1.
DR PROSITE; PS00599; AA_TRANSFR_CLASS_2; 1.
KM Acyltransferase; Complete proteome; Heme biosynthesis;
KM Pyridoxal phosphate; Transferase.
FT BINDING 244
SQ SEQUENCE 414 AA; 4616 MW; 9763C4E1966A2822 CRC64;

Query Match 62.1%; Score 41; DB 1; Length 414;
Best Local Similarity 61.5%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 76 SGGTRNIGNNIS 88

RESULT 27
Q68VS3 PRELIMINARY; PRT; 414 AA.
AC Q68VS3;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE 5-aminolevulinic acid synthase (EC 2.3.1.37).
GN Name=hema; OrderedLocNames=RT0829;
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxId=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Williamston;
RX PubMed=15317790; DOI=10.1128/JB.186.17.5842-5855.2004;
RA McLeod M.P., Qin X., Karpach S.E., Giola J., Highlander S.K.,
RA Fox G.B., McNeill T.Z., Jiang H., Muzny D., Jacob L.S., Hawes A.C.,
RA Sodergren E., Gill R., Hume J., Morgan M., Fan G., Amin A.G.,
RA Glibbs R.A., Hong C., Yu X.-J., Walker D.H., Weinstein G.M.;
RT "Complete genome sequence of Rickettsia typhi and comparison with
RT sequences of other Rickettsiae."
RL J. Bacteriol. 186:5842-5855(2004).
DR EMBL; AE017197; AA004263.1; -
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR010961; Saminolev_synth.
DR InterPro; IPR003408; Ala_synthase.
DR InterPro; IPR004839; Aminotrans_1/IT.
DR InterPro; IPR01917; Aminotrans_1I.
DR Pfam; PF02490; Ala_synthase; 1.
DR Pfam; PF00155; Aminotran_1.2; 1.
DR TIGRfams; TIGR01821; Saminolev_synth; 1.
DR PROSITE; PS00599; AA_TRANSFR_CLASS_2; UNKNOWN 1.
KM Acyltransferase; Complete proteome; Transferase;
SQ SEQUENCE 414 AA; 46460 MW; 50293078A98D56D CRC64;

Query Match 62.1%; Score 41; DB 2; Length 414;
Best Local Similarity 61.5%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 76 SGGTRNIGNNIS 88

RESULT 28
Q6BK59 PRELIMINARY; PRT; 847 AA.
AC Q6BK59;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Similar to trl09C019 Candida albicans Canna6 protein.
GN ORFNames=DEHA0F26114g;
OS Debaryomyces hanseni CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Bakaryota; Fungi; Ascomycota; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxId=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreaye F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Ortiz S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA GenomeScope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382138; CAG89823.1; -
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR008803; RHD3.
DR Pfam; PF05879; RHD3; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 847 AA; 96135 MW; 66D78C51CB4B6ACD CRC64;

Query Match 62.1%; Score 41; DB 2; Length 847;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNY 11
Db 59 STSSSDIGNNY 69

RESULT 29
Q7RR78 PRELIMINARY; PRT; 958 AA.
AC Q7RR78;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Asparagine-rich protein, putative.
GN Name=PY00629;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=13239;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=17XNT;
RX PubMed=136865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Koof T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bickell S.L.,
RA Shallem S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
RA Cio J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000170; EAA17409.1; -.
DR InterPro; IPR011591; Botulinum.
DR ProDom; PD001963; Botulinum; 1.
SQ SEQUENCE 958 AA; 108049 MW; 134FC37BF03E088B CRC64;

Query Match 62.1%; Score 41; DB 2; Length 958;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSTSNIGNNYVS 13
DB 580 GSTSNIGNNNIS 591

RESULT 30
ID Q95SG4 PRELIMINARY; PRT; 1272 AA.
AC Q95SG4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE GH27809P.
GN Name=CG3189; ORFNames=CG30421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacled S.E., Paragas V., Park S., Phouenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY060809; AAL28357.1; -.
DR HSSP; O93009; INBF.
DR FLYBase; FBgn0050421; CG30421.
DR GO; GO:0004157; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50351; UCH_2_3; 1.
SQ SEQUENCE 1272 AA; 138909 MW; E9BBD8A3125CAD4 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1272;
Best Local Similarity 61.5%; Pred. No. 3.9e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13

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DB 928 SGSSNSGDRHVS 940

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||:| |::|

RESULT 31
ID Q9W117 PRELIMINARY; PRT; 1272 AA.
AC Q9W117;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG30421-Pa.
GN ORFNames=CG30421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer J.R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abriil J.F., Agbayan A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandal D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garcia N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liao P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodruff W., Worley K.C., Wu D., Yang S., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng X.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Ceiniker S.E., Wheeler D.A., Kromoller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacled J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN
RP SEQUENCE FROM N.A.

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RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitskas R.,
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
RA Beltenok B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Hartley N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN
RN [5]
RN SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN
RN [6]
RN SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003465; AAF47260.2; -.
DR HSP; Q93009; INB8.
DR FlyBase; FBgn0050421; CG30421.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50235; UCH_2_3; 1.
DR SEQUENCE 1272 AA; 138810 MW; 70783F26B8AC2306 CRC64;
SQ
Query Match 62.1%; Score 41; DB 2; Length 1272;
Best Local Similarity 61.5%; Pred. No. 3.9e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYS 13
DB 928 SGSSNSGDMWVS 940
RESULT 32
ID 0811E2 PRELIMINARY; PRT; 1298 AA.
AC 0811E2;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE CG30421-PA.
GN ORFNames=CG30421;
OS Drosophila pseudobacura (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Tucson 14011-0121.4;
RA Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
RA Gaitre A., Mungall C.J., Wang A.M., Krommiller B., Pacleb J., Park S.,
RA Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA Celniker S.E.;
RT "Assessing the impact of comparative genomic sequence data on the
RT functional annotation of the Drosophila genome.";

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RL Genome Biol. 3:research0086-research0086(2002).
DR EMBL; AY190942; AAC01028.1; -.
DR HSP; Q93009; INB8.
DR FlyBase; FBgn0064435; Dpse\CG30421.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; F:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50235; UCH_2_3; 1.
DR SEQUENCE 1298 AA; 141590 MW; 44D4C7CB21B05257 CRC64;
SQ
Query Match 62.1%; Score 41; DB 2; Length 1298;
Best Local Similarity 61.5%; Pred. No. 4e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYS 13
DB 924 SGSSNSGDMWVS 936
RESULT 33
ID 0811A0 PRELIMINARY; PRT; 1336 AA.
AC 0811A0;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE CG30421-PA.
GN ORFNames=CG30421;
OS Drosophila virilis (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Tucson 15010-1001.10;
RA Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
RA Gaitre A., Mungall C.J., Wang A.M., Krommiller B., Pacleb J., Park S.,
RA Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA Celniker S.E.;
RT "Assessing the impact of comparative genomic sequence data on the
RT functional annotation of the Drosophila genome.";
RL Genome Biol. 3:research0086-research0086(2002).
DR EMBL; AY190953; AAC01072.1; -.
DR HSP; Q93009; INB8.
DR FlyBase; FBgn0064534; Dilt\CG30421.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; F:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50235; UCH_2_3; 1.
DR SEQUENCE 1336 AA; 144636 MW; A8BB15BAE6F4CA66 CRC64;
SQ
Query Match 62.1%; Score 41; DB 2; Length 1336;
Best Local Similarity 61.5%; Pred. No. 4.1e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYS 13
DB 965 SGSSNSGDMWVS 977
RESULT 34
ID 081150 PRELIMINARY; PRT; 1701 AA.
AC 081150;

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DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DE Hypothetical protein.
GN ORFNames=PF11_0324;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Paul A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Sub B., Peterson J., Anguoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairhead A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McEdden G.I., Cummings L.M., Subramanian G.M., Wungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
RW EMBL; AE014840; AAN35908.1; -
KM Hypothetical protein.
SQ SEQUENCE 1701 AA; 206848 MW; B7823F13A5CEC9E7 CRC64;

Query Match
Best Local Similarity 62.1%; Score 41; DB 2; Length 1701;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 3 STSNIGNNYVS 13
Db 1306 SNNNISNNYIS 1316

RESULT 35
LV1F HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaet D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
RT the lambda light chain."
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; LIHUWA.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 97
FT DOMAIN 98 109 V segment.
FT DISULFID 22 89 J segment.
FT NON TER 109 109 By similarity.
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match
60.6%; Score 40; DB 1; Length 109;
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Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 2 GSTSNIGNNYV 12
Db 24 GSSSNGTGNVYV 34

RESULT 36
LV1B HUMAN STANDARD; PRT; 112 AA.
AC P01700;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region HA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71103824; PubMed=5532227;
RA Shinoda T., Titani K., Putnam F.W.;
RT "Amino acid sequence of human lambda chains. II. Chymotryptic peptides
RT and sequence of protein Ha."
RL J. Biol. Chem. 245:4475-4487(1970).
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01963; LIHUWA.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 106
FT MOD RES 1 1 Pyrolydione carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 11896 MW; 8D73378F5CD039 CRC64;

Query Match
Best Local Similarity 60.6%; Score 40; DB 1; Length 112;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 2 GSTSNIGNNYV 12
Db 25 GSSSNGTGNVYV 35

RESULT 37
O8GFB2 PRELIMINARY; PRT; 159 AA.
AC O8GFB2;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Orf23.
GN Name=orf23;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29486;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RX MEDLINE=21185117; PubMed=11286884; DOI=10.1016/S0966-842X(01)01978-3;
```


RA Waterfield N.R., Bowen D.J., Fetherston J.D., Perry R.D.,
 RA ffrench-constant R.H.;
 RT "The tc genes of Photobabidus: a growing family.";
 RL Trends Microbiol. 9:185-191(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT4;
 RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
 RA Waterfield N.R., Daborn P.J., ffrench-constant R.H.;
 RT "Genomic islands in Photobabidus.";
 RL Trends Microbiol. 10:541-545(2002).
 DR EMBL: AF346500; AAC07189.1;
 DR InterPro: IPR008514; DUF796.
 DR Pfam: PF05638; DUF796; 1.
 SQ SEQUENCE 159 AA; 18032 MW; FF35A023A8913ADC CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 159;
 Best Local Similarity 70.0%; Pred. No. 71;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GSTSNIGNNY 11
 DB 22 GSTSNIGNNY 31
 RESULT 38
 ID 076611 PRELIMINARY; PRT; 314 AA.
 AC 076611;
 DT 01-NOV-1998 (TRENDBLREL. 08, Created)
 DT 01-MAR-2003 (TRENDBLREL. 23, Last sequence update)
 DT 01-OCT-2003 (TRENDBLREL. 25, Last annotation update)
 DE Hypothetical protein T07H3.6.
 GN Name=T07H3.6; ORFNames=T07H3.6;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RX MEDLINE=9069613; PubMed=9851916;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX Wormbase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Beck C., O'Brien D., Kramer J.;
 RT "The sequence of C. elegans cosmid T07H3.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG Wormbase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF077540; AAC26307.2;
 DR PIR: T33378; T33378.
 DR Wormbase; WBGene00020329; T07H3.6.
 DR WormPep; T07H3.6; CE32065.
 DR InterPro; IPR002083; MATH.
 DR InterPro; IPR008974; Ttaf_like;
 RP

DR Pfam; PF00917; MATH; 1.
 DR SMART; SM00061; MATH; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 314 AA; 35980 MW; 47496DB8B1B09C11C CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 314;
 Best Local Similarity 72.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 STSNIGNNYVS 13
 DB 34 STSNIGNNYVS 44
 RESULT 39
 ID 08M1R8 PRELIMINARY; PRT; 315 AA.
 AC 08M1R8;
 DT 01-MAR-2002 (TRENDBLREL. 20, Created)
 DT 01-MAR-2002 (TRENDBLREL. 20, Last sequence update)
 DT 01-MAR-2004 (TRENDBLREL. 26, Last annotation update)
 DE Blind.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 NCBI_TaxID=4081;
 RX PubMed=11805344; DOI=10.1073/pnas.022516199;
 RA Schmitz G., Tillmann B., Carriero F., Flore C., Cellini F., Theres K.;
 RT "The tomato Blind gene encodes a MYB transcription factor that
 RT controls the formation of lateral meristems.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:1064-1069(2002).
 CC 1-1 SUBCELLULAR LOCATION: Nuclear (by similarity).
 CC 1-1 SIMILARITY: Contains 2 Myb-like domains.
 DR EMBL: AF426174; AL69334.1; -.
 DR HSSP; P06876; IMBK.
 DR TRANSFAC; T05529; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00249; Myb DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KW Nuclear protein.
 SQ SEQUENCE 315 AA; 35518 MW; 8FD393A69BBD97B6 CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 315;
 Best Local Similarity 58.3%; Pred. No. 1.4e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNY 12
 DB 285 SGSTSNIGNNY 296
 RESULT 40
 ID 08P1Z5 PRELIMINARY; PRT; 410 AA.
 AC 08P1Z5;
 DT 01-MAR-2003 (TRENDBLREL. 23, Created)
 DT 01-MAR-2003 (TRENDBLREL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENDBLREL. 23, Last annotation update)
 DE Hypothetical protein C1206.
 GN OrderedLocNames=C1206;
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=06:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=2388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016758; AAN79668.1; -.
 KM Complete proteome.
 SQ SEQUENCE 410 AA; 41613 MM; 958A652E860819DD CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 410;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SGGSTSNIGNN 10
 |||||
 Db 212 SGGSTLNAGNN 221

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 Job time : 88.4948 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 54.25 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-14

Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	AA79072	AA79072 Anti-fact
2	35	100.0	99	ADJ80338	ADJ80338 Vlamda g
3	35	100.0	109	AAU02544	AAU02544 Anti-adip
4	35	100.0	110	AA796060	AA796060 Human ant
5	35	100.0	110	AAU02558	AAU02558 Anti-adip
6	35	100.0	110	AAU02612	AAU02612 Anti-adip
7	35	100.0	110	AAU02627	AAU02627 Anti-adip
8	35	100.0	110	AAU02629	AAU02629 Anti-adip
9	35	100.0	111	AAU19883	AAU19883 CEA-speci
10	35	100.0	111	AAU02542	AAU02542 Anti-adip
11	35	100.0	111	AAU02551	AAU02551 Anti-adip
12	35	100.0	111	AAU02585	AAU02585 Anti-adip
13	35	100.0	111	ADK17416	ADK17416 Anti-huma
14	35	100.0	111	ADG42838	ADG42838 scfV Ab12
15	35	100.0	214	ABM85072	ABM85072 Human dia
16	35	100.0	236	ABM85084	ABM85084 Human dia
17	35	100.0	240	ABP45887	ABP45887 Human Bly
18	35	100.0	240	ADG96714	ADG96714 Single ch
19	35	100.0	241	ADP46044	ADP46044 Human Bly
20	35	100.0	241	ADG96871	ADG96871 Single ch
21	35	100.0	242	ADG34301	ADG34301 Neurokini
22	35	100.0	242	ADG34317	ADG34317 Neurokini
23	35	100.0	242	ADG34317	ADG34317 Neurokini
24	35	100.0	243	ADG96743	ADG96743 Single ch
25	35	100.0	243	ADG34310	ADG34310 Neurokini

26	35	100.0	243	8	ADG34306	ADG34306 Neurokini
27	35	100.0	244	8	ADG34303	ADG34303 Neurokini
28	35	100.0	245	5	ABP45915	ABP45915 Human Bly
29	35	100.0	245	7	ADG96742	ADG96742 Single ch
30	35	100.0	245	7	ADG98057	ADG98057 TNF proli
31	35	100.0	245	8	ADG83862	ADG83862 Chemokine
32	35	100.0	245	8	ADG34308	ADG34308 Neurokini
33	35	100.0	245	8	ADG34313	ADG34313 Neurokini
34	35	100.0	246	5	ABP45902	ABP45902 Human Bly
35	35	100.0	246	5	ABP45906	ABP45906 Human Bly
36	35	100.0	246	7	ADG96723	ADG96723 Single ch
37	35	100.0	246	7	ADG96729	ADG96729 Single ch
38	35	100.0	246	8	ADG83872	ADG83872 Chemokine
39	35	100.0	247	5	ABP45671	ABP45671 Human Bly
40	35	100.0	247	5	ABP45674	ABP45674 Human Bly
41	35	100.0	247	5	ABP45432	ABP45432 Human Bly
42	35	100.0	247	5	ABP45923	ABP45923 Human Bly
43	35	100.0	247	5	ABP45917	ABP45917 Human Bly
44	35	100.0	247	5	ABP45696	ABP45696 Human Bly
45	35	100.0	247	5	ABP45888	ABP45888 Human Bly

ALIGNMENTS

RESULT 1
AA79072
ID AA79072 standard; peptide; 7 AA.
XX
AC AA79072;
XX
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence.
XX
XX Complementarity determining region 2; CDR2; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
PN W0200012562-A1.
XX
PD 09-MAR-2000.
XX
PF 26-AUG-1999; 99WC-US019453.
XX
PR 28-AUG-1998; 98US-0098233P.
XX
PR 03-MAR-1999; 99US-0122767P.
XX
PA (GENTECH) GENENTECH INC.
XX
PI Adams CW, Devaux B, Eaton DL, Haas PE, Judice JK, Kirchhofer D;
PI Suggett S;
XX
XX WPI; 2000-256595/22.
XX
PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
PT stroke, and post myocardial infarction.
XX
XX Claim 8; Fig 2; 84pp; English.
XX
XX This sequence represents a complementarity determining region 2 (CDR2) of
XX the light chain variable domain of a human anti-factor IX/IXa Gla domain
XX antibody. Factor IXa is a vitamin K dependent plasma serine protease that
XX participates in the blood coagulation pathways. The Gla domain of factor
XX IXa and its zymogen factor IX contains important structural determinants
XX for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 1 DVSKRPS 7

RESULT 2

ADJ80338
ID ADJ80338 standard; protein; 99 AA.

XX AC ADJ80338;

XX DT 06-MAY-2004 (first entry)

DE Vlamda gene locus antibody amino acid sequence #7.

XX KM hybrid antibody; antibody; framework region; homology; immunogenicity.

XX OS Homo sapiens.

XX PN WO2003048321-A2.

XX PD 12-JUN-2003.

XX PF 03-DEC-2002; 2002WO-US038450.

XX PR 03-DEC-2001; 2001US-0336591P.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Rother R, Wu D;

XX DR WPI; 2003-513753/48.

XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively
XX linking the selected framework sequences to one or more complementarity
XX determining regions of the initial antibody.

XX PS Disclosure; SEQ ID NO 98; 77pp; English.

XX The invention relates to a method of producing a hybrid antibody or
XX hybrid antibody fragment by: (i) providing an initial antibody having
XX specificity for a target; (ii) determining the sequence of a variable
XX region of the initial antibody; (iii) selecting a first component of the
XX variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
XX sequence of the first component to sequences contained in a reference
XX database of antibody sequences or antibody fragment sequences from a
XX target species; (v) selecting a sequence from an antibody in the database
XX which demonstrates a high degree of homology to the first component; (vi)
XX selecting a second component of the variable region which is different
XX than the first component; the second component selected from the group
XX consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
XX second component to sequences contained in a reference database of the
XX antibody sequences or antibody fragment sequences from the target species
XX; (viii) selecting a sequence from the database which demonstrates a high
XX degree of homology to the second component and which is from a different
XX antibody than the selected antibody; and (ix) operatively linking the

CC selected framework sequences to one or more complementarity determining
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
CC hybrid antibody fragment. The method is useful for producing a hybrid
CC antibody or hybrid antibody fragment (claimed). The antibody and
CC fragments are useful for therapeutic and diagnostic purposes. The method
CC uses entire framework regions from a single antibody variable heavy or
CC variable light chain to receive the CDRs. This produces antibodies that
CC are highly homologous and exhibit reduced immunogenicity while
CC maintaining an optimum binding profile. This sequence represents the
CC amino acid sequence of an antibody from the Vlamda gene locus.

XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 35; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 3

AAU02544
ID AAU02544 standard; protein; 109 AA.

XX AC AAU02544;

XX DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 31.

XX KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR N-PSDB; AAS03444.

XX PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.

XX PS Claim 1; Page 120; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies

CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 109 AA;
Query Match 100.0%; Score 35; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 51 DVSKRPS 57
RESULT 4
AAV96060
ID AAV96060 standard; protein; 110 AA.
XX
AC AAV96060;
XX
DT 05-DEC-2000 (first entry)
XX
DE Human anti-DAF antibody LU30 light chain variable region.
XX
KM LU30; human; antibody; VL domain; decay accelerating factor; DAF;
KM phage display; subtractive panning; lung cancer; lung carcinoma;
KM lung adenocarcinoma; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 23..36 /label= CDR1
FT /note= "complementarity determining region I"
FT 25..35 /note= "hypervariable loop region"
FT 52..58 /label= CDR2
FT /note= "complementarity determining region II"
FT 52..54 /note= "hypervariable loop residues"
FT /note= "hypervariable loop residues"
FT 91..100 /label= CDR3
FT /note= "complementarity determining region III"
FT 93..99 /note= "hypervariable loop residues"
FT Region
XX
XX WO20052054-A2.
XX
XX 08-SEP-2000.
XX
XX 29-FEB-2000; 2000WO-US005352.
XX
XX 01-MAR-1999; 99US-0122262P.
XX
XX (GETH) GENENTECH INC.
XX
XX Carter PJ, Ridgway JB;
XX
XX WPI; 2000-594169/56.
XX
XX Making antibodies (e.g. anti-decay accelerating factor antibody) for
PT diagnosing or treating e.g. lung cancer comprises identifying an antigen
PT that is differentially expressed on the surface of two or more distinct
PT cell populations.
XX
XX Disclosure; Fig 5A; 52pp; English.
XX
XX The present sequence is that of the light chain variable region (VL) of
CC the anti-decay accelerating factor (DAF) human antibody LU30. The VH of
CC region is given in AAV96063. LU30 has a binding affinity (Kd) for DAF of
CC about 13 nM. It was produced using a novel method for making antibodies
CC which can be used for cancer diagnosis or therapy. The method comprises:

CC (a) binding an antibody phage from a naive antibody phage library to a
CC live cancer cell; (b) selecting an antibody phage or antibody which binds
CC selectively to the live cancer cell; and (c) identifying an antigen to
CC which the antibody phage or antibody binds. To obtain LU30, a human scFv
CC library was used to search for tumour-associated antigens by panning the
CC lung adenocarcinoma cell line 1264, and counter-selecting with a non-
CC tumour bronchial epithelial cell line, BEAS-2B. The invention also
CC describes a method for identifying an antigen which is differentially
CC expressed on the surface of 2 or more distinct cell populations. The anti-
CC -DAF human antibody, or a composition comprising the antibody, is useful
CC for in vivo cancer diagnosis or therapy. In particular, the antibody is
CC useful for diagnosing or treating lung cancer, e.g. small-cell lung
CC cancer, non-small cell lung cancer, large cell lung carcinoma, lung
CC adenocarcinoma, or squamous cell lung carcinoma (all claimed)
XX
SQ Sequence 110 AA;
Query Match 100.0%; Score 35; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 52 DVSKRPS 58
RESULT 5
AAU02558
ID AAU02558 standard; protein; 110 AA.
XX
AC AAU02558;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, PAT 44.
XX
DE Anti-adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BW, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX
XX N-PSDB; AAS03458.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
XX Claim 1; Page 128-129; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the

CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

XX Sequence 110 AA;
XQ

Query Match	100.0%;	Score 35;	DB 4;	Length 110;
Best Local Similarity	100.0%;	Pred. No. 6.1;		
Matches	7;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	1	DVSKRPS	7	
Db	51	DVSKRPS	57	

RESULT 6
AAU02612
ID AAU02612 standard; protein; 110 AA
XY

DT 29-AUG-2001 (first entry)
xx

DE Anti-adipocyte monoclonal antibody light chain, FAT 99.

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat
KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

PN WO200127279-A1.

PD 19-APR-2001

PF 11-OCT-2000; 2000WO-GB003900
VY

PR 12-OCT-1999; 99US-0158812P.
VY

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Edwards BM, Main SH, Vaughan TJ;

DR WPI; 2001-282031/29.

XX

PT Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

PS Claim 1; Page 163; 182pp; English.

AAU025501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

Query Match	100.0%	Score 35;	DB 4;	Length 110;
Best Local Similarity	100.0%	Pred. No. 6.1;		
Matches	7;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	1	DVSKRPS	7	
Db	51	DVSKRPS	57	

RESULT 7
AAU02627
ID AAU02627 standard; protein; 110 AA
VV

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 112.

KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 KW

OS Homo sapiens

PN WO200127279-A1

PD 19-APR-2001

PF. 11-OCT-2000; 2000WO-GB003900.

PR 12-OCT-1999; 99US-0158812P.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
VY

PI Edwards BM, Main SH, Vaughan TJ;

DR WPI; 2001-282031/29.

XX
XX
Page 1 of 1

PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.

PS Claim 1; Page 172; 182pp; English.

CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarily determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

Query Match	100.0%	Score 35;	DB 4;	Length 110;
Best Local Similarity	100.0%	Pred. No. 6.1;		
Matches	7;	Conservative 0;	Mismatches 0;	Gaps 0;

QY	1	DVSKRPS	7
Db	51	DVSKRPS	57

RESULT 8
AAU02629
ID AAU02629 standard; protein; 110 AA.
XX
AC AAU02629;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 113.
XX
KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN W0200127279-A1.
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
DR N-PSDB; AAS03529.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS Claim 1; Page 173; 182pp; English.
XX
CC AAU02601-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
CC
XX
SQ Sequence 110 AA;
Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 07-DEC-1997 (first entry)
XX
XX CEA-specific antibody CEAL, CEA2, CEA3 VL sequence.
DE
XX
KM Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
XX lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 23..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..56
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 90..100
FT /label= CDR3
FT /note= "complementarity determining region 3"
XX
PN W09720932-A1.
PD 12-JUN-1997.
XX
PF 09-DEC-1996; 96WO-GB003043.
XX
PR 07-DEC-1995; 95GB-00025004.
PR 23-MAY-1996; 96GB-00010824.
PR 11-OCT-1996; 96GB-00021295.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Osbourn JK, Allen DJ, McCafferty JG;
XX
DR WPI; 1997-319779/29.
DR N-PSDB; AAT72133.
XX
PT Specific binding members for human carcinoembryonic antigen - bind to the
PT A3-B3 extracellular domain of hCEA and are substantially non-cross-
PT reactive with human liver cells; used for diagnosing cancer.
XX
PS Claim 14; Fig 1b; 128pp; English.
XX
CC This polypeptide sequence comprises the light chain variable region (VL)
CC of human carcinoembryonic antigen (hCEA)-specific antibodies CEAL, CEA2
CC and CEA3. VH (AAT72126-32) and VL (AAT72133-35) gene sequences were
CC obtained for anti-hCEA antibodies CEAL-CEA3 (see AAM19876-85). A claimed
CC specific binding member (A) comprises an hCEA specific antibody antigen
CC binding domain that has a dissociation constant for hCEA of less than 1 x
CC 10⁻⁸ M, is non-cross-reactive with human liver cells, and
CC preferentially binds to the A3-B3 extracellular domain of hCEA and/or to
CC cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include
CC pairings of VH and VL sequences from CEAL-7, or their CDR sequences, as
CC well as CEA6 VH and VL variants. (A) is used to detect cells expressing
CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer,
CC e.g. adenocarcinoma of the colon, lung or breast
XX
SQ Sequence 111 AA;
Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
AAM19883
ID AAM19883 standard; protein; 111 AA.
XX
AC AAM19883;
XX

RESULT 10
AAU02542
ID AAU02542 standard; protein; 111 AA.
XX
AC AAU02542;
XX

XX 29-AUG-2001 (first entry)
 XX Anti-adipocyte monoclonal antibody light chain, FAT 30.
 DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 OS WO200127279-A1.
 PN 19-APR-2001.
 XX 11-OCT-2000; 2000WO-GB003900.
 PF 12-OCT-1999; 99US-0158812P.
 XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Edwards BM, Main SH, Vaughan TJ;
 PI WPI; 2001-282031/29.
 DR N-PSDB; AAS03442.
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX Claim 1; Page 118-119; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC Sequence 111 AA;
 SQ

Query Match 100.0%; Score 35; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 51 DVSKRPS 57

RESULT 11
 AAU02551
 ID AAU02551 standard; protein; 111 AA.
 XX AAU02551;
 AC 29-AUG-2001 (first entry)
 XX Anti-adipocyte monoclonal antibody light chain, FAT 37.
 DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 XX

OS Homo sapiens.
 XX WO200127279-A1.
 PN 19-APR-2001.
 XX 11-OCT-2000; 2000WO-GB003900.
 PF 12-OCT-1999; 99US-0158812P.
 XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Edwards BM, Main SH, Vaughan TJ;
 PI WPI; 2001-282031/29.
 DR N-PSDB; AAS03451.
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX Claim 1; Page 124; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC Sequence 111 AA;
 SQ

Query Match 100.0%; Score 35; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58

RESULT 12
 AAU02585
 ID AAU02585 standard; protein; 111 AA.
 XX AAU02585;
 AC 29-AUG-2001 (first entry)
 XX Anti-adipocyte monoclonal antibody light chain, FAT 72.
 DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 OS WO200127279-A1.
 PN 19-APR-2001.
 XX 11-OCT-2000; 2000WO-GB003900.
 PF

PR 12-OCT-1999, 99US-0158812P.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TU;
XX
XX WPI; 2001-282031/29.
DR N-PSDB; AAS03485.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
XX Claim 1; Page 146; 182pp; English.
XX
CC AAU02501-AAU02655, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 13
ADK17416
ID ADK17416 standard; protein; 111 AA.
XX
XX ADK17416;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human CXCR4 loop 6 ScFv antibody VI region.
XX
KM anti-HIV; cytosstatic; virucide; single chain antibody; yeast;
KM HIV; cancer; CCR5.
XX
OS Synthetic.
XX
XX WO2003066830-A2.
XX
PD 14-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-US003763.
XX
XX 08-FEB-2002; 2002US-00071866.
XX
PR 08-FEB-2002; 2002US-00072031.
PR 25-APR-2002; 2002US-00133978.
XX
XX (GENE-) GENETASTIX CORP.
XX
XX Hua S, Pauling MH, Zhu L;
XX

DR WPI; 2003-731501/69.
XX
XX Selecting an scFv against a peptide target by expressing a target fusion
PT protein having a DNA binding domain or activation domain of a
PT transcription activator, useful for diagnosing, preventing and/or
PT treating HIV infection and cancer.
XX
XX Claim 123; SEQ ID NO 61; 150pp; English.
XX

CC The invention relates to a method of selecting a single chain antibody
CC (scFv) against a peptide target in a yeast by expressing a library of
CC scFv fusion proteins in yeast cells, expressing a target fusion protein
CC in the yeast cells expressing the scFv fusion proteins having either the
CC DNA binding domain or the activation domain of the transcription
CC activator which is not comprised in the scFv fusion proteins, and a
CC target peptide, and selecting those yeast cells in which a reporter gene
CC is expressed. Each scFv fusion protein comprises either an activation
CC domain or a DNA binding domain of a transcription activator and a scFv
CC having a heavy chain of a variable region (VH) of antibody whose sequence
CC varies within the library, a light chain of a variable region (VL) of
CC antibody whose sequence varies within the library independently of the VH
CC and a linker peptide which links the VH and VL. The expression of the
CC reporter gene is activated by a reconstituted transcriptional activator
CC formed by binding of the scFv fusion protein to the target fusion
CC protein. The methods and compositions of the present invention are useful
CC for preventing and/or treating HIV infection and cancer. This sequence
CC corresponds to the VI region of an anti-human CXCR4 loop 6 antibody gene
CC and used to generate the scFv antibody of the invention.
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 7; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 14
ADG42838
ID ADG42838 standard; protein; 111 AA.
XX
XX ADG42838;
XX
DT 26-FEB-2004 (first entry)
XX
DE scFv Ab124 light chain variable region.
XX
XX HIV infection; HIV type 1; HIV type 2; cancer; breast; prostate; liver;
KM renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon;
KM lymphoma; leukaemia; pancreas; chemokine receptor; antibody.
XX
OS Synthetic.
XX
XX US2003206909-A1.
XX
XX 06-NOV-2003.
XX
XX 07-FEB-2003; 2003US-00360828.
XX
XX 08-FEB-2002; 2002US-00071866.
XX
PR 08-FEB-2002; 2002US-00072201.
PR 25-APR-2002; 2002US-00133978.
XX
XX (HUA S.) HUA S.
XX (PAULING M H.) PAULING M H.
XX (ZHU L.) ZHU L.
XX
XX Hua S, Pauling MH, Zhu L;
XX
XX WPI; 2004-051479/05.
XX

DR N-PSDB; ADG42836.
XX Antibody binding loop of human chemokine receptor useful for the
PT treatment of HIV infection and cancer.
XX
XX
PS Claim 6; SEQ ID NO 61; 74pp; English.
XX
CC The invention relates to an antibody that binds to loop 6 of human
CC chemokine receptor (CXCR4). The antibody is useful in the treatment or
CC prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer
CC of (e.g. breast, prostate, liver, renal, lung, skin, ovarian, cervical,
CC brain, thyroid, stomach, colon, lymphoma, leukaemia and pancreas cancer
CC cells), for screening drugs, for diagnosing disease or condition
CC associated with interaction with chemokine receptor. The present sequence
CC is used in the exemplification of the present invention.
XX
SQ Sequence 111 AA;
Query Match 100.0%; Score 35; DB 8; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58
RESULT 15
ABM85072
ID ABM85072 standard; protein; 214 AA.
XX
AC ABM85072;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5321.
XX
KM gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P;
PI Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzen D;
PI Patursy S, Shi X, Suarez CJ;
XX
XX
DR WPI, 2004-329368/30.
DR N-PSDB; ACN43724.
XX
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The ditnp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germ-line
CC gene therapy. The present sequence represents a ditnp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 214 AA;
Query Match 100.0%; Score 35; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVSKRPS 7
Db 71 DVSKRPS 77
RESULT 16
ABM85084
ID ABM85084 standard; protein; 236 AA.
XX
AC ABM85084;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5333.
XX
KM gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P;
PI Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzen D;
PI Patursy S, Shi X, Suarez CJ;
XX
XX
DR WPI, 2004-329368/30.
DR N-PSDB; ACN43736.
XX
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germ-line
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 236 AA;

Query Match 100.0%; Score 35; DB 8; Length 236;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
|||
Db 71 DVSKRPS 77

RESULT 17

ABP45887 ID ABP45887 standard; protein; 240 AA.

XX AC ABP45887;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1898.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID, AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293489P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX PT WPI; 2002-114799/15.

XX DR
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2666-2667; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and actively such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX SQ Sequence 240 AA;

Query Match 100.0%; Score 35; DB 5; Length 240;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
|||
Db 181 DVSKRPS 187

RESULT 18

ADG96714 ID ADG96714 standard; protein; 240 AA.

XX AC ADG96714;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 1898.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scFv; myasthenia gravis;
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antirheumatic; antihypertensive; neuroprotective;
XX antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0311469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;

XX PT WPI; 2003-505530/47.

XX DR
XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 1898; 394pp; English.

XX CC This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX heavy chain antibody molecules (scFvs) derived, preferably, from the variable
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the

CC aberrant expression or inappropriate function of BLyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antisthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BLyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 35; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 181 DVSKRPS 187

RESULT 19
ABP46044
ID ABP46044 standard; protein; 241 AA.
XX
AC ABP46044;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 2055.
XX
KW BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
DR
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2849-2850; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (BLyS) polypeptides. BLyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 35; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 20
ADG96871
ID ADG96871 standard; protein; 241 AA.
XX
AC ADG96871;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds BLyS SeqID 2055.
XX
KW antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
KW antiinflammatory; antisthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (BLyS), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 2055; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey BLyS. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of BLyS or its receptor. As

CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiallergic and cytoprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytoprotective. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 241 AA;

Query Match 100.0%; Score 35; DB 7; Length 241;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 21

ADG34301
ID ADG34301 standard; protein; 242 AA.

XX ADG34301;

XX 26-FEB-2004 (first entry)

DE Neurokinin B antibody SEQ ID NO:24.

XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.

XX Synthetic.

XX WO2003102136-A2.

XX 11-DEC-2003.

XX 29-MAY-2003; 2003WO-US016802.

XX 30-MAY-2002; 2002US-0383802P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX WPI; 2004-053456/05.

DR N-PSDB; ADG34282.

XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.

XX Claim 2; SEQ ID NO 24; 127bp; English.

XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.

XX Sequence 242 AA;

Query Match 100.0%; Score 35; DB 8; Length 242;

Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
XX

Db 182 DVSKRPS 188

RESULT 22

ADG34317
ID ADG34317 standard; protein; 242 AA.

XX ADG34317;

XX 26-FEB-2004 (first entry)

DE Neurokinin B antibody SEQ ID NO:40.

XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;

KM hypertension; pre-eclampsia; NKB.

XX Synthetic.

XX WO2003102136-A2.

XX 11-DEC-2003.

XX 29-MAY-2003; 2003WO-US016802.

XX 30-MAY-2002; 2002US-0383802P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX WPI; 2004-053456/05.

DR N-PSDB; ADG34296.

XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.

XX Claim 2; SEQ ID NO 40; 127bp; English.

XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.

XX Sequence 242 AA;

Query Match 100.0%; Score 35; DB 8; Length 242;

Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 23

ABP45916
ID ABP45916 standard; protein; 243 AA.

XX ABP45916;

XX 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1927.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineutritic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CYID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.
XX
PN W0200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2700-2701; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 35; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DVSKRPS 7
DB 183 DVSKRPS 189
XX
RESULT 24
ADG36743
XX ID ADG36743 standard; protein; 243 AA.
XX
AC ADG36743;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SeqID 1927.
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antineoplastic; antiallergic; neuroprotective;
KM antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
XX Unidentified.
OS
XX

PN W02003055979-A2.
XX
XX 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
XX 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1927; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antineoplastic, antiallergic, neuroprotective,
XX antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
XX polypeptide sequence is a single chain antibody that binds Blys of the
XX invention. NOTE: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format
XX directly from WFO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 35; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DVSKRPS 7
DB 183 DVSKRPS 189
XX
RESULT 25
ADG34310
XX ID ADG34310 standard; protein; 243 AA.
XX
AC ADG34310;
XX
DT 26-FEB-2004 (first entry)
XX
DE Neurokinin B antibody SEQ ID NO:33.
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKG.
XX
XX Synthetic.
XX
XX W02003102136-A2.
XX
XX 11-DEC-2003.
PD

XX 29-MAY-2003; 2003WO-US016802.
PF 30-MAY-2002; 2002US-0383802P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2004-053456/05.
DR N-PSDB; ADG34291.
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 33; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
XX Sequence 243 AA;
SQ
QY 1 DVSKRPS 7
Db 183 DVSKRPS 189
Query Match 100.0%; Score 35; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 26
ADG34306
ID ADG34306 standard; protein; 243 AA.
XX
XX ADG34306;
AC
XX 26-FEB-2004 (first entry)
DT
XX
XX Neurokinin B antibody SEQ ID NO:29.
DE
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
XX Synthetic.
OS
XX
XX WO2003102136-A2.
PN
XX
XX 11-DEC-2003.
PD
XX
XX 29-MAY-2003; 2003WO-US016802.
PF
XX
XX 30-MAY-2002; 2002US-0383802P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2004-053456/05.
DR
XX
XX N-PSDB; ADG34287.
DR
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 29; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC activity, and may have a use in gene therapy. The antibody is useful for

CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
XX Sequence 243 AA;
SQ
QY 1 DVSKRPS 7
Db 183 DVSKRPS 189
Query Match 100.0%; Score 35; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 27
ADG34303
ID ADG34303 standard; protein; 244 AA.
XX
XX ADG34303;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Neurokinin B antibody SEQ ID NO:26.
DE
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
XX Synthetic.
OS
XX
XX WO2003102136-A2.
PN
XX
XX 11-DEC-2003.
PD
XX
XX 29-MAY-2003; 2003WO-US016802.
PF
XX
XX 30-MAY-2002; 2002US-0383802P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2004-053456/05.
DR
XX
XX N-PSDB; ADG34284.
DR
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 26; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
XX Sequence 244 AA;
SQ
QY 1 DVSKRPS 7
Db 184 DVSKRPS 190
Query Match 100.0%; Score 35; DB 8; Length 244;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 28
ABP45915
ID ABP45915 standard; protein; 245 AA.
XX
XX ABP45915;
AC

```

XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1926.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1, Page 2699-2700; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX Sequence 245 AA;
XX
XX Query Match 100.0%; Score 35; DB 5; Length 245;
XX Best Local Similarity 100.0%; Pred. No. 14;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 DVSRRPS 7
XX |||||
XX |||||
XX Db 185 DVSRRPS 191
XX
XX RESULT 29
XX ADG96742
XX ID ADG96742 standard; protein; 245 AA.
XX AC
XX ADG96742;
XX

```

DT	11-MAR-2004 (first entry)	
DE	Single chain antibody that immunospecifically binds Blys Seqid 1926.	
XX		
KW	antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;	
KW	B cell proliferation; differentiation; scfv; myasthenia gravis;	
KW	multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;	
KW	carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;	
KW	antiinflammatory; antiaesthetic; antiallergic; cytostatic.	
XX		
OS	Unidentified.	
XX		
PN	WO2003055979-A2.	
XX		
PD	10-JUL-2003.	
XX		
PF	14-NOV-2002; 2002WO-US036496.	
XX		
PR	16-NOV-2001; 2001US-031469P.	
XX		
PR	19-DEC-2001; 2001US-0340817P.	
XX		
PA	(HDM-A) HDMAN GENOME SCT INC.	
PI		
PI	Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;	
XX		
XX	WPI; 2003-505530/47.	
XX		
PT	Novel antibody that immunospecifically binds to a B lymphocyte stimulator	
PT	(Blys), useful for detecting and treating diseases or disorders e.g.	
PT	rheumatoid arthritis, asthma and leukemia.	
XX		
PS	Example 1; SEQ ID NO 1926; 394pp; English.	
XX		
XX	This invention relates to novel antibodies that immunospecifically bind	
CC	to B lymphocyte stimulator (Blys). The Blys gene has been mapped to	
CC	chromosome 13q34 and encodes a protein that is a member of the tumour	
CC	necrosis factor superfamily and induces both in vivo and in vitro B cell	
CC	proliferation and differentiation. Specifically, it refers to single	
CC	chain antibody molecules (scFvs) derived, preferably, from the variable	
CC	heavy CDR3 region that immunospecifically bind to a polypeptide, or	
CC	fragment thereof, of either human, murine, rat or monkey Blys. The	
CC	present invention refers to the use of such antibodies in various methods	
CC	for the detection, diagnosis and prognosis of diseases related to the	
CC	aberrant expression or inappropriate function of Blys or its receptor. As	
CC	such, these compositions are useful for identifying immune disorders	
CC	including myasthenia gravis and multiple sclerosis, inflammatory	
CC	disorders e.g. asthma and rheumatoid arthritis, infectious diseases such	
CC	as AIDS and proliferative disorders including leukaemia, carcinoma and	
CC	lymphoma. Accordingly, they can be described as exhibiting various	
CC	activities such as antirheumatic, antiallergic, neuroprotective,	
CC	antiinflammatory, antiaesthetic, antiallergic and cytostatic. This	
CC	polypeptide sequence is a single chain antibody that binds Blys of the	
CC	invention. NOTE: The sequence data for this patent did not form part of	
CC	the printed specification, but was obtained in electronic format	
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
XX		
XX	Sequence 245 AA;	
XX		
Query Match	100.0%; Score 35; DB 7; Length 245;	
Best Local Similarity	100.0%; Prod. NO. 14;	
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 DVSKRPS 7	
DB	185 DVSKRPS 191	
XX		
RESULT 30		
ID	ADG98057	
XX	ADG98057 standard; protein; 245 AA.	
XX		
XX	ADG98057;	
XX		

DT 11-MAR-2004 (first entry)
XX
DE TNF proliferation inducing protein ligand (APRIL) seqid 3241.
XX
KW human; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineoplastic; antiarthritic; neuroprotective;
KW antiinflammatory; antisthmatic; antiallergic; cytostatic; APRIL; TNF;
KW ligand.
XX
OS unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0311469P.
XX 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX WPI; 2003-505530/47.
XX
DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX
PS Claim 1; SEQ ID NO 3241; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumor
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antineoplastic, antirheumatic, neuroprotective,
XX antiinflammatory, antisthmatic, antiallergic and cytostatic. This
XX polypeptide sequence is an APRIL protein, a TNF proliferation inducing
XX ligand that can form a fusion protein with a Blys protein of the
XX invention.
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 35; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSRRPS 7
DB 185 DVSRRPS 191
RESULT 31
ADE83862
ID ADE83862 standard; protein; 245 AA.
XX
AC ADE83862;
XX

DT 29-JAN-2004 (first entry)
XX
DE Chemokine beta-4 binding antibody F081C09 protein SEQ ID NO:21.
XX
KW antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
KW antipruritic; dermatological; antiinflammatory; immunosuppressive;
KW antineoplastic; antirheumatic; neuroprotective; cytostatic; anti-HIV;
KW vulnery; dermatitis; autoimmune disease; rheumatoid arthritis;
KW systemic lupus erythematosus; autoimmune encephalitis; cancer;
KW HIV infection; wound; inflammatory disorder; human; psoriasis.
XX
OS Synthetic.
XX
PN WO2003092597-A2.
XX
PD 13-NOV-2003.
XX
PF 30-APR-2003; 2003WO-US013414.
XX
PR 01-MAY-2002; 2002US-0376561P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX WPI; 2004-022614/02.
XX
DR N-PSDB; ADE83845.
XX
DR New antibody that specifically binds to a chemokine beta-4 polypeptide,
XX useful for diagnosing, treating, preventing or ameliorating psoriasis,
XX rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
XX and wounds.
XX
PS Claim 1; SEQ ID NO 21; 181pp; English.
XX
XX The present invention describes an antibody (I) that specifically binds
XX to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
XX amino acid sequence at least 95% identical to a second amino acid
XX sequence comprising a VH complementarily determining region (CDR) or VL
XX CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
XX sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
XX (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
XX (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
XX cell comprising the vector of (3); (5) a cell line engineered to express
XX (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
XX that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
XX method for detecting aberrant expression of CK-B4 polypeptide, comprising
XX assaying the level of CK-B4 polypeptide expression in a first biological
XX sample of an individual using at least one of (1), and comparing the
XX level of CK-B4 polypeptide assayed in the biological sample with a
XX standard level of CK-B4 polypeptide expression or level of CK-B4
XX polypeptide in a second, normal biological sample, where an increase or
XX decrease in the assayed level of CK-B4 polypeptide in the first
XX biological sample compared to the standard level is indicative of
XX aberrant expression; and (9) a method of treating, preventing or
XX ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
XX administering (1) to the animal. (1) has antipruritic, dermatological,
XX antiinflammatory, immunosuppressive, antineoplastic, antirheumatic,
XX cerebroprotective, cytostatic, anti-HIV and vulnery activities. The
XX methods and compositions of the present invention are useful for
XX diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
XX an autoimmune disease such as rheumatoid arthritis, systemic lupus
XX erythematosus and autoimmune encephalitis. They can also be used in
XX cancer, HIV infection, wounds and inflammatory disorders. The present
XX sequence is used in the exemplification of the present invention.
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 35; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 185 DVSKRPS 191

RESULT 32
ADG34308 standard; protein; 245 AA.
ID ADG34308 standard; protein; 245 AA.
XX
AC ADG34308;
XX
DT 26-FEB-2004 (first entry)
XX
DE Neurokinin B antibody SEQ ID NO:31.
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
XX
PR 29-MAY-2003; 2003WO-US016802.
XX
PS 30-MAY-2002; 2002US-0383802P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2004-053456/05.
XX
N-PSDB; ADG34289.
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
composition for treating or preventing hypertension or preeclampsia.
XX
PS Claim 2; SEQ ID NO 31; 127pp; English.
XX
CC The invention relates to a novel antibody specifically binding neurokinin
B. An antibody of the invention has hypotensive, and gynaecological
activity, and may have a use in gene therapy. The antibody is useful for
preparing a composition for treating or preventing hypertension or pre-
eclampsia. The present sequence is used in the exemplification of the
invention.
XX
SQ Sequence 245 AA;

Qy 1 DVSKRPS 7
Db 185 DVSKRPS 191

RESULT 33
ADG34313 standard; protein; 245 AA.
ID ADG34313 standard; protein; 245 AA.
XX
AC ADG34313;
XX
DT 26-FEB-2004 (first entry)
XX
DE Neurokinin B antibody SEQ ID NO:36.
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX

PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
XX
PR 30-MAY-2002; 2002US-0383802P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2004-053456/05.
XX
N-PSDB; ADG34294.
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
composition for treating or preventing hypertension or preeclampsia.
XX
PS Claim 2; SEQ ID NO 36; 127pp; English.
XX
CC The invention relates to a novel antibody specifically binding neurokinin
B. An antibody of the invention has hypotensive, and gynaecological
activity, and may have a use in gene therapy. The antibody is useful for
preparing a composition for treating or preventing hypertension or pre-
eclampsia. The present sequence is used in the exemplification of the
invention.
XX
SQ Sequence 245 AA;

Qy 1 DVSKRPS 7
Db 185 DVSKRPS 191

RESULT 34
ABP45902 standard; protein; 246 AA.
ID ABP45902 standard; protein; 246 AA.
XX
AC ABP45902;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1913.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
tumour necrosis factor; B cell proliferation; B cell differentiation;
immunomodulatory; immunostimulant; immunomodulatory; antineoplastic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX
XX Claim 1; Page 2683-2684; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX
SQ Sequence 246 AA;
XX
XX
Query Match 100.0%; Score 35; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DVSKRPS 7
|||
186 DVSKRPS 192
DB
XX
XX
RESULT 35
ABP45906
ID ABP45906 standard; protein; 246 AA.
XX
XX ABP45906;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human Blys binding scFv SEQ ID 1917.
DE
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX
XX WO200202641-A1.
PN
XX
XX 10-JAN-2002.
PD
XX
XX 15-JUN-2001; 2001WO-US019110.
PF
XX
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTI BODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI
XX

DR WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX
XX Claim 1; Page 2688-2689; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX
SQ Sequence 246 AA;
XX
XX
Query Match 100.0%; Score 35; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DVSKRPS 7
|||
186 DVSKRPS 192
DB
XX
XX
RESULT 36
ADG96733
ID ADG96733 standard; protein; 246 AA.
XX
XX ADG96733;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Single chain antibody that immunospecifically binds Blys SeqID 1917.
DE
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
KW carcinoma; lymphoma; antineumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
XX Unidentified.
OS
XX
XX WO2003055979-A2.
PN
XX
XX 10-JUL-2003.
PD
XX
XX 14-NOV-2002; 2002WO-US036496.
PF
XX
XX 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI
XX
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX

PS Example 1; SEQ ID NO 1917; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CD3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic and cyostatic.
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 35; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 186 DVSKRPS 192

RESULT 37

ID ADE83872 standard; protein; 246 AA.

XX ADG96729;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds Blys SegID 1913.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antiinflammatory; antiallergic; neuroprotective;
KM antiinflammatory; antiallergic; antiallergic; cyostatic.
XX
XX Unidentified.

OS
PN WO2003055979-A2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-031469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1913; 394pp; English.

XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CD3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic and cyostatic.
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 246 AA;

Query Match 100.0%; Score 35; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 186 DVSKRPS 192

RESULT 38

ID ADE83872 standard; protein; 246 AA.

XX ADE83872;

DT 29-JAN-2004 (first entry)

DE Chemokine beta-4 binding antibody P002C08 protein SEQ ID NO:31.

XX antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
KM antipruritic; dermatological; antiinflammatory; immunosuppressive;
KM antirheumatic; antiallergic; cerebroprotective; cyostatic; anti-HIV;
KM vulnery; dermatitis; autoimmune disease; rheumatoid arthritis;
KM systemic lupus erythematosus; autoimmune encephalitis; cancer;
KM HIV infection; wound; inflammatory disorder; human; psoriasis.
XX

OS Synthetic.

OS Homo sapiens.

PN WO2003092597-A2.

PD 13-NOV-2003.

PF 30-APR-2003; 2003WO-US013414.

PR 01-MAY-2002; 2002US-0376561P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX WPI; 2004-022614/02.

XX N-PSDB; ADE83855.
DR New antibody that specifically binds to a chemokine beta-4 polypeptide,
PT useful for diagnosing, treating, preventing or ameliorating psoriasis,

PT rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
 PT and wounds.
 XX
 PS Claim 1; SEQ ID NO 31; 181bp; English.

XX The present invention describes an antibody (1) that specifically binds
 CC to a chemokine beta-4 (CK-B4) polypeptide. Where (1) comprises a first
 CC amino acid sequence at least 95% identical to a second amino acid
 CC sequence comprising a VH complementarity determining region (CDR) or VL
 CC CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
 CC sequences of 245-253 amino acids (ADB83861 to ADB83877). Also described:
 CC (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
 CC (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
 CC cell comprising the vector of (3); (5) a cell line engineered to express
 CC (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
 CC that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
 CC method for detecting aberrant expression of CK-B4 polypeptide, comprising
 CC assaying the level of CK-B4 polypeptide expression in a first biological
 CC sample of an individual using at least one of (1), and comparing the
 CC level of CK-B4 polypeptide assayed in the biological sample with a
 CC standard level of CK-B4 polypeptide expression or level of CK-B4
 CC polypeptide in a second, normal biological sample, where an increase or
 CC decrease in the assayed level of CK-B4 polypeptide in the first
 CC biological sample compared to the standard level is indicative of
 CC aberrant expression; and (9) a method of treating, preventing or
 CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
 CC administering (1) to the animal. (1) has antipsoriatic, dermatologic,
 CC antiinflammatory, immunosuppressive, antirheumatic, antineuritic,
 CC cerebroprotective, cytostatic, anti-HIV and vulnereary activities. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
 CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
 CC erythematosus and autoimmune encephalitis. They can also be used in
 CC cancer, HIV infection, wounds and inflammatory disorders. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 246 AA;

Query Match 100.0%; Score 35; DB 8; Length 246;
 Best Local Similarity 100.0%; Pred. NO. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 186 DVSKRPS 192

RESULT 39
 ABP45671
 ID ABP45671 standard; protein: 247 AA.
 XX
 AC ABP45671;

DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1682.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antineuritic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCT INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2409-2410; 3148bp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineuritic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 35; DB 5; Length 247;
 Best Local Similarity 100.0%; Pred. NO. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 187 DVSKRPS 193

RESULT 40
 ABP45674
 ID ABP45674 standard; protein: 247 AA.
 XX
 AC ABP45674;

DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1685.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antineuritic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX

PI Ruben SM, Baraeh SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX

PS Claim 1; Page 2413-2414; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytototoxic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineoplastic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 35; DB 5; Length 247;

Best Local Similarity 100.0%; Pred. NO. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 188 DVSKRPS 194

Search completed: March 31, 2005, 12:02:31
 Job time : 55.25 secs

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OM protein - protein search, using BW model

Run on: March 31, 2005, 11:51:44 ; Search time 13.6719 Seconds
(without alignments)
36.220 Million cell updates/sec

Title: US-10-614-959-14

Perfect score: 35

Sequence: 1 DVSKRPS 7

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	7	US-09-383-667-14	Sequence 14, Appl
2	35	100.0	111	US-08-652-816A-15	Sequence 15, Appl
3	35	100.0	112	US-09-025-769B-19	Sequence 19, Appl
4	35	100.0	112	US-09-490-070A-19	Sequence 19, Appl
5	35	100.0	112	US-09-490-153-19	Sequence 19, Appl
6	35	100.0	112	US-09-490-324-19	Sequence 19, Appl
7	31	88.6	7	US-09-383-667-25	Sequence 25, Appl
8	31	88.6	7	US-09-424-840B-125	Sequence 125, Appl
9	31	88.6	235	US-08-378-939-12	Sequence 10, Appl
10	31	88.6	236	US-08-487-550-10	Sequence 10, Appl
11	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
12	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
13	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
14	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
15	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
16	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
17	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
18	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
19	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
20	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
21	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
22	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
23	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
24	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
25	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
26	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
27	31	88.6	236	US-09-526-098-10	Sequence 10, Appl

28	28	80.0	366	4	US-09-270-767-43922	Sequence 43922, A
29	28	80.0	514	4	US-09-252-991A-18161	Sequence 18161, A
30	28	80.0	692	4	US-09-540-236-2750	Sequence 2750, Ap
31	28	80.0	894	2	US-08-867-941-15	Sequence 15, Appl
32	28	80.0	898	2	US-08-867-941-11	Sequence 11, Appl
33	28	80.0	1118	4	US-09-538-092-423	Sequence 423, App
34	28	80.0	2150	4	US-09-321-987B-2	Sequence 2, Appl1
35	28	80.0	2165	4	US-09-800-729-155	Sequence 155, App
36	28	80.0	2432	3	US-09-074-658-15	Sequence 15, Appl
37	28	80.0	2439	3	US-09-074-658-11	Sequence 11, Appl
38	27	77.1	70	4	US-09-107-532A-7296	Sequence 7296, Ap
39	27	77.1	77	4	US-09-248-796A-17949	Sequence 17949, A
40	27	77.1	78	4	US-09-270-767-38080	Sequence 38080, A
41	27	77.1	78	4	US-09-270-767-53297	Sequence 53297, A
42	27	77.1	81	3	US-08-858-207A-476	Sequence 476, App
43	27	77.1	108	4	US-09-248-796A-22912	Sequence 22912, A
44	27	77.1	116	4	US-09-583-110-4891	Sequence 4891, Ap
45	27	77.1	124	4	US-09-107-433-3333	Sequence 3333, Ap

ALIGNMENTS

RESULT 1
US-09-383-667-14
; Sequence 14, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-14
Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. NO. 4.1e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DVSKRPS 7
Db 1 DVSKRPS 7
RESULT 2
US-08-652-816A-15
; Sequence 15, Application US/08652816A
; Patent No. 5672215
; GENERAL INFORMATION:
; APPLICANT: Oebourtn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-15

Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 3
US-09-025-769B-19
Sequence 19, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
FAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-19

Query Match 100.0%; Score 35; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 4
US-09-490-070A-19
Sequence 19, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McCaulliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-490-070A-19

Query Match 100.0%; Score 35; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58

RESULT 5
 US-09-490-153-19
 Sequence 19, Application US/09490153
 Patent No. 6706484
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,153
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-490-153-19

Query Match 100.0%; Score 35; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58

RESULT 6
 US-09-490-324-19
 Sequence 19, Application US/09490324
 Patent No. 6828422
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-490-324-19

Query Match 100.0%; Score 35; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58

RESULT 7
 US-09-383-667-25
 Sequence 25, Application US/09383667

Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Devaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Haas, Philip E.
APPLICANT: Judice, J. Kevin
APPLICANT: Kirchofer, Daniel
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 25
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-25

Query Match 88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSRRPS 7
DB 1 EVSRKPS 7

RESULT 8
US-09-424-840B-125
Sequence 125, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 125
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-125

Query Match 88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSRRPS 7
DB 1 EVSRKPS 7

RESULT 9
US-08-378-939-12
Sequence 12, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-939-12

Query Match 88.6%; Score 31; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSRRPS 7
DB 71 EVSRKPS 77

RESULT 10
US-08-487-550-10
Sequence 10, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONALD, SWECKER & MATHIAS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Teekin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-131
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 236 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-487-550-10

Query Match      88.6%; Score 31; DB 3; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
       |:|||||
Db      71 DINRPS 77

RESULT 11
: US-09-526-098-10
: Sequence 10, Application US/09526098
: Patent No. 6492134
: GENERAL INFORMATION:
: APPLICANT: Anderson, Darrell R.
: TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
: TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
: NUMBER OF INVENTION: IMMUNOSUPPRESSANTS"
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/526,098
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/383,916
: FILING DATE:
: APPLICATION NUMBER: US 08/487,550
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Teekin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-131
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 236 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-526-098-10

Query Match      88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
       |:|||||
Db      71 DINRPS 77

RESULT 12
: US-09-383-916-10
: Sequence 10, Application US/09383916
: Patent No. 6709654
: GENERAL INFORMATION:
: APPLICANT: Anderson, Darrell R.
: TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
: TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
: NUMBER OF INVENTION: IMMUNOSUPPRESSANTS"
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/383,916
: FILING DATE: 26-AUG-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/487,550
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Teekin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-131
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 236 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-383-916-10

Query Match      88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
       |:|||||
Db      71 DINRPS 77

RESULT 13
: US-09-949-016-7859
: Sequence 7859, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: QUERY MATCH
: BEST LOCAL SIMILARITY
: MATCHES
: CONSERVATIVE
: MISMATCHES
: INDELS
: GAPS
```

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7859
LENGTH: 1039
TYPE: PRT
ORGANISM: Human
US-09-949-016-7859

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 1039;
Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
Db 915 DVSKRP 920

RESULT 14
US-09-369-364A-13
Sequence 13, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apce, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1882
TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-9
FEATURE:
NAME/KEY: MOD RES
LOCATION: (468)
OTHER INFORMATION: Xaa = C
NAME/KEY: MOD RES
LOCATION: (521)
OTHER INFORMATION: Xaa = Y
US-09-369-364A-13

Query Match
Best Local Similarity 88.6%; Score 31; DB 3; Length 1882;
Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
Db 1543 DVSKRP 1548

RESULT 15
US-09-025-769B-33
Sequence 33, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-33

Query Match
Best Local Similarity 85.7%; Score 30; DB 3; Length 110;
Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 16
US-09-025-769B-53
Sequence 53, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-53

Query Match 85.7%; Score 30; DB 3; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSNRPS 58

RESULT 17
US-09-490-070A-33
Sequence 33, Application US/09490070A
Patent No. 6696248

GENERAL INFORMATION:
APPLICANT: Knappik, Achim

Ilag, Vic
Ge, Liming
Moroney, Simon

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-490-070A-33

Query Match 85.7%; Score 30; DB 4; Length 110;

Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSNRPS 58

RESULT 18
US-09-490-070A-53
Sequence 53, Application US/09490070A
Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ilag, Vic
Ge, Liming
Moroney, Simon

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-09-490-070A-53

Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSNRPS 58

RESULT 19
US-09-490-153-33
Sequence 33, Application US/09490153
Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ilag, Vic

Query Match 85.7%; Score 30; DB 4; Length 110;

Ge, Lining
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-490-153-33
Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVSRRPS 7
Db 52 DVSRRPS 58
RESULT 20
US-09-490-153-53
Sequence 53, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Lining
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-490-153-53
Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVSRRPS 7
Db 52 DVSRRPS 58
RESULT 21
US-09-490-324-33
Sequence 33, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Lining
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-490-324-33

Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 52 EVNKRPS 58

RESULT 22
US-09-490-324-53
Sequence 53, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-490-324-53

Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 52 EVNKRPS 58

RESULT 23
US-09-247-373B-42
Sequence 42, Application US/09247373B
Patent No. 6168954
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 42
LENGTH: 215
TYPE: PRT
ORGANISM: SOYBEAN
US-09-247-373B-42

Query Match 82.9%; Score 29; DB 3; Length 215;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 197 DISSRPS 203

RESULT 24
US-09-232-290-17
Sequence 17, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUECKHUHN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONGGGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapiens
US-09-232-290-17

Query Match 80.0%; Score 28; DB 4; Length 111;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 52 EVNKRPS 58

RESULT 25
US-09-252-991A-23989
Sequence 23989, Application US/09252991A
Patent No. 6551795

```
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23989
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23989

Query Match      80.0%; Score 28; DB 4; Length 140;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSRRPS 7
Db      73 DASKRPS 79

RESULT 26
US-09-134-000C-5577
; Sequence 5577, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5577
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (25)-(37)
; OTHER INFORMATION: Amino acids 25 & 37 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-5577

Query Match      80.0%; Score 28; DB 4; Length 217;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSRRPS 7
Db      160 DLSKQPS 166

RESULT 27
US-09-134-000C-4555
; Sequence 4555, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
```

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; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4555
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4555

Query Match      80.0%; Score 28; DB 4; Length 294;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSRRPS 7
Db      27 DASKRPS 33

RESULT 28
US-09-270-767-43922
; Sequence 43922, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43922
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43922

Query Match      80.0%; Score 28; DB 4; Length 366;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSRRPS 7
Db      297 DVERRPS 303

RESULT 29
US-09-252-991A-18161
; Sequence 18161, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18161
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18161

Query Match      80.0%; Score 28; DB 4; Length 514;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSRRPS 7
```


Db 44 DVSKRPS 50

RESULT 30

US-09-540-236-2750
; Sequence 2750, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2750
; LENGTH: 692
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2750

Query Match 80.0%; Score 28; DB 4; Length 692;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
Db 300 DVKRRPA 306

RESULT 31

US-08-867-941-15
; Sequence 15, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867.941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 894 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-867-941-15

Query Match 80.0%; Score 28; DB 2; Length 894;
Best Local Similarity 71.4%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
Db 287 DVKRRPA 293

RESULT 32

US-08-867-941-11
; Sequence 11, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867.941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-867-941-11

Query Match 80.0%; Score 28; DB 2; Length 898;
Best Local Similarity 71.4%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
Db 287 DVKRRPA 293

RESULT 33

US-09-538-092-423
; Sequence 423, Application US/09538092
; Patent No. 675314
; GENERAL INFORMATION:
; APPLICANT: Gloc, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538.092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352

;; PRIOR FILING DATE: 1999-04-01
;; PRIOR APPLICATION NUMBER: 60/1178,965
;; PRIOR FILING DATE: 2000-02-01
;; NUMBER OF SEQ ID NOS: 1387
;; SOFTWARE: CurataseqFormatter Version 0.9
;; SEQ ID NO: 423
;; LENGTH: 1118
;; TYPE: PRT
;; ORGANISM: Saccharomyces cerevisiae
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (0)...(0)
;; OTHER INFORMATION: Polypeptide Accession Number Y1151C
US-09-538-092-423

Query Match 80.0%; Score 28; DB 4; Length 1118;
Best Local Similarity 71.4%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 94 DVSKRPS 100

RESULT 34
US-09-321-987B-2
;; Sequence 2, Application US/09321987B
;; Patent No. 6730820
;; GENERAL INFORMATION:
;; APPLICANT: Kimble, Judith E
;; APPLICANT: Bielloch, Robert H
;; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
;; FILE REFERENCE: 960236.95386
;; CURRENT APPLICATION NUMBER: US/09/321,987B
;; CURRENT FILING DATE: 1999-05-28
;; PRIOR APPLICATION NUMBER: 60/087,170
;; PRIOR FILING DATE: 1998-05-29
;; PRIOR APPLICATION NUMBER: 60/129,023
;; PRIOR FILING DATE: 1999-04-13
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 2
;; LENGTH: 2150
;; TYPE: PRT
;; ORGANISM: Caenorhabditis elegans
US-09-321-987B-2

Query Match 80.0%; Score 28; DB 4; Length 2150;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 1452 DVQKRPT 1458

RESULT 35
US-09-800-729-155
;; Sequence 155, Application US/09800729
;; Patent No. 6605592
;; GENERAL INFORMATION:
;; APPLICANT: N1 et al.
;; TITLE OF INVENTION: 32 Human secreted proteins
;; FILE REFERENCE: P2044P1
;; CURRENT APPLICATION NUMBER: US/09/800,729
;; CURRENT FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: PCT/US00/26013
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: 60/155,709
;; PRIOR FILING DATE: 1999-09-24
;; NUMBER OF SEQ ID NOS: 217
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 155

;; LENGTH: 2165
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-800-729-155

Query Match 80.0%; Score 28; DB 4; Length 2165;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 1467 DVQKRPT 1473

RESULT 36
US-09-074-658-15
;; Sequence 15, Application US/09074658
;; Patent No. 6184371
;; GENERAL INFORMATION:
;; APPLICANT: Loomore, Sheena M
;; APPLICANT: Run-Pan Du
;; APPLICANT: Qijun Wang
;; APPLICANT: Yang, Yan-Ping
;; APPLICANT: Klein, Michel H
;; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
;; NUMBER OF SEQUENCES: 78
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: 6th Floor, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/074,658
;; FILING DATE: 08-MAY-1998
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-795
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2432 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-074-658-15

Query Match 80.0%; Score 28; DB 3; Length 2432;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 287 DVKKRPA 293

RESULT 37
US-09-074-658-11
;; Sequence 11, Application US/09074658
;; Patent No. 6184371
;; GENERAL INFORMATION:
;; APPLICANT: Loomore, Sheena M
;; APPLICANT: Run-Pan Du

APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2439 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-074-658-11

Query Match 80.0%; Score 28; DB 3; Length 2439;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSRKPS 7
Db 287 DVKRRPA 293

RESULT 38
US-09-107-532A-7296
Sequence 7296, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7296:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...70
SEQUENCE DESCRIPTION: SEQ ID NO: 7296:
US-09-107-532A-7296

Query Match 77.1%; Score 27; DB 4; Length 70;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSRKPS 7
Db 15 DCSRPS 21

RESULT 39
US-09-248-796A-17949
Sequence 17949, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCES: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17949
LENGTH: 77
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-17949

Query Match 77.1%; Score 27; DB 4; Length 77;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSRKPS 7
Db 6 NLSKPS 12

RESULT 40
US-09-270-767-38080
Sequence 38080, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCES: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 38080
 ; LENGTH: 78
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-38080

Query Match 77.1%; Score 27; DB 4; Length 78;
 Best Local Similarity 71.4%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
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 Db 47 DAKKRPS 53

Search completed: March 31, 2005, 12:13:27
 Job time : 13.6719 secs

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OM protein - protein search, using bw model

Run on: March 31, 2005, 12:10:00 ; Search time 39.1562 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	99	US-10-308-817-98	Sequence 98, Appl
2	35	100.0	99	US-10-453-698-98	Sequence 98, Appl
3	35	100.0	110	US-10-447-331-1	Sequence 1, Appl
4	35	100.0	111	US-10-360-828-61	Sequence 61, Appl
5	35	100.0	240	US-09-880-748-1898	Sequence 1898, Ap
6	35	100.0	240	US-10-293-418-1898	Sequence 1898, Ap
7	35	100.0	241	US-09-880-748-1898	Sequence 1898, Ap
8	35	100.0	241	US-10-293-418-1898	Sequence 1898, Ap
9	35	100.0	243	US-09-880-748-1898	Sequence 1898, Ap
10	35	100.0	243	US-10-293-418-1898	Sequence 1898, Ap
11	35	100.0	245	US-09-880-748-1898	Sequence 1898, Ap
12	35	100.0	245	US-10-293-418-1898	Sequence 1898, Ap
13	35	100.0	245	US-10-293-418-1898	Sequence 1898, Ap

14	35	100.0	246	US-09-880-748-1898	Sequence 1898, Ap
15	35	100.0	246	US-09-880-748-1898	Sequence 1898, Ap
16	35	100.0	246	US-10-293-418-1898	Sequence 1917, Ap
17	35	100.0	246	US-10-293-418-1898	Sequence 1917, Ap
18	35	100.0	247	US-09-880-748-1898	Sequence 1443, Ap
19	35	100.0	247	US-09-880-748-1898	Sequence 1682, Ap
20	35	100.0	247	US-09-880-748-1898	Sequence 1685, Ap
21	35	100.0	247	US-09-880-748-1898	Sequence 1685, Ap
22	35	100.0	247	US-09-880-748-1898	Sequence 1685, Ap
23	35	100.0	247	US-09-880-748-1898	Sequence 1685, Ap
24	35	100.0	247	US-09-880-748-1898	Sequence 1685, Ap
25	35	100.0	247	US-10-293-418-1898	Sequence 1443, Ap
26	35	100.0	247	US-10-293-418-1898	Sequence 1443, Ap
27	35	100.0	247	US-10-293-418-1898	Sequence 1443, Ap
28	35	100.0	247	US-10-293-418-1898	Sequence 1443, Ap
29	35	100.0	247	US-10-293-418-1898	Sequence 1443, Ap
30	35	100.0	247	US-10-293-418-1898	Sequence 1443, Ap
31	35	100.0	247	US-10-293-418-1898	Sequence 1443, Ap
32	35	100.0	249	US-09-880-748-1898	Sequence 1419, Ap
33	35	100.0	249	US-09-880-748-1898	Sequence 1419, Ap
34	35	100.0	249	US-09-880-748-1898	Sequence 1419, Ap
35	35	100.0	249	US-09-880-748-1898	Sequence 1419, Ap
36	35	100.0	249	US-10-293-418-1898	Sequence 1419, Ap
37	35	100.0	249	US-10-293-418-1898	Sequence 1419, Ap
38	35	100.0	249	US-10-293-418-1898	Sequence 1419, Ap
39	35	100.0	249	US-10-293-418-1898	Sequence 1419, Ap
40	35	100.0	250	US-09-880-748-1898	Sequence 1419, Ap
41	35	100.0	250	US-09-880-748-1898	Sequence 1419, Ap
42	35	100.0	251	US-09-880-748-1898	Sequence 1419, Ap
43	35	100.0	251	US-09-880-748-1898	Sequence 1419, Ap
44	35	100.0	251	US-09-880-748-1898	Sequence 1419, Ap
45	35	100.0	251	US-09-880-748-1898	Sequence 1419, Ap

ALIGNMENTS

RESULT 1
US-10-308-817-98
Sequence 98, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russel
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version 3.1
SEQ ID NO 98
LENGTH: 99
TYPE: PRT
ORGANISM: human
US-10-308-817-98

Query Match: 100.0%; Score 35; DB 15; Length 99;
Best Local Similarity: 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58
RESULT 2
US-10-453-698-98
Sequence 98, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
APPLICANT: Rother, Russel
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)

;; CURRENT APPLICATION NUMBER: US/10/453,698
;; CURRENT FILING DATE: 2003-06-03
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 98
;; LENGTH: 99
;; TYPE: PRT
;; ORGANISM: human
US-10-453-698-98

Query Match 100.0%; Score 35; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 52 DVSKRPS 58

RESULT 3
US-10-447-331-1
;; Sequence 1, Application US/10447331
;; Publication No. US20030219434A1
;; GENERAL INFORMATION:
;; APPLICANT: Carter, Paul J.
;; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
;; FILE REFERENCE: GENENT.122A
;; CURRENT APPLICATION NUMBER: US/10/447,331
;; CURRENT FILING DATE: 2003-05-28
;; PRIOR APPLICATION NUMBER: US/09/515,825
;; PRIOR FILING DATE: 2000-02-29
;; PRIOR APPLICATION NUMBER: 60/122262
;; PRIOR FILING DATE: 1999-03-01
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 110
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-447-331-1

Query Match 100.0%; Score 35; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 52 DVSKRPS 58

RESULT 4
US-10-360-828-61
;; Sequence 61, Application US/10360828
;; Publication No. US20030206909A1
;; GENERAL INFORMATION:
;; APPLICANT: Hua, Shaobing
;; APPLICANT: Pauling, Michelle H.
;; APPLICANT: Zhu, Li
;; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
;; FILE REFERENCE: 2636-727
;; CURRENT APPLICATION NUMBER: US/10/360,828
;; CURRENT FILING DATE: 2003-02-07
;; PRIOR APPLICATION NUMBER: US 10/071,866
;; PRIOR FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: US 10/072,301
;; PRIOR FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: US 10/133,978
;; PRIOR FILING DATE: 2002-04-25
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 61

;; LENGTH: 111
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VL of scFv Ab124
US-10-360-828-61

Query Match 100.0%; Score 35; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 52 DVSKRPS 58

RESULT 5
US-09-880-748-1898
;; Sequence 1898, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P5523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1898
;; LENGTH: 240
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match 100.0%; Score 35; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
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Db 181 DVSKRPS 187

RESULT 6
US-10-293-418-1898
;; Sequence 1898, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P5523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21

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; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1898

```

```

Query Match          100.0%; Score 35; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DVSKRPS 7
        |||||
Db      181 DVSKRPS 187

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RESULT 7
US-09-880-748-2055
; Sequence 2055, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2055

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Query Match          100.0%; Score 35; DB 10; Length 241;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DVSKRPS 7
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Db      182 DVSKRPS 188

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RESULT 8
US-10-293-418-2055
; Sequence 2055, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19

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; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2055

```

```

Query Match          100.0%; Score 35; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DVSKRPS 7
        |||||
Db      182 DVSKRPS 188

```

```

RESULT 9
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

```

```

Query Match          100.0%; Score 35; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DVSKRPS 7
        |||||
Db      183 DVSKRPS 189

```

```

RESULT 10
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2

```

```

; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927
```

```

Query Match      100.0%; Score 35; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 DVSKRPS 7
      |||||
Db      183 DVSKRPS 189
```

```

RESULT 11
US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926
```

```

Query Match      100.0%; Score 35; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 DVSKRPS 7
      |||||
Db      185 DVSKRPS 191
```

```

RESULT 12
US-10-293-418-1926
```

```

; Sequence 1926, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926
```

```

Query Match      100.0%; Score 35; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 DVSKRPS 7
      |||||
Db      185 DVSKRPS 191
```

```

RESULT 13
US-10-293-418-3241
; Sequence 3241, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3241
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3241
```


Query Match 100.0%; Score 35; DB 15; Length 245;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 185 DVSKRPS 191

RESULT 14

US-09-880-748-1913
 ; Sequence 1913, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1913
 ; LENGTH: 246
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-1913

Query Match 100.0%; Score 35; DB 10; Length 246;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 186 DVSKRPS 192

US-09-880-748-1917
 ; Sequence 1917, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1917
 ; LENGTH: 246
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-1917

Query Match 100.0%; Score 35; DB 10; Length 246;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 186 DVSKRPS 192

RESULT 16

US-10-293-418-1913
 ; Sequence 1913, Application US/10293418
 ; Publication No. US2003022396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 1913
 ; LENGTH: 246
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-293-418-1913

Query Match 100.0%; Score 35; DB 15; Length 246;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 186 DVSKRPS 192

US-10-293-418-1917
 ; Sequence 1917, Application US/10293418
 ; Publication No. US2003022396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1917
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1917

Query Match 100.0%; Score 35; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 186 DVSKRPS 192

RESULT 18
US-09-880-748-1443
Sequence 1443, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1443
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1443

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 187 DVSKRPS 193

RESULT 19
US-09-880-748-1682
Sequence 1682, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1682
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1682

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 187 DVSKRPS 193

RESULT 20
US-09-880-748-1685
Sequence 1685, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1685
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1685

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 188 DVSKRPS 194

RESULT 21
US-09-880-748-1707
Sequence 1707, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17

;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 1707
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1707

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 22
US-09-880-748-1899
;; Sequence 1899, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 1899
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1899

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 23
US-09-880-748-1928
;; Sequence 1928, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816

;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 1928
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1928

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 24
US-09-880-748-1934
;; Sequence 1934, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 1934
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1934

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 25
US-10-293-418-1443
;; Sequence 1443, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523p2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; PRIOR FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1443
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1443

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
DB 187 DVSKRPS 193

RESULT 26
US-10-293-418-1682
Sequence 1682, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1682
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1682

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
DB 187 DVSKRPS 193

RESULT 27

US-10-293-418-1685
Sequence 1685, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1685
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1685

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
DB 188 DVSKRPS 194

RESULT 28
US-10-293-418-1707
Sequence 1707, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1707
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1707

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 29

US-10-293-418-1899
; Sequence 1899, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1899

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 30

US-10-293-418-1928
; Sequence 1928, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1928

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 31

US-10-293-418-1934
; Sequence 1934, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1934

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 32

US-09-880-748-1419
; Sequence 1419, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT FILING DATE: 2001-06-15

```

; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1419
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1419

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 33
US-09-880-748-1618
; Sequence 1618, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1618

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 34
US-09-880-748-2049
; Sequence 2049, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
```

```

; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2049
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2049

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 35
US-09-880-748-2065
; Sequence 2065, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2065
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2065

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 36
US-10-293-418-1419
; Sequence 1419, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
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```

; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1419
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1419

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
        |||||
Db      189 DVSKRPS 195

RESULT 37
US-10-293-418-1618
; Sequence 1618, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1618

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
        |||||
Db      189 DVSKRPS 195
```

```

Db      189 DVSKRPS 195

RESULT 38
US-10-293-418-2049
; Sequence 2049, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2049
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2049

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
        |||||
Db      189 DVSKRPS 195

RESULT 39
US-10-293-418-2065
; Sequence 2065, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2065
```

LENGTH: 249
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-293-418-2065

Query Match 100.0%; Score 35; DB 15; Length 249;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 189 DVSKRPS 195

RESULT 40
 US-09-880-748-859
 ; Sequence 859, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PFS23
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 859
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-859

Query Match 100.0%; Score 35; DB 10; Length 250;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 192 DVSKRPS 198

Search completed: March 31, 2005, 12:46:10
 Job time : 40.1562 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 9.95312 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	99	2 S36057	Ig lambda chain -
2	34	97.1	646	2 G85056	probable receptor-
3	32	91.4	60	2 A24626	Ig lambda chain V-
4	32	91.4	103	2 A38923	AL type amyloid fi
5	32	91.4	111	1 L2HUTR	Ig lambda chain V-
6	32	91.4	423	2 F64690	type IIS restricti
7	31	88.6	110	2 S51149	antibody light cha
8	31	88.6	111	1 L2HUTN	Ig lambda chain V-
9	31	88.6	111	2 S36281	Ig lambda chain V
10	30	85.7	112	2 S31515	Ig lambda chain V
11	30	85.7	112	2 S44105	Ig lambda chain V-
12	30	85.7	416	2 S26836	type II site-speci
13	29	82.9	74	2 A92642	hypothetical prote
14	29	82.9	88	2 A97425	hypothetical prote
15	29	82.9	337	1 E70191	conserved hypotet
16	29	82.9	377	2 A32548	homeobox protein M
17	29	82.9	404	2 T00750	probable protein p
18	29	82.9	685	2 T21466	hypothetical prote
19	29	82.9	690	2 T21806	hypothetical prote
20	29	82.9	735	2 T00850	probable receptor-
21	29	82.9	972	2 H84903	hypothetical prote
22	29	82.9	1033	2 T37715	actin-interacting
23	29	82.9	1077	2 T21800	hypothetical prote
24	29	82.9	1245	2 G84897	hypothetical prote
25	28	80.0	91	2 T09711	ADP carrier pr
26	28	80.0	111	1 L2HUMC	Ig lambda chain V-
27	28	80.0	189	2 AE1316	GTP cyclolhydroase
28	28	80.0	189	2 AE1688	GTP cyclolhydroase
29	28	80.0	235	2 S25759	Ig lambda chain -

30	28	80.0	235	2 S14675	Ig lambda chain -
31	28	80.0	259	2 T40075	60s ribosomal prot
32	28	80.0	292	2 A64624	hypothetical prote
33	28	80.0	296	2 D71891	hypothetical prote
34	28	80.0	300	2 A82017	probable lipoprote
35	28	80.0	301	2 AE0243	hypothetical prote
36	28	80.0	309	2 B83999	mutants block spor
37	28	80.0	310	2 B97777	thioredoxin-disulf
38	28	80.0	310	2 D71703	thioredoxin reduct
39	28	80.0	348	2 G87604	thioredoxin reduct
40	28	80.0	440	2 S65358	familial Alzheimer
41	28	80.0	447	2 S35481	SRPM54 protein - M
42	28	80.0	452	2 T40769	hypothetical prote
43	28	80.0	458	1 Z2BPC2	gene 12 protein -
44	28	80.0	463	2 P04422	4-Hydroxybutyryl-C
45	28	80.0	498	1 HYBSPA	pseudolysin (EC 3.

ALIGNMENTS

RESULT 1
S36057
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36057
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <MW>
A:Cross-references: EMBL:Z22196, NID:G312319, PIDN:CA80208.1, PID:G312320
C:Superfamily: immunoglobulin V region, immunoglobulin homology.
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSKRPS 58

RESULT 2
G85056
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C:Accession: G85056
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; MUID:20083488; PMID:10617158
A:Accession: G85056
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-646 <STO>
A:Cross-references: UNIPROT:Q9XEC7, GB:INC_001268, NID:G7267207, PIDN:CA877918.1, GSPDB:G
C:Gene: AT4G04500
A:Map position: 4
C:Superfamily: protein kinase homology

Query Match 97.1%; Score 34; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 606 DISKPS 612

|||||

RESULT 3

A24626

Ig lambda chain V-II region (Har) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996

C/Accession: A24626

R/Eulitz, M.; Linke, R.

Biol. Chem. Hoppe-Seyler 366, 907-915, 1985

A/Title: Amyloid fibrils derived from V-region together with C-region fragments from a

A/Reference number: A24626; MUID:86077295; PMID:3935132

A/Accession: A24626

A/Molecule type: protein

A/Residues: 1-60 <EUL>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 91.4%; Score 32; DB 2; Length 60;

Best Local Similarity 85.7%; Pred. No. 3.1;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

|||||

Db 45 DVNRKPS 51

RESULT 4

A38923

AL type amyloid fibril protein precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C/Accession: A38923

R/Eulitz, M.; Linke, R.P.

Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993

A/Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amy

A/Reference number: A38923; MUID:93356823; PMID:8352801

A/Accession: A38923

A/Molecule type: protein

A/Residues: 1-95/96-103 <EUL>

C/Comment: This protein is derived from an immunoglobulin light chain of lambda type.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: amyloid; immunoglobulin

F/1-58/Product: AL type amyloid fibril protein #status predicted <MAT>

F/7-83/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 32; DB 2; Length 103;

Best Local Similarity 85.7%; Pred. No. 5.4;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

|||||

Db 43 DVNRKPS 49

RESULT 5

L2HUTR

Ig lambda chain V-II region (Tro) - human (tentative sequence)

C/Species: Homo sapiens (man)

C/Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004

C/Accession: A01973

R/Scholz, R.; Yang, C.; Hilschmann, N.

Hope-Seyler's Z. Physiol. Chem. 360, 1903-1918, 1979

A/Title: Zur Struktur der Antikörper. Die Primärstruktur eines monoklonalen Iga 1

A/Reference number: A01973; MUID:80114123; PMID:118915

A/Accession: A01973

A/Molecule type: protein

A/Residues: 1-111 <SCH>

A/Cross-references: UNIPROT:P01707

C/Comment: This chain was isolated from a myeloma protein.

C/Genetics:

A/Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap-

tain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into la

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: blocked amino end; heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

F/1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

F/22-90/Disulfide bonds: #status predicted

Query Match 91.4%; Score 32; DB 1; Length 111;

Best Local Similarity 85.7%; Pred. No. 5.9;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

|||||

Db 52 DVNRKPS 58

RESULT 6

F64690

Type IIS restriction enzyme R protein - Helicobacter pylori (strain 26695)

C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C/Accession: F64690

R/Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.

Nature 386, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.;

A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: F64690

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-423 <TOM>

A/Cross-references: UNIPROT:O25919; GB:AE000637; GB:AE000511; NID:G2314536; PIDN:AD08411

Query Match 91.4%; Score 32; DB 2; Length 423;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

|||||

Db 71 DVNRKPS 77

RESULT 7

S51149

antibody light chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C/Accession: S51149

R/de Kruij, V.; Boel, E.; Logtenberg, T.

submitted to the EMBL Data Library, January 1995

A/Description: Selection and application of human SCFV antibody fragments from a semi-sy

A/Reference number: S51147

A/Accession: S51149

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-110 <DEK>

A/Cross-references: EMBL:X83712

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/13-90/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 110;

Best Local Similarity 85.7%; Pred. No. 9.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

|||||

Db 50 EVSKRPS 56

RESULT 8

L2HWMN

Ig Lambda chain V-II region (Win) - human (tentative sequence)

C/Species: Homo sapiens (man)

C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004

C/Accession: A01978

R/Chen, B.L.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.

Biochim. Biophys. Acta 537, 9-21, 1978

A/Title: Amino acid sequence of the human myeloma lambda chain Win.

A/Reference number: A01978; MUID:79062503; PMID:102365

A/Accession: A01978

A/Molecule type: protein

A/Residues: 1-111 <CHE>

A/Cross-references: UNIPROT:P01712

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: blocked amino end; heterotetramer

F/15-92/Domain: immunoglobulin homology <IMM>

F/22-90/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 88.6%; Score 31; DB 1; Length 111;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 DVSKRPS 58

RESULT 9

S36281

Ig Lambda chain V region (clone alpha-FOG1-A3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C/Accession: S36281

R/Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MUID:93178448; PMID:7679990

A/Accession: S36281

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-111 <GR1>

A/Cross-references: EMBL:Z18623; NID:G33414; PIDN:CAA79275.1; PID:G939907

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.6%; Score 31; DB 2; Length 111;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 EVSKRPS 58

RESULT 10

S31515

Ig Lambda chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S31515

R/van der Heijden, R.W.J.; Uytendaele, F.G.C.M.; Osterhaus, A.D.M.E.

submitted to the EMBL Data Library, January 1993

A/Description: V-Lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody

A/Reference number: S31515

A/Accession: S31515

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-112 <VAN>

A/Cross-references: EMBL:Z19546; NID:G33754; PIDN:CAA79606.1; PID:G33755

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 112;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 DVSKRPS 58

RESULT 11

S44105

Ig Lambda chain V-J region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C/Accession: S44105

R/Hawkins, R.E.; Zhu, D.; Orecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

submitted to the EMBL Data Library, March 1994

A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A/Reference number: S44105

A/Accession: S44105

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-112 <HAN>

A/Cross-references: EMBL:Z31388; NID:G472959; PIDN:CAA83263.1; PID:G940517

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 112;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 DVSKRPS 58

RESULT 12

S26836

Type II site-specific deoxyribonuclease (EC 3.1.21.4) MboII - Moraxella bovis

C/Species: Moraxella bovis

C/Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S26836

R/Bocklage, H.; Heeger, K.; Mueller-Hill, B.

Nucleic Acids Res. 19, 1007-1013, 1991

A/Title: Cloning and characterization of the MboII restriction-modification system.

A/Reference number: S26835; MUID:91212177; PMID:2020540

A/Accession: S26836

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-416 <BOC>

A/Cross-references: UNIPROT:P23191; EMBL:X56977; NID:G44180; PIDN:CAA40298.1; PID:G44182

C/Keywords: hydrolase

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 416;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6

Db 66 DISKRP 71

RESULT 13
A:Title: hypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
A:Accession: AH2642
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
A:Accession: AH2642
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreppan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH2642
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-74 <KUR>
A:Cross-references: UNIPROT:Q8UHW8; GB:AB008688; PIDN:AAL41558.1; PID:g17738891; GSPDB:G
C:Genetics:
A:Gene: Atu0540
A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 74;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|:|:|:|
Db 2 DISKPS 8

RESULT 14
A:Title: hypothetical protein AGR_C_956 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
A:Accession: A97425
R:Goodner, B.; Hinkley, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A97425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <KUR>
A:Cross-references: UNIPROT:Q8UHW8; GB:AB007869; PIDN:AAK86354.1; PID:g15155478; GSPDB:G
C:Genetics:
A:Gene: AGR_C_956
A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 88;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|:|:|:|
Db 16 DISKPS 22

RESULT 15
A:Title: conserved hypothetical protein BB0734 - Lyme disease spirochete
A:Accession: E70191
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: E70191
R:Fraser, C.M.; Casjens, S.; Hwang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kevlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Yugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70191
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <KUR>
A:Cross-references: UNIPROT:O51676; GB:AE001173; GB:AE000783; NID:g2688665; PIDN:AA6708
A:Experimental source: strain B31
C:Superfamily: translation factor, SUN5 type

Query Match 82.9%; Score 29; DB 1; Length 337;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|:|:|:|
Db 141 DISKPS 147

RESULT 16
A:Title: homeobox protein Mix.1 - African clawed frog
A:Accession: A32548
C:Species: Xenopus laevis (African clawed frog)
C:Date: 05-Oct-1989 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
A:Accession: A32548
R:Roza, F.M.
Cell 57, 965-974, 1989
A:Title: Mix.1, a homeobox mRNA inducible by mesoderm inducers, is expressed mostly in t
A:Reference number: A32548; MUID:89288302; PMID:2567635
A:Accession: A32548
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-377 <ROS>
A:Cross-references: UNIPROT:P21711; GB:M27063; NID:g532660; PIDN:AAA49903.1; PID:g532661
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
P:97-153/Domains: homeobox homology <HOX>

Query Match 82.9%; Score 29; DB 2; Length 377;
Best Local Similarity 71.4%; Pred. No. 98;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|:|:|:|
Db 260 DISKPS 266

RESULT 17
A:Title: probable protein phosphatase 2C [imported] - Arabidopsis thaliana
A:Accession: T00750
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
A:Accession: T00750; G84834
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence.
A:Reference number: Z14159
A:Accession: T00750
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-404 <ROU>
A:Cross-references: UNIPROT:Q22200; EMBL:AC002409; NID:g2623294; PID:g2623300
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84834

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <STO>
A:Cross-references: GB:AE002093; NID:g2623300; PIDN:AAH86446.1; GSPDB:GN00139
C:Genetics:
A:Gene: T20B5.6; At2g40860
A:Map position: 2
A:Introns: 178/1; 200/2; 273/3; 308/3; 340/3

Query Match 82.9%; Score 29; DB 2; Length 404;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 43 DVSKRPS 49

RESULT 18

T21466

hypothetical protein F28B1.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21466

R:Matthews, L.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19426

A:Accession: T21466

A>Status: preliminary; translated from GB/EMBL/DBDUT

A:Molecule type: DNA

A:Residues: 1-685 <WIL>

A:Cross-references: UNIPROT:O45415; EMBL:Z81517; PIDN:CAB04212.1; GSPDB:GN00023; CESP:F2

C:Experimental source: clone F28B1

C:Genetics:

A:Gene: CESP:F28B1.5

A:Map position: 5

A:Introns: 31/3; 156/3; 258/3; 305/1; 384/3; 500/3; 600/3; 641/3

Query Match 82.9%; Score 29; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSKRPS 7
Db 347 VSKRPS 352

RESULT 19

T21806

hypothetical protein F35G12.3b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21806

R:Chui, C.

submitted to the EMBL Data Library, October 1994

A:Reference number: Z19473

A:Accession: T21806

A>Status: preliminary; translated from GB/EMBL/DBDUT

A:Molecule type: DNA

A:Residues: 1-690 <WIL>

A:Cross-references: UNIPROT:Q20056; EMBL:Z46242; PIDN:CAA6332.1; GSPDB:GN00021; CESP:F3

C:Experimental source: clone F35G12

C:Genetics:

A:Gene: CESP:F35G12.3b

A:Map position: 3

A:Introns: 37/1; 56/1; 96/3; 132/1; 244/1; 295/1; 332/3; 431/3; 538/2; 612/1

C:Superfamily: yeast hypothetical protein YNL020c; protein kinase homology

Query Match 82.9%; Score 29; DB 2; Length 690;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 301 DVNRPS 307

RESULT 20

T00850

probable receptor-like protein kinase [imported] - Arabidopsis thaliana

N/Alternate names: hypothetical protein T20F6.8

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Aug-2004

C:Accession: T00850; G84440

R:Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, March 1998

A:Description: Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence.

A:Reference number: Z14206

A:Accession: T00850

A>Status: translated from GB/EMBL/DBDUT

A:Molecule type: DNA

A:Residues: 1-735 <ROU>

A:Cross-references: UNIPROT:O64505; EMBL:AC002521; NID:g2947056; PID:g2947063

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Yankken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84440

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-735 <STO>

A:Cross-references: GB:AE002093; NID:g2947063; PIDN:AA05344.1; GSPDB:GN00139

C:Genetics:

A:Gene: T20F6.8; At2g02780

A:Map position: 2

A:Introns: 421/1; 472/3; 555/1; 619/3; 652/3

C:Superfamily: protein kinase homology

Query Match 82.9%; Score 29; DB 2; Length 735;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 695 DVSKRPS 701

RESULT 21

H84903

hypothetical protein At2g46520 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84903

R:Jan, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vancken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84903

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-972 <STO>

A:Cross-references: UNIPROT:Q9ZPY7; GB:AE002093; NID:g4415933; PIDN:AA020163.1; GSPDB:GN

C:Genetics:

A:Gene: At2g46520

A:Map position: 2

Query Match 82.9%; Score 29; DB 2; Length 972;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 311 DVSKRPS 317

RESULT 22

T37715

actin-interacting homolog SPAC15A10.16 [imported] - fission yeast (schizosaccharomyces p

C/Species: Schizosaccharomyces pombe

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000

C/Accession: T37715

R/Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1997

A/Reference number: Z21738

A/Accession: T37715

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1033 <MUR>

A/Cross-references: EMBL:Z97208; PIDN:CA81012.1; GSPDB:GN00066; SPDB:SPAC15A10.16

A/Experimental source: strain 972h; cosmid c15A10

C/Genetics:

A/Map position: 1

Query Match

Best Local Similarity 82.9%; Score 29; DB 2; Length 1033;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 298 VSKRPS 303

RESULT 23

T21800

hypothetical protein F35G12.3a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T21800

R/Chui, C.

submitted to the EMBL Data Library, October 1994

A/Reference number: Z19473

A/Accession: T21800

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1077 <MTL>

A/Cross-references: UNIPROT:Q20050; EMBL:Z46242; PIDN:CAA66326.1; GSPDB:GN00021; CESP:F3

A/Experimental source: clone F35G12

C/Genetics:

A/Map position: 3

A/Introns: 37/1; 56/1; 96/3; 132/1; 244/1; 295/1; 332/3; 431/3; 538/2; 612/1; 654/1; 688

Query Match

Best Local Similarity 82.9%; Score 29; DB 2; Length 1077;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 301 DVNRPS 307

RESULT 24

G84897

hypothetical protein At2g46020 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: G84897

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

ues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: G84897

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1245 <STO>

A/Cross-references: UNIPROT:O82366; GB:AE002093; NID:G3702343; PIDN:AC62900.1; GSPDB:GN

C/Genetics:

A/Map position: 2

Query Match

Best Local Similarity 82.9%; Score 29; DB 2; Length 1245;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 633 DLKSRPS 639

RESULT 25

T09711

ADP,ATP carrier protein CANT2 - upland cotton (fragment)

N/Alternate names: adenine nucleotide translocator 2

C/Species: Gossypium hirsutum (upland cotton)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T09711

R/Shin, H.; Brown, R.M.

submitted to the EMBL Data Library, June 1997

A/Reference number: Z16832

A/Accession: T09711

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-91 <SHI>

A/Cross-references: UNIPROT:O22343; EMBL:AF006490; NID:G2463665; PID:G2463666

A/Experimental source: strain Texas marker1; fiber

C/Genetics:

A/Map position: 2

Query Match

Best Local Similarity 80.0%; Score 28; DB 2; Length 91;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 3 DSKRPS 9

RESULT 26

L2HDMC

Ig lambda chain V-II region (Mcg) - human

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C/Accession: A90381; A01975

R/Felt, J.W.; Deutsch, H.F.

Biochemistry 13, 4102-4114, 1974

A/Title: Primary structure of the Mcg lambda chain.

A/Reference number: A90381; MUID:75013804; PMID:4415202

A/Accession: A90381

A/Molecule type: protein

A/Residues: 1-111 <FEY>

A/Cross-references: UNIPROT:P01709

A/Note: the C region of this chain has the Kern+ and Mcg+ markers

R/Felt, J.W.; Deutsch, H.F.

Immunochimistry 12, 643-652, 1975

A/Title: A new lambda-chain gene.

A/Reference number: A91745; MUID:76093781; PMID:812801

A/Contents: annotation; lambda chain genes

A/Note: the Mcg-type C region appears to be correlated with a very unusual V-region subet

R/Bunderson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.

Biochemistry 14, 3953-3961, 1975

A/Title: Rotational allomerism and divergent evolution of domains in immunoglobulin light

A:Reference number: A90391
A:Contents: annotation; X-ray crystallography, 2.3 angstroms
A:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (Kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotrimer
F:15-92/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status F:22-90/Disulfide bonds: #status predicted

Query Match 80.0%; Score 28; DB 1; Length 111;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
|||:|
Db 52 EVNKRPS 58

RESULT 27
AE1316
GTP cyclohydrolase I homolog Imo1933 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1316
R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schlueker, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <GUA>
A:Cross-references: UNIPROT:Q8Y5X1; GB:NC_003210; PIDN:CAD00011.1; PID:G16411386; GSPDB: A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: Imo1933
C:Superfamily: GTP cyclohydrolase I

Query Match 80.0%; Score 28; DB 2; Length 189;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRP 6
|||:|
Db 112 DVSRRP 117

RESULT 28
AE1688
GTP cyclohydrolase I homolog Lin2047 [imported] - Listeria innocua (strain C1p11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1688
R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schlueker, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1688
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-189 <GUA>
A:Cross-references: UNIPROT:Q92A75; GB:AL592022; PIDN:CAC97277.1; PID:G16414548; GSPDB:G A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: Lin2047
C:Superfamily: GTP cyclohydrolase I

Query Match 80.0%; Score 28; DB 2; Length 189;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRP 6
|||:|
Db 112 DVSRRP 117

RESULT 29
S25759
Ig lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25759
R:Combario, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lambda F:150-218/Domain: immunoglobulin homology <IMM>
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25759
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57824; NID:933747; PIDN:CAA40961.1; PID:933748
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 28; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
|||:|
Db 71 DVSGRPS 77

RESULT 30
S14675
Ig lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C:Accession: S14675; S12445
R:Vaaiček, T.J.
submitted to the EMBL Data Library, February 1990
A:Reference number: S14675
A:Accession: S14675
A:Molecule type: DNA
A:Residues: 1-235 <VAS1>
A:Cross-references: UNIPROT:Q8WTK4; EMBL:X51754
R:Vaaiček, T.J.; Leder, P.
J. Exp. Med. 172, 609-620, 1990
A:Title: Structure and expression of the human immunoglobulin lambda genes.
A:Reference number: S12440; MUID:90324881; PMID:2115572
A:Accession: S12445
A:Cross-references: EMBL:X51754
C:Genetics:
A:Introns: 16/1; 130/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 28; DB 2; Length 235;

Best Local Similarity 71.4%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 71 EVTKRPS 77

RESULT 31

T40075

60s ribosomal protein l8 - fission yeast (Schizosaccharomyces pombe)

N/Alternate names: ribosomal protein L7; ribosomal protein L7a, cytosolic

C/Species: Schizosaccharomyces pombe

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T40075; T45223

R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Voicakeart, G.

submitted to the EMBL Data Library, March 1998

A/Reference number: Z21904

A/Accession: T40075

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-259 <LUN>

A/Cross-references: UNIPROT:O13672; EMBL:AL022239; PIDN:CAA18381.1; GSPDB:GN00067; SPDB:

A/Experimental source: strain 972h-; cosmid C29A3

R/Marchfelder, A.; Clayton, D.A.; Brennick, A.

Biochim. Biophys. Acta 1397, 146-150, 1998

A/Title: The gene for ribosomal protein L7a in Schizosaccharomyces pombe contains an int

A/Reference number: Z22944; MUID:98234301; PMID:9565672

A/Accession: T45223

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-259 <MAR>

A/Cross-references: EMBL:AJ001133; NID:g3123704; PIDN:CAA04548.1; PID:g3123705

C/Genetics:

A/Gene: rp18-1; SPBC29A3.04; L7A

A/Map position: 2

A/Intons: 1/3

C/Superfamily: rat ribosomal protein L7a

Query Match 80.0%; Score 28; DB 2; Length 259;

Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRP 6
Db 124 DVSKRP 129

RESULT 32
A64624
hypothetical protein HP0833 - Helicobacter pylori (strain 26695)

C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C/Accession: A64624

R/Tomb, J.F.; White, O.; Kexlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Knaluk, H.G.; Glodek, A.; McKenna

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: A64624

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-292 <TOM>

A/Cross-references: UNIPROT:O25504; GB:AE000594; GB:AE000511; NID:g2313957; PIDN:AD0788

C/Genetics:

A/Start codon: TTG

C/Superfamily: Helicobacter pylori hypothetical protein jhp0772

Query Match 80.0%; Score 28; DB 2; Length 292;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 38 DGSKRPS 44

RESULT 33

D71891

hypothetical protein jhp0772 - Helicobacter pylori (strain J99)

C/Species: Helicobacter pylori

A/Variety: strain J99

C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C/Accession: D71891

R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Iyevs, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.;

Nature 397, 176-180, 1999

A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A/Reference number: A71800; MUID:99120557; PMID:9923682

A/Accession: D71891

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-296 <ANR>

A/Cross-references: UNIPROT:Q9ZL10; GB:AE001507; GB:AE001439; NID:g4155326; PIDN:AA06351

A/Experimental source: strain J99

C/Genetics:

A/Gene: jhp0772

C/Superfamily: Helicobacter pylori hypothetical protein jhp0772

Query Match 80.0%; Score 28; DB 2; Length 296;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 38 DGSKRPS 44

RESULT 34
A82017
probable lipoprotein NMA0225 [imported] - Neisseria meningitidis (strain Z2491 serogroup

C/Species: Neisseria meningitidis

C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: A82017

R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell

Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: A82017

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-300 <PAR>

A/Cross-references: UNIPROT:Q9QUV3; GB:AL16752; GB:AL157959; NID:g7378778; PIDN:CAB83536

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: NMA0225

Query Match 80.0%; Score 28; DB 2; Length 300;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 217 DISRPS 223

RESULT 35
AE0243
hypothetical protein YP01996 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C/Accession: AE0243

R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.B.;

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AB0243

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-301 <KUR>
A/Cross-references: UNIPROT:Q8ZF00; GB:AL590842; PIDN:CMC90809.1; PID:g15980010; GSPDB:C
C/Genetics:
A/Gene: YPO1996

Query Match 80.0%; Score 28; DB 2; Length 301;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|:|:|
Db 142 DLSORPS 148

RESULT 36

EB3999
mutants block sporulation after engulfment spoIIIA [imported] - *Bacillus halodurans* (st
C/Species: *Bacillus halodurans*
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: EB3999
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A/Reference number: AB3650; MUID:20512582; PMID:11058132
A/Accession: EB3999

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-309 <STO>
A/Cross-references: UNIPROT:Q9K953; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB065
A/Experimental source: strain C-125
C/Genetics:
A/Gene: spoIIIA

Query Match 80.0%; Score 28; DB 2; Length 309;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|:|:|
Db 263 EVSKRPA 269

RESULT 37

B97777
thioredoxin-disulfide reductase (EC 1.8.1.9) - *Rickettsia conorii* (strain Malish 7)

C/Species: *Rickettsia conorii*
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: B97777

R/Ogata, H.; Andic, S.; Renato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A/Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A/Reference number: A57700; MUID:21442074; PMID:11557893
A/Accession: B97777

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-310 <KUR>
A/Cross-references: UNIPROT:Q92102; GB:AE006914; PIDN:AAL03156.1; PID:g15619703; GSPDB:C
C/Genetics:
A/Gene: trxB1
C/Superfamily: thioredoxin reductase; thioredoxin reductase homology
C/Keywords: oxidoreductase

Query Match 80.0%; Score 28; DB 2; Length 310;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
|:|:|
Db 87 DLSKRP 92

RESULT 38

D71703
thioredoxin reductase (trxB1) RP445 - *Rickettsia prowazekii*

C/Species: *Rickettsia prowazekii*
C/Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C/Accession: D71703

R/Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Scharitz-Ponten, T.; Almark, U
Nature 396, 133-140, 1998
A/Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
A/Reference number: A71630; MUID:99039499; PMID:9828893
A/Accession: D71703

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-310 <AND>
A/Cross-references: UNIPROT:Q9ZD97; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA1490
A/Experimental source: strain Madrid E
C/Genetics:
A/Gene: trxB1; RP445
C/Superfamily: thioredoxin reductase; thioredoxin reductase homology
F,1-308/Domain: thioredoxin reductase homology <TRXB>

Query Match 80.0%; Score 28; DB 2; Length 310;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
|:|:|
Db 87 DLSKRP 92

RESULT 39

G87604
thioredoxin reductase [imported] - *Caulobacter crescentus*

C/Species: *Caulobacter crescentus*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: G87604

R/Nieman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Land, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of *Caulobacter crescentus*.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: G87604

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-348 <STO>
A/Cross-references: UNIPROT:Q9A4G3; GB:AE005673; NID:g13424487; PIDN:AAK24835.1; GSPDB:C
C/Genetics:
A/Gene: CC2871
C/Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 80.0%; Score 28; DB 2; Length 348;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
|:|:|
Db 104 DLSKRP 109

RESULT 40

S65358
familial Alzheimer's disease protein 1 - human

C/Species: *Homo sapiens* (man)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S65358
R/Matsumoto, A.; Matsumoto, R.; Fujiwara, Y.

Eur. J. Biochem. 230, 337-343, 1995
 A;Title: Molecular cloning of human CDNA with a sequence highly similar to that of the d
 A;Reference number: S65358; MUID:95324544; PMID:7601120
 A;Accession: S65358
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-440 <MAT>
 A;Cross-references: UNIPROT:Q7M4L1

Query Match 80.0%; Score 28; DB 2; Length 440;
 Best local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 ||:||||
 Db 204 DVGRRPS 210

Search completed: March 31, 2005, 12:11:17
 Job time : 11.9531 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 46.4844 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	646	2	Q9XEC7 arabidopsis
2	32	91.4	111	1	P01707 homo sapien
3	32	91.4	236	2	Q6PIQ7 homo sapien
4	32	91.4	423	2	Q25919 helicobacte
5	31	88.6	111	1	P01712 homo sapien
6	31	88.6	130	2	Q7MUS6 porphyromon
7	31	88.6	233	2	Q7S4H3 neurospora
8	31	88.6	400	2	Q7SZL9 brachydanio
9	31	88.6	402	2	Q64WES bacteroides
10	31	88.6	486	2	Q828G3 streptomyce
11	31	88.6	728	2	Q7SF90 neurospora
12	31	88.6	1292	2	Q6SLD6 cochllobolu
13	31	88.6	1766	2	Q7SEB6 ashyba goss
14	31	88.6	1935	1	AT9S HUMAN
15	30	85.7	164	1	BR11 MAMGNG
16	30	85.7	212	2	Q9V6F8 drosophila
17	30	85.7	233	2	Q6FUA3 homo sapien
18	30	85.7	236	2	Q6P5S3 homo sapien
19	30	85.7	267	2	Q9BTM2 homo sapien
20	30	85.7	279	1	Y170 BUCBP
21	30	85.7	283	2	Q70914 prunus necr
22	30	85.7	283	2	Q70918 prunus necr
23	30	85.7	285	2	Q71142 prunus necr
24	30	85.7	327	2	Q86V04 homo sapien
25	30	85.7	378	2	Q9XY82 enchytraeus
26	30	85.7	385	2	Q7S098 neurospora
27	30	85.7	401	2	Q6DHY1 moraxella b
28	30	85.7	416	1	T2M2 MORBO
29	30	85.7	508	2	Q80U48 mus musculu
30	30	85.7	530	2	Q6PHCO mus musculu
31	30	85.7	654	2	Q8CA22 mus musculu

32	30	85.7	674	2	Q9DBJ2 mus musculu
33	30	85.7	706	1	TM24_HUMAN
34	30	85.7	706	1	TM24_MOUSE
35	30	85.7	747	2	Q6DOL7 erwinia car
36	30	85.7	833	2	Q6ADP4 leifsonia x
37	30	85.7	1036	2	Q6LMO4 methanococc
38	30	85.7	1059	2	Q64QOL bacteroides
39	30	85.7	1372	2	Q8SX99 drosophila
40	30	85.7	1372	2	Q9VN46 drosophila
41	29	82.9	59	2	Q6YEX3 vltis vinif
42	29	82.9	74	2	Q8UHW8 agrobacteri
43	29	82.9	80	2	Q6LK05 photobacter
44	29	82.9	88	2	Q7D190 agrobacteri
45	29	82.9	103	2	Q6D0T2 erwinia car

ALIGNMENTS

RESULT 1
Q9XEC7 PRELIMINARY, PRT: 646 AA.
AC Q9XEC7, 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative receptor-like protein kinase.
GN Name=TR26N6.11; Synonyms=AT9404500;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parnell L.D.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y., Mewes H.W.,
RL Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF076243; AAD29752.1; -;
DR EMBL; AL161500; CAB77918.1; -;
DR PIR; G85056; G85056.
DR HSSP; P06239; 3LCK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002902; DUF26.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot. kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR Pfam; PF01657; DUF26; 2.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00106; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW transferase.
SQ SEQUENCE 646 AA; 73439 MW; E1200574D5864207 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 646;
 Best Local Similarity 85.7%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 606 DISKPS 612

RESULT 2
 LV2D HUMAN STANDARD; PRT; 111 AA.
 AC P01707;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 05-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda chain V-II region TRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

QY 1 DVSKRPS 7
 DB 606 DISKPS 612

RESULT 3
 O6PIQ7 PRELIMINARY; PRT; 236 AA.
 AC O6PIQ7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.B., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.

QY 1 DVSKRPS 7
 DB 71 DVNKRPS 77

RESULT 4
 O25919 PRELIMINARY; PRT; 423 AA.
 AC O25919;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Type IIS restriction enzyme R protein (MBOIIR).
 GN OrderedlocusNames=HP1366;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 1 DVSKRPS 7
 DB 71 DVNKRPS 77

RESULT 4
 O25919 PRELIMINARY; PRT; 423 AA.
 AC O25919;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Type IIS restriction enzyme R protein (MBOIIR).
 GN OrderedlocusNames=HP1366;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 1 DVSKRPS 7
 DB 71 DVNKRPS 77

RESULT 4
 O25919 PRELIMINARY; PRT; 423 AA.
 AC O25919;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Type IIS restriction enzyme R protein (MBOIIR).
 GN OrderedlocusNames=HP1366;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 1 DVSKRPS 7
 DB 71 DVNKRPS 77

RESULT 4
 O25919 PRELIMINARY; PRT; 423 AA.
 AC O25919;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Type IIS restriction enzyme R protein (MBOIIR).
 GN OrderedlocusNames=HP1366;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Glodok A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Matthey L., Mallin B., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.,
RT "The complete genome sequence of the gastric pathogen *Helicobacter*
RT *pylori*.";
RL Nature 388:539-547(1997).
DR EMBL: AE000637; AAC08410.1; -
DR PIR: F64690; F64690.
DR TIGR: HPI366; -
DR InterPro: IPR003615; HNH_nuc.
DR SMART: SM00507; HNH; 1.
KW Complete proteome.
SQ SEQUENCE 423 AA; 50047 MW; 908651C8FE4E58E CRC64;

Query Match 91.4%; Score 32; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
|:|||||
Db 71 DVSKRPS 77

RESULT 5

LV21_HUMAN STANDARD; PRT; 111 AA.

AC P01712;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-II region WTN.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=7062503; PubMed=102365; DOI=10.1016/0005-2795(78)90598-6;
RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.U.;
RT "Amino acid sequence of the human myeloma lambda chain Wtn."
RL Biochim. Biophys. Acta 537:9-21(1978).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A01978; L2HWN.
DR HSBP; P01709; IDCL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF0047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT DOMAIN 1 106
FT MOD_RES 1 1
FT DISULFID 22 90
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11694 MW; 8C9CB95FE721B07C CRC64;

Query Match 88.6%; Score 31; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
|:|||||
Db 52 DVSKRPS 58

RESULT 6

O7MUS6 PRELIMINARY; PRT; 130 AA.
AC O7MUS6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PG1409;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxId=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/01.185.18.5591-5601.2003.
RA Nelson K.E., Fleischmann R.D., Desoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Taiton L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT *Porphyromonas gingivalis* strain W83."
RL J. Bacteriol. 185:5591-5601(2003).
DR EMBL: AE017176; AA066466.1; -
DR TIGR: PG1409; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 130 AA; 14455 MW; 3F2E1F64F23E5805 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 130;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
|:|||||
Db 107 DVSKRPS 113

RESULT 7

O7S4H3 PRELIMINARY; PRT; 233 AA.

AC O7S4H3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU0220.1;
OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seitzmunkhoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
RA Keith G.O., Jedd G., Mewes W., Steben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Navlyar J., Thumann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krystofova S., Kasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.U., Osmant S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*."

-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

```

CC      preliminary data.
DR      EMBL: AABX0100366; EAAJ0397.1; -.
DR      GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR      GO: GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
DR      InterPro: IPR001853; DSB_A.
DR      InterPro: IPR010986; DsbA_insertion.
DR      Pfam: PF01323; DSB_A; 1.
KM      Hypothetical protein.
SQ      SEQUENCE 233 AA; 25367 MW; 50B8FA369168929 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSRRPS 7
Db      222 DVSRRPS 228

RESULT 8
Q7SZL9 PRELIMINARY; PRT; 400 AA.
AC Q7SZL9;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ATP-gated Ionotropic P2X receptor subunit 2.
GN Name=p2rx2; Synonyms=p2rx2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22943235; PubMed=14580944; DOI=10.1016/S0306-4522(03)00566-9;
RA Kucenas S., Li Z., Cox J.A., Egan T.M., Voigt M.M.;
RT "Molecular characterization of the zebrafish P2X receptor subunit gene
family.";
RL Neuroscienc 121:935-945(2003).
DR EMBL: AY292650; AAC21195.1; -.
DR ZFIN: ZDB-GENE-030319-2; p2rx2.
DR GO: GO:0009503; C:light-harvesting complex (sensu Viridiplantae); IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0005216; F:ion channel activity; IEA.
DR GO: GO:0016978; F:lipoate-protein ligase B activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0006091; P:energy pathway; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR InterPro: IPR000066; Antenna_a/b.
DR InterPro: IPR001429; P2X receptor.
DR Pfam: PF00864; P2X receptor; 1.
DR TIGRfams: TIGR00863; P2X; 1.
KM Receptor.
SQ SEQUENCE 400 AA; 45752 MW; E8571C00171609F5 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSRRPS 7
Db      369 DVSRRPS 375

RESULT 9
Q64WES PRELIMINARY; PRT; 402 AA.
AC Q64WES;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

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DE      Predicted nucleoside-diphosphate sugar epimerase.
GN ORNames=SP1430;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kubara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT interons regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL: AP006841; BAD48181.1; -.
SQ SEQUENCE 402 AA; 45596 MW; 2D56A6DAF87797CC CRC64;

Query Match      88.6%; Score 31; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSRRP 6
Db      348 DVSRRP 353

RESULT 10
Q828G3 PRELIMINARY; PRT; 486 AA.
AC Q828G3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative cytochrome P450.
GN Name=cyp24; OrderedLocNames=SAV6706;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osomoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
CC - - SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL: AP005047; BAC74417.1; -.
DR HSSP: Q9L142; IGMT.
DR GO: GO:0004497; F:monooxygenase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR002397; BP450.
DR InterPro: IPR001128; Cytochrome_P450.
DR PRINTS: PR00359; BP450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN 1.
KM Complete proteome: Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 486;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;

```

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||:||||
Db 428 DVSKRPS 434

RESULT 11

Q7SEF90 PRELIMINARY; PRT; 728 AA.

AC Q7SEF90; (TRENBLrel. 26, Created)

DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Predicted protein.

GN Name=NCU00559.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=OR74A; Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Galagan J.E., FitzHugh W., Ma L.-Y., Smirnov S., Purcell S., Rehman B.,
RA Jaffe D., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Elkins T., Tankelev P., Pedersen D., Nelson M., Washburne M.,
RA Qiu D., Ianakiev C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Seitzmunkoff C.P., Mewes W., Steben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mancini E., Bielke R., Rudd S., Frisman D.,
RA Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catheide D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).

CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

CC EMBL; AABX0100022; EAA35484.1; -
SQ SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 728;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||:||||
Db 336 DVSKRPS 342

RESULT 12

Q6SLD6 PRELIMINARY; PRT; 1292 AA.

AC Q6SLD6; (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Putative histidine kinase HKK1p.

GN Name=HKK1;

OS Cochliobolus heterostrophus (Drechslera maydis).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;

OC Pleosporales; Pleosporaceae; Cochliobolus.

OX NCBI_TaxID=5016;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C4;

RX PubMed:1465450; DOI=10.1128/EC.2.6.1151-1161.2003;

RA Catlett N.L., Yoder O.C., Turgeon B.G.;

RT "Whole-genome analysis of two-component signal transduction genes in

RT fungal pathogenes.",
RL Eukaryotic Cell 2:1151-1161(2003).

CC -1- SIMILARITY: Contains 1 histidine kinase domain.

EMBL; AY456014; AAR29890.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.

DR GO; GO:0000156; F:two-component response regulator activity; IEA.

DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.

DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.

DR InterPro; IPR004358; Bact_sens_pr_C.

DR InterPro; IPR011006; Chey_like.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR003661; His_kin_N.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; HSKA; 1.

DR Pfam; PF00072; Response_reg; 1.

DR PRINTS; PR00344; BCTRLSENSOR.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; HSKA; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KM Kinase; Phosphorylation; Sensory transduction.

SQ SEQUENCE 1292 AA; 144730 MW; 57010F00609FF49B CRC64;

Query Match 88.6%; Score 31; DB 2; Length 1292;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||:||||
Db 45 DVSKRPS 51

RESULT 13

Q7SE06 PRELIMINARY; PRT; 1766 AA.

AC Q7SE06; (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE ABL133Cp.

GN ORFNames=ABL133C;

OS Asbya gossypii (Yeast) (Eremothecium gossypii).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Eremothecium.

OX NCBI_TaxID=33169;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 10895;

RA Voegelé S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE016815; AAS50638.1; -

DR AGD; ABL133C; -

SQ SEQUENCE 1766 AA; 179132 MW; BEC73A1CF69F2EA3 CRC64;

Qy 1 DVSKRPS 7
|||:||||
Db 1445 DVSKRPS 1451

RESULT 14

Query Match 88.6%; Score 31; DB 2; Length 1766;
Best Local Similarity 85.7%; Pred. No. 9.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


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FT CARBOHYD 1806 1806 N-linked (GlcNAc...) (Potential).
FT VASAPLIC 1064 1072 CLVTGKGH -> VAMEGCTFP (in isoform 3).
FT VASAPLIC 1073 1935 Missing (in isoform 3).
FT VASAPLIC 1624 1629 CSVTGC -> VPSWEL (in isoform 2).
FT VASAPLIC 1630 1935 /FTId=VSP_007548.
FT VASAPLIC 1630 1935 Missing (in isoform 2).
FT CONFLICT 46 46 /FTId=VSP_007549.
FT CONFLICT 96 96 S -> G (in Ref. 1).
FT CONFLICT 182 182 P -> S (in Ref. 1).
FT CONFLICT 367 367 D -> G (in Ref. 2).
FT CONFLICT 1117 1117 F -> L (in Ref. 1).
FT CONFLICT 1117 1117 V -> G (in Ref. 3).
SQ SEQUENCE 1935 AA; 216556 MW; FD3D51E88300A3C6 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 1935;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
Db 1596 DVSKRP 1601

RESULT 15
BFR1_MAGMG STANDARD; PRT; 164 AA.
ID BFR1_MAGMG
AC 050171;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bacterioferritin subunit 1 (BFR 1).
GN Name=bfr1.
OS Magnetospirillum magnetotacticum (Aquaespirillum magnetotacticum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Magnetospirillum.
OX NCBI_TaxID=188;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS-1;
RX MEDLINE=96072426; PubMed=9409768; DOI=10.1016/S0378-1119(97)00424-1;
RA Bettand L.E., Huang J.S., Weir B.A., Kirichynk J.L.;
RT "Evidence for two types of subunits in the bacterioferritin of
Magnetospirillum magnetotacticum."
RL Gene 20131-36(1997).
CC -1- FUNCTION: May perform analogous functions in iron detoxification
and storage to that of animal ferritins (By similarity).
CC -1- COFACTOR: Binds 1 heme b (iron-protoporhyrin IX) group per
monomer (Potential).
CC -1- SUBUNIT: Oligomer of 24 identical subunits (By similarity).
CC -1- MISCELLANEOUS: The di-iron binding site functions as active site
where iron ions are oxidized from iron(II) to iron(III) before
they are stored (By similarity).
CC -1- SIMILARITY: Belongs to the bacterioferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
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CC EMBL: AF001959; AAC91253.1; -.
DR HSSP: P11056; 1BCF.
DR InterPro: IPR002024; Bacterioferritin.
DR InterPro: IPR009078; Ferritin/RR_like.
DR InterPro: IPR008331; Ferritin_DPs.
DR InterPro: IPR009040; Ferritin_like.
DR Pfam: PF00210; Ferritin_1.
DR PRINTS: PR00601; BACTERIFERRITIN.

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DR ProDom: PD002269; Bacterioferritin; 1.
DR TIGRFAMs: TIGR00754; Bfr, 1.
DR PROSITE: PS00549; BACTERIOFERRITIN; 1.
DR PROSITE: PS09005; FERRITIN LIKE; 1.
KW Heme; Iron; Iron storage; Metal-binding.
FT DOMAIN 1 147 Ferritin-like diiron.
FT METAL 18 18 Iron 1 (By similarity).
FT METAL 49 49 Iron (heme axial ligand) (Potential).
FT METAL 51 51 Iron 2 (By similarity).
FT METAL 51 51 Iron 2 (By similarity).
FT METAL 54 54 Iron 1 (By similarity).
FT METAL 94 94 Iron 2 (By similarity).
FT METAL 129 129 Iron 1 (By similarity).
FT METAL 129 129 Iron 2 (By similarity).
FT METAL 132 132 Iron 2 (By similarity).
SQ SEQUENCE 164 AA; 18491 MW; 6B837DCAFCDD72358 CRC64;

Query Match 85.7%; Score 30; DB 1; Length 164;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
Db 70 DVSKRP 75

RESULT 16
Q9V6F8 PRELIMINARY; PRT; 212 AA.
ID Q9V6F8
AC Q9V6F8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE CG30052-PA (GH25962P).
GN Name=Odp49a; ORFNames=CG30052;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekline R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E.B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Duthin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glisdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heitman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.U., Wei M.H., Ibegam C.,
RA Jaraal M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liao P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekurov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy I., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paley J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheefer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,

```

RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yen R.F., Zaveri J.S., Zhan M., Zhang M., Zhang Q., Zheng L.,
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Change M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatic
 RT genome perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426099; PubMed=12537572;
 RA Mirza S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hirdsey P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.D., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN
 RP SEQUENCE FROM N.A.
 RX
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RX
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RX
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RX
 RL STRAIN=Berkeley;
 RA Stapleton M., Bricestein P., Hong L., Aghayani A., Carlson J.,
 RA Change M., Chavez C., Dorsett V., Dresnek D., Fattan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E.,
 RA Celniker S.;
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE003821; AAF58469.2; -;
 DR EMBL; AY118821; AAM50661.1; -;
 DR INAC; Q9V6F8; -;
 DR FLYBase; FBgn0050053; CG30053.
 DR FLYBase; FBgn0050052; ODP49A.
 SO SEQUENCE 212 AA; 23472 MW; 9449E602F390B469 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 212;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 DVSKRPS 7
 |||||

DB 25 DSKRPS 31
 RESULT 17
 ID 06P53 PRELIMINARY; PRT; 233 AA.
 AC 06P53;
 DT 05-JUL-2004 (TRENDEL. 27, Created)
 DT 05-JUL-2004 (TRENDEL. 27, Last sequence update)
 DE 05-JUL-2004 (TRENDEL. 27, Last annotation update)
 OS Homo sapiens (Human).
 OC Hypothetical protein.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshimaki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravinsky M.I., Skaleja U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN
 RP EMBL; BC018749; AAH18749.1; -;
 DR HSSP; P01709; 1ABJ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SO SEQUENCE 233 AA; 24509 MW; AA0588B008C9F09 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 233;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 DVSKRPS 7
 |||||
 71 DVSKRPS 77

RESULT 18
 ID 06P53 PRELIMINARY; PRT; 236 AA.
 AC 06P53;

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DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Glndular pool - thyroid;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold S.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Raley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RP TISSUE=Glandular pool - thyroid;
RA Strausberg R.;
RC Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062711; AAH62711.1; -
DR HSP; P01709; IABJ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SO SEQUENCE 236 AA; 24928 MW; C036D7FA63468E0D CRC64;

Query Match 85.7%; Score 30; DB 2; Length 236;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 71 DVSNRPS 77

RESULT 19
Q9BTM2 PRELIMINARY; PRT; 267 AA.
AC Q9BTM2;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE KIAA0285 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold S.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Raley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Strausberg R.;
RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003598; AAH03598.2; -
SO SEQUENCE 267 AA; 28233 MW; 400C27CCEB1EA107 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 267;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 168 DISRPS 174

RESULT 20
Y170_BUCBP STANDARD; PRT; 279 AA.
AC Q89A52;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein bnp170 (ybaz).
CN OrderedLocustNames=bnp170;
OS Buchnera aphidicola (subsp. Baizongia pistaciae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=135842;
[1]
SEQUENCE FROM N.A.
RP PubMed=12522265; DOI=10.1073/pnas.0235961100;
RA van Ham R.C.H.J., Kamerbeek U., Palacios C., Rausell C., Abascal F.,
RA Baatolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
RT "Reductive genome evolution in Buchnera aphidicola."
RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
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CC EMBL; AE014016; AAO26903.1; -

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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 279 AA; 31460 MW; 616FDB0C3821009D CRC64;

Query Match 85.7%; Score 30; DB 1; Length 279;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 114 DISKRP 119

RESULT 21

070914 PRELIMINARY; PRT; 283 AA.
AC 070914;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative movement protein.
OS Prunus necrotic ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=37733;
RN [1]
RP SEQUENCE FROM N.A.
RA Scott S.W., Zimmermann M.T., Ge X., Mackenzie D.J.;
RT "The coat proteins and putative movement proteins of isolates of Prunus necrotic ringspot virus from different host species and geographic origins are extensively conserved."
RL Eur. J. Plant Pathol. 104:155-161(1998).
DR EMBL; AF013285; AAC16498.1;
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP.1.
SQ SEQUENCE 283 AA; 31568 MW; 4BA16CAD1F8B191A CRC64;

Query Match 85.7%; Score 30; DB 2; Length 283;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 3 DVSKNPS 9

RESULT 22

070918 PRELIMINARY; PRT; 283 AA.
AC 070918;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative movement protein.
OS Prunus necrotic ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=37733;
RN [1]
RP SEQUENCE FROM N.A.
RA Scott S.W., Zimmermann M.T., Ge X., Mackenzie D.J.;
RT "The coat proteins and putative movement proteins of isolates of Prunus necrotic ringspot virus from different host species and geographic origins are extensively conserved."
RL Eur. J. Plant Pathol. 104:155-161(1998).
DR EMBL; AF013287; AAC16502.1;
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP.1.
SQ SEQUENCE 283 AA; 31459 MW; DEB602B59309123 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 283;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 3 DVSKNPS 9

RESULT 23

071142 PRELIMINARY; PRT; 285 AA.
AC 071142;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative movement protein.
OS Prunus necrotic ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=37733;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CH71;
RX MEDLINE=98343741; PubMed=9680147;
RA Hammond R.W., Crosslin J.M.;
RT "Virulence and molecular polymorphism of Prunus necrotic ringspot virus isolates."
RL J. Gen. Virol. 79:1815-1823(1998).
DR EMBL; AF034995; AAC1036.1;
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP.1.
SQ SEQUENCE 285 AA; 31795 MW; 3247584F7B73F506 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 285;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 3 DVSKNPS 9

RESULT 24

086V04 PRELIMINARY; PRT; 327 AA.
AC 086V04;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE KIA0285 Protein (Fragment).
GN Name=KIA0285;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schmeich A., Schein J.E.,
RA Jones S.J., Maitra W.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052246; AAH52246.1; -.
FT NON TER 1
SQ SEQUENCE 327 AA; 34509 MW; D21FF6223ED711FC CRC64;

Query Match 85.7%; Score 30; DB 2; Length 327;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 228 DISERP 234

RESULT 25
ID Q9XY82 PRELIMINARY; PRT; 378 AA.
AC Q9XY82;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Elongation factor 1-alpha (Fragment).
OS Enchytraeus sp. 'Enc'.
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Tubificata; Enchytraeidae; Enchytraeus.
OX NCBI_TaxID=89370;
RN [1]
RP SEQUENCE FROM N.A.
RA Regier J.C., Shultz J.W.;
RT "Molecular phylogeny of arthropods and the significance of the
RT Cambrian 'explosion' for molecular systematics.";
RL Am. Zoologist 38:918-928 (1998).
DR EMBL; AF063418; AAD21857.1; -.
DR HSSP; P02994; IFE0.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR004539; EFT_alpha.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR000795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat_Factor.
DR Pfam; PF00009; GTP_EFTU_D2; 1.
DR Pfam; PF03144; GTP_EFTU_D3; 1.
DR PRINTS; PR00315; ELONGATNFCM.
DR TIGRfams; TIGR00483; EF-1_alpha; 1.
DR PROSITE; PS00301; EFACOR_GTP; 1.
KW Elongation factor; GTP-binding; Protein biosynthesis.
FT NON TER 1
FT TER 378
SQ SEQUENCE 378 AA; 41429 MW; 1793787C653C5F5B CRC64;

Query Match 85.7%; Score 30; DB 2; Length 378;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 191 DVKRP 197

RESULT 26

Q7S098
ID Q7S098 PRELIMINARY; PRT; 385 AA.
AC Q7S098;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU10037.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Galvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-Y., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endlitz M.,
RA Qiu D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamyselis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Nativig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nudbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0 (2003).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA00100518; EAA28730.1; -.
SQ SEQUENCE 385 AA; 44471 MW; 6FF21B8053B0309B CRC64;

Query Match 85.7%; Score 30; DB 2; Length 385;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 379 DVSNRPS 385

RESULT 27
ID Q6DHX1 PRELIMINARY; PRT; 401 AA.
AC Q6DHX1;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefel C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahney J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC075833; AAF75832.1; -
 DR InterPro; IPR008973; C2_CabD.
 KW Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 401 AA; 42633 MW; 80E3C52006A6DFPA CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 401;
 Best Local Similarity 71.4%; Pred. No. 3.5e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 302 DISERPS 308
 RESULT 28
 T2M2 MORBO STANDARD; PRT; 416 AA.
 ID T2M2 MORBO
 AC P23191;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Type IIS restriction enzyme MboII (EC 3.1.21.4) (Endonuclease MboII)
 (R.MboII).
 GN Name=MboII;
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5; 7-12 AND 15-19.
 RC STRAIN=ATCC 10900;
 RX MEDLINE=91212177; PubMed=2020540;
 RA Bocklage H., Heeger K., Mueller-Hill B.;
 RT "Cloning and characterization of the MboII restriction-modification
 RT system";
 RL Nucleic Acids Res. 19:1007-1013 (1991).
 CC -1- FUNCTION: Recognizes the double-stranded sequences GAGA and TCTTC
 CC and cleaves respectively 13 bases after G-1 and 7 bases before T-
 CC 1, leaving a single 3' protruding nucleotide.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -1- Cofactor: Magnesium.
 CC -----
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 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL; X56977; CAA40298.1; -
 DR PIR; S26836; S26836.
 DR REBASE; 1205; MboII.
 KW Direct protein sequencing; Endonuclease; Hydrolase; Magnesium;
 KM Nuclease; Restriction system.
 SQ SEQUENCE 416 AA; 48617 MW; CSA0008775B635CPC CRC64;

Query Match 85.7%; Score 30; DB 1; Length 416;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRP 6
 DB 66 DISKRP 71
 RESULT 29
 Q80U48 PRELIMINARY; PRT; 508 AA.
 ID Q80U48
 AC Q80U48;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE MKIAA0285 protein (Fragment).
 GN Name=MKIAA0285;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22579291; PubMed=12693553;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
 RA Nakajima D., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT cDNAs identified by screening of terminal sequences of 400 mouse KIAA-homologous
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:35-48 (2003).
 DR EMBL; AK122237; BAC65519.1; -
 FT NON TER
 SQ SEQUENCE 508 AA; 54979 MW; 2331C7AE26845EAI CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 508;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 409 DISERPS 415
 RESULT 30
 Q6PHCO PRELIMINARY; PRT; 530 AA.
 ID Q6PHCO
 AC Q6PHCO;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Tmem24 protein.
 GN Name=Tmem24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tohyiuki S., Carninci P., Prange C.,
 RA Raha S.S., Locuselli N.A., Peters G.J., Abramson R.D., Mullady S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor. C3;
 RA Strusberg R.;
 RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC056612; AAH56612.1; -;
 DR InterPro, IPR008973; C2_GALB.
 SQ SEQUENCE 530 AA; 5686 MW; FAAEE290EAF13504 CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 530;
 Best Local Similarity 71.4%; Pred. No. 4.6e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DVSKRPS 7
 Db 431 DISERPS 437
 RESULT 31
 ID 08CA2 PRELIMINARY; PRT; 654 AA.
 AC 08CA2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched
 DE library, clone:A230109H5 product:hypothetical C2 domain
 DE (Calcium/lipid-binding domain, CalB) structure containing protein,
 DE full insert sequence.
 GN Name=Tem24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT Nature 420:563-573(2002).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Atzawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuwa T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA Adachi J., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirao K., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AK039220; BAC30281.1; -;
 DR MGD, MGI:1919014; Tem24.
 DR InterPro, IPR008973; C2_GALB.
 KW Hypothetical protein.
 SQ SEQUENCE 654 AA; 70454 MW; 63472C1D12BAF05D CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 654;
 Best Local Similarity 71.4%; Pred. No. 5.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DVSKRPS 7
 Db 607 DISERPS 613
 RESULT 32
 ID 09DBJ2 PRELIMINARY; PRT; 674 AA.
 AC 09DBJ2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
 DE library, clone:130006023 product:hypothetical C2 domain
 DE (Calcium/lipid-binding domain, CalB) structure containing protein,
 DE full insert sequence.
 GN Name=Tem24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[3]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA The PANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[4]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carinini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
[5]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carinini P.,
RA Kono H., Akiyama J., Nishi K., Kitsuina T., Teshiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada M.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wakahagi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
[6]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Adachi J., Aizawa K., Akabira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carinini P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Katsukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Muramatsu T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK004920; BAB3671.1; -
DR MGI; MGI:1919014; Tmem24.
DR InterPro; IPR008973; C2_GaLB.
RW Hypothetical protein.
SQ SEQUENCE 674 AA; 72442 MW; BA290F25B6258E83 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 674;
Best Local Similarity 71.4%; Pred. No. 6e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSXKPS 7
|:|:|
Db 575 DISRPS 581

RESULT 33
ID TM24 HUMAN STANDARD. PRT. 706 AA.
AC O14523; O86UT7; Q8NS22; Q8TBM4; Q96G10;
DT 15-JUL-1998 (Rel. 36, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane protein 24 (DINB23 protein).
GN Name=TMEM24; Synonyms=KIAA0285;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP SEQUENCE FROM N.A.
RA Kubo T., Arai Y., Ohira M., Gamou T., Maeno G., Sakiyama T.,
RA Toyoda A., Hatori M., Sakaki Y., Nakagawa A., Ohki M.,
RT "Identification of a 500-kb region of common allelic loss in
RT chromosome 11q23 in non-MYC amplified type of neuroblastoma."
RL Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.
[2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Pancreas;
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marud A.K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schermer A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN
RP SEQUENCE OF 49-706 FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=9732306; PubMed=9179496;
RA Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Nomura N.,
RT "Construction and characterization of human brain cDNA libraries
RT suitable for analysis of cDNA clones encoding relatively large
RT proteins."
RL DNA Res. 4:53-59(1997).
[4]
RN
RP REVISIONS.
RA Ohara O., Nagase T., Kikuno R., Nomura N.,
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
CC
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CC
DR EMBL; AB094094; BAC76048.1; -
DR EMBL; BC010071; AAH10071.1; ALT_INT.
DR EMBL; BC021254; AAH21254.1; ALT_INT.
DR EMBL; BC022219; AAH22219.1; -
DR EMBL; BC033083; AAH33083.1; -
DR EMBL; AB006623; BAA22954.2; -
DR Genew; HGNC:29000; TMEM24.
DR InterPro; IPR008973; C2_GaLB.
KW Transmembrane.
FT TRANSMEM 10
FT CONFLICT 497 R -> PG (in Ref. 1).
SQ SEQUENCE 706 AA; 76180 MW; 9301ABDF6D4D5B6 CRC64;
Query Match 85.7%; Score 30; DB 1; Length 706;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|:|:|
Db 607 DISERPS 613

RESULT 34
TM24_MOUSE STANDARD; PRT; 706 AA.

AC O80X80; 2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane protein 24.
GN Name=tmem24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
[1]

SEQUENCE FROM N. A.
RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralline P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra W.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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CC EMBL; BC049875; AAH49875.1; -
DR EMBL; BC060156; AAH60156.1; -
DR MGI; MGI:1919014; 1300006023Rik.
DR Interpro; IPR008973; C2_CalB.

FT TRANSMEM 10 30 Potential.
FT CONFLICT 550 550 V -> A (in Ref. 1; AAH49875).
SQ SEQUENCE 706 AA; 76356 MW; 2F8B63D26FF1F91 CRC64;

Query Match 85.7%; Score 30; DB 1; Length 706;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|:|:|
Db 607 DISERPS 613

RESULT 35
Q6D0L7

ID Q6D0L7 PRELIMINARY; PRT; 747 AA.

AC Q6D0L7;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE TONB dependent siderophore receptor.
GN Name=lepa; Synonyms=lepf, leub; OrderedLocustNames=ECA5781;
OS Erwina carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
NCBI_Taxid=29471;
[1]

SEQUENCE FROM N. A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holava M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Baeson N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.,
RT "Genome sequence of the enterobacterial phytopathogen Erwina
carotovora subsp. atroseptica and characterization of virulence
factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).

DR EMBL; BX950851; CAG76680.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0016820; F:hydrolase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002086; Alderhyd. dehydros.
DR InterPro; IPR000568; ATPsyn. Asub.
DR InterPro; IPR010916; TONB_Box_N.
DR InterPro; IPR010917; TONB_recept_C.
DR InterPro; IPR010105; TONB_sdp_recept.
DR TIGRFAMs; TIGR01783; TONB-siderophor; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00449; ATPASE_A; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
DR PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
KW Complete proteome; Receptor.

SQ SEQUENCE 747 AA; 81581 MW; 8E8A5D2505CBB065 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
|:|:|
Db 56 DISKRP 61

RESULT 36
Q6ADP4 PRELIMINARY; PRT; 833 AA.

AC Q6ADP4;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Telchoic acid synthase.
GN Name=tagF; OrderedLocustNames=Lxx17460;
OS Leifsonia xyl1 (subsp. xyl1).
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Micrococciaceae; Microbacteriaceae; Leifsonia.
NCBI_Taxid=59736;
[1]

RP SEQUENCE FROM N. A.
RC STRAIN=CTCB07;
RX PubMed=15305603;
Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,

RA Kitaajima J.P., Truffei D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Taitia M.A., da Silva A.C.R., Putian L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F., Jr., Carter H., Coutinho L.L., El-Dorry H.A.,
RA Ferro M.I.T., Gagliardi P.R., Giglioli E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.W., Zanca A.S., Simpson A.J.G., Brumley S.W., Seubert U.C.,
RT "The genome sequence of the Gram-positive sugarcane pathogen *Telifonia*
RT *xyl* subsp. *xyl1*.",
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL: AE016832; AAT89502.1; -
DR GO:GO:0016020; C:membrane; IEA.
DR GO:GO:0047355; F:CDP-glycerol glycerophosphotransferase actl. .; IEA.
DR GO:GO:0009058; P:biosynthesis; IEA.
DR GO:GO:0019350; P:telcholic acid biosynthesis; IEA.
DR InterPro: IPR001296; Glyco_trans_1.
DR InterPro: IPR007554; Glycos_transf.
DR Pfam: PF00534; Glycos_transf_1; 1.
DR Pfam: PF0464; Glyphos_transf; 1.
KW Complete proteome.
SO SEQUENCE 833 AA; 92594 MW; 3C321CDABF67FC99 CRC64;

Query Match	85.7%	Score 30;	DB 2;	Length 833;
Best Local Similarity	85.7%	Pred. No. 7.4e+02;		
Matches	6;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;
QY	1	DVSKRPS	7	
Db	119	DPSKRPS	125	

RESULT 37	06LW04	PRELIMINARY;	PRT; 1036 AA.
ID	06LW04		
AC	06LW04;		
DT	05-JUL-2004 (TEMBirel, 27, Created)		
DT	05-JUL-2004 (TEMBirel, 27, last sequence update)		
DT	05-JUL-2004 (TEMBirel, 27, last annotation update)		
DE	Hypothetical protein.		
GN	OrderedlocusNames=MMP1653;		
OS	Methanococcus maripaludis.		
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;		
OC	Methanococcaceae; Methanococcus.		
OX	NCBI_TaxId=39152;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=82 / LL;		
RA	Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,		
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,		
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,		
RA	Moore B., Porat I., Overbeek R., Palmieri A., Rouse G.,		
RA	Saenphimachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,		
RA	Leigh J.A.,		
RT	"Complete genome sequence of the mesophilic hydrogenotrophic		
RT	methanogen <i>Methanococcus maripaludis</i> ."		
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX57223; CAF31209.1; -		
DR	InterPro; IPR006938; ARM.		
KM	Complete proteome.		
QO	SEQUENCE 1036 AA; 121756 MW; A79CBFI0B2060575 CRC64;		

	85.7%;	Score 30;	DB 2;	Length 1036;
Best Local Similarity	85.7%;	Pred. No. 9.3e+02;		
Matches	6;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	1 DVSKRPS	7		
DG	808 DYSKRPS	814		

RESULT 38

064001		
ID	064001	PRELIMINARY; PRR; 1059 AA.
AC	064001;	
DT	25-OCT-2004 (TREMblrel. 28, Created)	
DT	25-OCT-2004 (TREMblrel. 28, Last sequence update)	
DT	25-OCT-2004 (TREMblrel. 28, Last annotation update)	
DE	Putative outer membrane protein probably involved in nutrient binding.	
GN	ORFNames=BF3437;	
OS	Bacteroides fragilis.	
OC	Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;	
OC	Bacteroidaceae; Bacteroides.	
OX	NCBI_TaxID=817;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=YCH46;	
RA	Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,	
RA	Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;	
RT	"Genomic analysis of Bacteroides fragilis reveals extensive DNA	
RT	inversions regulating cell surface adaptation.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).	
DR	EMBL; AF006841; BAD50180.1;	
SO	SEQUENCE	1059 AA; 118250 NM; F15E945F7DBFDA5 CRC64;

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Query Match      85.7%:  Score 30;  DB 2;  Length 1059;
Best Local Similarity  83.3%:  Pred. No. 9.6e+02;
Matches      5;  Conservative      1;  Mismatches      0;  Gaps      0;

QY      1 DVSKRP 6
      |:|||
      |:|||
Db      158 DISKRP 163

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RESULT 39			
08SX99			
ID	08SX99	PRELIMINARY;	PRT; 1372 AA.
AC	08SX99;		
DT	01-JUN-2002	(TRMBLrel. 21, Created)	
D7	01-JUN-2002	(TRMBLrel. 21, Last sequence update)	
D7	01-MAR-2003	(TRMBLrel. 23, Last annotation update)	
DE	GH25780p.		
GN	Name=CG1054; ORFName=CG1513;		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxId=7227;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Berkeley;		
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,		
RA	Champe M., Chavez C., Dorett V., Drensek D., Farfan D., Frise E.,		
RA	George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,		
RA	Miranda A., Mungall C.J., Nuno U.J., Paele J., Parages V., Park S.,		
RA	Patel S., Phouanavong S., Wan C., Yu C., Lewis S.E., Rubin G.M.,		
RA	Celniker S.;		
RL	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: AY094730; AAA11083.1; -.		
DR	flyBase; FBgn0051531; CG1513.		
DR	SEQUENCE 1372 AA; 149239 MW; 389B643E74C2658E CRC64;		

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Query Match      85.7%; Score 30; DB 2; Length 1372;
Best Local Similarity 85.7%;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 DVSKRPS 7
        | | | | |
Db       722 DFKSRPS 728

```

RESULT 40
Q9VN46
ID Q9VN46 PRELIMINARY; PRT, 1372 AA

AC Q9VNA6;
 DT 01-MAR-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG31531-PA (CG31531-pb).
 GN ORFNames=CG31531;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TextID=7227;
 RN
 RP
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Aghayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Buttis K.C., Busam D.A., Butler H., Cadelu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ihegama C.,
 RA Jalaali M., Kalush F., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN
 RP
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclab J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J.,
 RA Svitskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN
 RP
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miya S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.U., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003605; AAF52105.2; -
 DR FlyBase: FBgn0051531; CG31531.
 SQ SEQUENCE 1372 AA; 149298 MW; 726436F41803F4D7 CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 1372;
 Best local similarity 85.7%; Pred. No. 1.3e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 | | | | |
 DB 722 DFSSKPS 728

Search completed: March 31, 2005, 12:09:45
 Job time : 48.651 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 85.25 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseq_16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	3	AA79073 Anti-fact
2	58	100.0	104	2	AA880087 Aar80087 Human der
3	58	100.0	104	2	AA95485 Aar95485 Human der
4	58	100.0	109	4	AAU02544 Anti-adip
5	58	100.0	110	4	AAU02558 Anti-adip
6	58	100.0	110	4	AAU02612 Anti-adip
7	58	100.0	110	4	AAU02627 Anti-adip
8	58	100.0	110	4	AAU02629 Anti-adip
9	58	100.0	111	2	AAU19883 CEA-speci
10	58	100.0	111	4	AAU02542 Anti-adip
11	58	100.0	111	4	AAU02551 Anti-adip
12	58	100.0	111	4	AAU02585 Anti-adip
13	58	100.0	111	4	AAU02606 Anti-adip
14	58	100.0	242	8	ADG34301 Neurokini
15	58	100.0	242	8	ADG34317 Neurokini
16	58	100.0	243	5	ABP45916 Human Bly
17	58	100.0	243	7	ADG96743 Single ch
18	58	100.0	243	7	ADG96743 Single ch
19	58	100.0	244	8	ADG34306 Neurokini
20	58	100.0	244	8	ADG34303 Neurokini
21	58	100.0	245	5	ABP45915 Human Bly
22	58	100.0	245	7	ADG96742 Single ch
23	58	100.0	245	7	ADG98057 TNF proli
24	58	100.0	245	8	ADG83862 Chemokine
25	58	100.0	245	8	ADG34308 Neurokini

26	58	100.0	246	5	ABP45902	ADP45902 Human Bly
27	58	100.0	246	5	ABP45906	ADP45906 Human Bly
28	58	100.0	246	7	ADG96733	ADG96733 Single ch
29	58	100.0	246	7	ADG96729	ADG96729 Single ch
30	58	100.0	246	8	ADG83872	ADG83872 Chemokine
31	58	100.0	247	5	ABP45671	ABP45671 Human Bly
32	58	100.0	247	5	ABP45432	ABP45432 Human Bly
33	58	100.0	247	5	ABP45923	ABP45923 Human Bly
34	58	100.0	247	5	ABP45917	ABP45917 Human Bly
35	58	100.0	247	5	ABP45696	ABP45696 Human Bly
36	58	100.0	247	5	ABP45888	ABP45888 Human Bly
37	58	100.0	247	7	ADG30413	ADG30413 Human GMB
38	58	100.0	247	7	ADG30455	ADG30455 Human GMB
39	58	100.0	247	7	ADG96715	ADG96715 Single ch
40	58	100.0	247	7	ADG96498	ADG96498 Single ch
41	58	100.0	247	7	ADG96744	ADG96744 Single ch
42	58	100.0	247	7	ADG96259	ADG96259 Single ch
43	58	100.0	247	7	ADG96750	ADG96750 Single ch
44	58	100.0	247	7	ADG96523	ADG96523 Single ch
45	58	100.0	247	8	ADG83874	ADG83874 Chemokine

ALIGNMENTS

RESULT 1
AA79073
ID AA79073 standard; peptide, 11 AA.

12-JUN-2000 (first entry)

Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence.
Complementarity determining region 3, CDR3; antibody; Gla domain;
factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
arterial thrombosis; unstable angina; post myocardial infarction;
coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
percutaneous transluminal coronary angioplasty; PTCA; inflammation;
septic shock; hypotension; adult respiratory distress syndrome; ARDS;
arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

26-AUG-1999; 99WO-US019453.

28-AUG-1998; 98US-0098233P.

03-MAR-1999; 99US-0122767P.

(GETH) GENENTECH INC.

Adams CW, Devaux B, Baton DL, Hase PE, Judice JK, Kirchofer D;
Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
stroke, and post myocardial infarction.

Claim 8, Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of
the light chain variable domain of a human anti-factor IX/IXa domain
antibody. Factor IXa is a vitamin K dependent plasma serine protease that
participates in the blood coagulation pathways. The Gla domain of factor
IXa and its zymogen factor IX contains important structural determinants
for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/XIa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

CC Sequence 11 AA;

Query Match 100.0%; Score 58; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSSEFL 11
 Db 1 AAMDLSSEFL 11

RESULT 2
 AAR80087
 ID AAR80087 standard; protein; 104 AA.
 AC AAR80087;
 XX 23-MAY-1996 (first entry)
 XX Human derived light chain RT3 phage antibody.
 DE Human derived light chain RT3 phage antibody.
 XX Light chain; RT3; human; catalytic antibody; bacteriophage.
 XX Homo sapiens.
 XX OS
 XX Key Location/Qualifiers
 FH Region 7..15
 FT /note= "framework region 1"
 FT Region 16..28
 FT /note= "complementarity determining region 1"
 FT Region 29..42
 FT /note= "framework region 2"
 FT Region 43..50
 FT /note= "complementarity determining region 2"
 FT Region 51..82
 FT /note= "framework region 3"
 FT Region 83..93
 FT /note= "complementarity determining region 3"
 FT Region 94..104
 FT /note= "framework region 4"

XX WO9527045-A1.
 XX 12-OCT-1995.
 XX 30-MAR-1994; 94WO-US003420.
 XX 30-MAR-1994; 94WO-US003420.
 XX (IGEN-) IGEN INC.
 XX Smith RG, Mc Cafferty J, Chiswell D, Darsley MJ, Fitzgerald K;
 PI Kenten JH, Martin MT, Tiltas RC, Williams RO;
 XX WPI: 1995-358624/46.
 XX N-PSDB; AAT04634.
 XX Production of catalytic antibodies displayed on phage - by generating a
 PT gene library of antibody-derived domains and expressing it in phage
 PT vectors.
 XX Disclosure; Fig 20; 133pp; English.

XX AAT04634 encodes AAR80087 human derived light chain RT3 phage antibody.
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing
 CC bacteriophage. The CAe can be used to activate/deactivate a biological
 CC function in an animal by enhancing the rate of cleavage, or formation of
 CC a specific bond within a mol. in vivo

CC Sequence 104 AA;

Query Match 100.0%; Score 58; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSSEFL 11
 Db 83 AAMDLSSEFL 93

RESULT 3
 AAW95485
 ID AAW95485 standard; protein; 104 AA.
 AC AAW95485;
 XX 29-MAR-1999 (first entry)
 XX Human-derived RT3 phage antibody light chain genetic sequence.
 DE Human-derived RT3 phage antibody; phage display; immunising; phage expression vector;
 XX Catalytic; antibody; phage display; immunising; phage expression vector;
 KW prodng; scfv; RT3.
 XX Homo sapiens.
 XX OS
 XX US5855885-A.
 XX 05-JAN-1999.
 XX 14-JUL-1994; 94US-00273146.
 XX 22-JAN-1993; 93US-00007684.

XX (MCCA/) MCCAFFERTY J.
 PA (CHIS/) CHISWELL D.
 PA (DARS/) DARSLEY M J.
 PA (TITM/) TITMAS R C.
 PA (MART/) MARTIN M T.
 PA (KENT/) KENTEN J H.
 PA (SMIT/) SMITH R.
 PA (FITZ/) FITZGERALD K.
 PA (WILL/) WILLIAMS R O.
 XX Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
 PI Kenten JH, Chiswell D, McCafferty J, Tiltas RC;
 XX WPI: 1999-105036/09.
 XX N-PSDB; AAX00884.
 XX Production of catalytic antibodies displayed on bacteriophages -
 PT comprises generating a gene library of antibody-derived domains inserting
 PT coding into a phage expression vector and isolating the catalytic
 PT antibodies.
 XX Example; Fig 20B; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies
 CC displayed on a phage. The method comprises: (a) generating a gene library
 CC of antibody-derived domains; (b) inserting coding for the domains into a
 CC phage expression vector; and (c) isolating the catalytic antibodies. The
 CC phage expression vector incorporates a histidine peptide in tandem with a
 CC myc peptide. The catalytic antibodies can be isolated by preparing an
 CC antigen, optionally immunising an animal with the antigen; generating a
 CC library of VH and VL domains from the immunised animal; cloning the VH
 CC and VL domains into a phage expression vector to generate phage display

CC antibodies; selecting phage display antibodies which bind specifically to
CC the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a prodrug.
CC Sequences AA955484-489 represent genetic sequences of heavy and light
CC chains of RT3 specific phage antibodies selected from a naive human phage
CC antibody library
CC
SQ Sequence 104 AA;

Query Match 100.0%; Score 58; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSLEFL 11
|||
Db 83 AAMDLSLEFL 93

RESULT 4
AAU02544
ID AAU02544 standard; protein; 109 AA.
AC AAU02544;
XX
XX 29-AUG-2001 (first entry)
DT
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 31.
DE
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KM heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX 12-OCT-1999; 99US-0158812P.
PR
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
XX Edwards BM, Main SH, Vaughan TJ;
PI
XX WPI; 2001-282031/29.
DR N-PSDB; AAS03444.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PS diseases.
XX
XX Claim 1; Page 120; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-

CC abdominal fat associated with heart disease
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 58; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSLEFL 11
|||
Db 90 AAMDLSLEFL 100

RESULT 5
AAU02558
ID AAU02558 standard; protein; 110 AA.
AC AAU02558;
XX
XX 29-AUG-2001 (first entry)
DT
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 44.
DE
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KM heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX 12-OCT-1999; 99US-0158812P.
PR
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
XX Edwards BM, Main SH, Vaughan TJ;
PI
XX WPI; 2001-282031/29.
DR N-PSDB; AAS03458.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PS diseases.
XX
XX Claim 1; Page 128-129; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 DB 90 AAWDSISEFL 100

RESULT 6
 AAU02612
 ID AAU02612 standard; protein; 110 AA.

AC AAU02612;
 DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 99.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

XX MO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000MO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03512.

PT Panel of specific binding members of antibody molecules which bind to
 whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 163; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 DB 90 AAWDSISEFL 100

RESULT 7
 AAU02627
 ID AAU02627 standard; protein; 110 AA.

XX AAU02627;
 AC
 DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 112.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

XX MO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000MO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03527.

PT Panel of specific binding members of antibody molecules which bind to
 whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 172; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 DB 90 AAWDSISEFL 100

RESULT 8
 AAU02629
 ID AAU02629 standard; protein; 110 AA.

AC AAU02629;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 113.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KW heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 XX WO200127279-A1.
 PN 19-APR-2001.
 PD 11-OCT-2000; 2000WO-GB003900.
 PE 12-OCT-1999; 99US-0158812P.
 PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Edwards BM, Main SH, Vaughan TJ;
 PI WPI, 2001-282031/29.
 DR N-PSDB; AAS03529.
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 PS Claim 1; Page 173; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC XX
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAWDLSSEFL 11
 Db 90 AAWDLSSEFL 100
 RESULT 9
 AAU19883
 ID AAU19883 standard; protein; 111 AA.
 XX AAU19883;
 AC
 XX 07-DEC-1997 (first entry)
 DT
 XX CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
 DB
 XX Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
 KW lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
 XX Homo sapiens.
 OS
 XX Key
 FT Region
 FT Location/Qualifiers
 FT 23..35
 FT /label= CDR1
 FT /note= "complementarity determining region 1"

FT Region 50..56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 90..100
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN WO9720932-A1.
 PD 12-JUN-1997.
 PE 09-DEC-1996; 96WO-GB003043.
 PR 07-DEC-1995; 95GB-00025004.
 PR 23-MAY-1996; 96GB-00010824.
 PR 11-OCT-1996; 96GB-00021285.
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Osbourn JK, Allen DJ, McCafferty JG;
 PI WPI, 1997-319779/29.
 DR N-PSDB; AAT72133.
 XX Specific binding members for human carcinoembryonic antigen - bind to the
 PT A3-B3 extracellular domain of hCEA and are substantially non-cross-
 PT reactive with human liver cells; used for diagnosing cancer.
 PS Claim 14; Fig 1b; 128pp; English.
 XX This polypeptide sequence comprises the light chain variable region (VL)
 CC of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2
 CC and CEA3. VH (AAU72126-32) and VL (AAT72133-35) gene sequences were
 CC obtained for anti-hCEA antibodies CEA1-CEA3 (see AAU19876-85). A claimed
 CC specific binding member (A) comprises an hCEA specific antibody antigen
 CC binding domain that has a dissociation constant for hCEA of less than 1 x
 CC 10⁻⁸ M, is non-cross-reactive with human liver cells, and
 CC preferentially binds to the A3-B3 extracellular domain of hCEA and/or to
 CC cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include
 CC pairings of VH and VL sequences from CEA1-7, or their CDR sequences, as
 CC well as CEA6 VH and VL variants. (A) is used to detect cells expressing
 CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer,
 CC e.g. adenocarcinoma of the colon, lung or breast
 CC XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 58; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAWDLSSEFL 11
 Db 90 AAWDLSSEFL 100
 RESULT 10
 AAU02542
 ID AAU02542 standard; protein; 111 AA.
 XX AAU02542;
 AC
 XX 29-AUG-2001 (first entry)
 DT
 XX Anti-adipocyte monoclonal antibody light chain. PAT 30.
 DB
 XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 OS
 XX Key
 FT Region
 FT WO200127279-A1.
 FT 19-APR-2001.

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XX 11-OCT-2000; 2000WO-GB003900.
XX 12-OCT-1999; 99US-0158812P.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Edwards BM, Main SH, Vaughan TJ;
XX N-PSDB; AAS03442.
XX WPI; 2001-282031/29.
XX DR
XX PT Panel of specific binding members of antibody molecules which bind to
XX PT whole adipocytes is used in the treatment of obesity and obesity related
XX PT diseases.
XX PS Claim 1; Page 118-119; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX
XX Sequence 111 AA;
XX
XX Query Match 100.0%; Score 58; DB 4; Length 111;
XX Best Local Similarity 100.0%; Pred.No. 0.025;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAWDSLSEFL 11
XX |||||
XX 90 AAWDSLSEFL 100
XX
XX RESULT 11
XX AAU02551
XX AAU02551 standard; protein; 111 AA.
XX
XX DT 29-AUG-2001 (first entry)
XX
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 37.
XX
XX XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX KW heart disease; complementarity determining region; CDR.
XX
XX OS Homo sapiens.
XX
XX XX WO200127279-A1.
XX PN
XX PD 19-APR-2001.
XX
XX PF 11-OCT-2000; 2000WO-GB003900.
XX PR 12-OCT-1999; 99US-0158812P.
XX
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Edwards BM, Main SH, Vaughan TJ
XX
XX

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XX	WPI: 2001-282031/29.
DR	N-PSDB; AAS03451.
XX	
PT	Panel of specific binding members of antibody molecules which bind to
PT	whole adipocytes is used in the treatment of obesity and obesity related
XX	diseases.
XX	
XX	Claim 1; Page 124; 182pp; English.
XX	
CC	AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC	sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC	and heavy chain complementarity determining regions (CDR) of the
CC	invention. The antibodies can be used in the treatment of obesity and
CC	obesity related diseases. The antibodies can be used to deliver drugs or
CC	pro-drugs directly to the fat mass of an obese patient or the antibody
CC	can be used as a therapeutic itself. Antibodies binding specifically to
CC	adipocytes can be used to activate the immune system to destroy the cells
CC	by complement mediated lysis. The antibodies may be labeled with a
CC	detectable label such as radiolabel, fluorescent or chemical group and
CC	used in methods of diagnosis in human subjects e.g. to determine the
CC	presence of adipocyte antigen on the surface of an adipocyte to detect or
CC	determine the presence or level of adipocytes in a cell or tissue sample.
CC	The antibodies can be used as an alternative means of treatment for obese
CC	patients other than undergoing surgery to remove excess fat. Antibodies
CC	for different types of fat deposits can also be produced e.g. intra-
CC	abdominal fat associated with heart disease
SQ	
SQ	Sequence 111 AA;
Query Match	100.0%; Score 58; DB 4; Length 111;
Best Local Similarity	100.0%; Pred. No. 0.025;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 AAMDLSSEFL 11
Db	91 AAMDLSSEFL 101
RESULT 12	
AAU02585	
ID	AAU02585 standard; protein; 111 AA.
XX	
AC	AAU02585;
XX	
DT	29-AUG-2001 (first entry)
XX	
DE	Anti-adipocyte monoclonal antibody light chain, FAT 72.
XX	
KW	Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW	heart disease; complementarity determining region; CDR.
XX	
OS	Homo sapiens.
XX	
PN	WO200127279-A1.
XX	
PD	19-APR-2001.
XX	
PF	11-OCT-2000; 2000WO-GB003900.
XX	
PR	12-OCT-1999; 99US-0158812P.
XX	
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	
PI	Edwards BM, Main SH, Vaughan TV;
XX	
DR	WPI; 2001-282031/29.
XX	
DR	N-PSDB; AAS03485.
XX	
PT	Panel of specific binding members of antibody molecules which bind to
PT	whole adipocytes is used in the treatment of obesity and obesity related
XX	diseases.
XX	

PS Claim 1; Page 146; 182pp; English.
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
CC
SQ Sequence 111 AA;

Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
DQ 90 AAMDLSSEFL 100

RESULT 13
AAU02606
ID AAU02606 standard; protein; 111 AA.
XX AAU02606;
AC
XX
XX
DT 29-AUG-2001 (first entry)
XX
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 95.
XX
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX
OS Homo sapiens.
XX
XX WO200127279-A1.
XX
XX PD 19-APR-2001.
XX
XX PE 11-OCT-2000; 2000WO-GB003900.
XX
XX PR 12-OCT-1999; 99US-0158812P.
XX
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Edwards BM, Main SH, Vaughan TJ;
XX
XX DR WPI; 2001-282031/29.
XX
XX DR N-PSDB; AAS03506.
XX
XX PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX PS Claim 1; Page 159; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody

CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
CC
SQ Sequence 111 AA;

Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
DQ 91 AAMDLSSEFL 101

RESULT 14
ADG34301
ID ADG34301 standard; protein; 242 AA.
XX ADG34301;
AC
XX
XX
DT 26-FEB-2004 (first entry)
XX
XX
DE Neurokinin B antibody SEQ ID NO:24.
XX
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KW hypertension; pre-eclampsia; NKB.
XX
XX
OS Synthetic.
XX
XX WO2003102136-A2.
XX
XX PD 11-DEC-2003.
XX
XX PF 29-MAY-2003; 2003WO-US016802.
XX
XX PR 30-MAY-2002; 2002US-0383802P.
XX
XX PA (HDMA-) HDMA GENOME SCT INC.
XX
XX PI Rosen CA, Ruben SM;
XX
XX DR WPI; 2004-053456/05.
XX
XX DR N-PSDB; ADG34282.
XX
XX PT New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.
XX
XX PS Claim 2; SEQ ID NO 24; 127pp; English.
XX
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 58; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
DQ 11 AAMDLSSEFL 11

XX	Hom sapiens.
PN	MO200202641-A1.
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US019110.
XX	
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
PA	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	
XI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,
PI	WPI; 2002-114799/15.
DR	
XX	
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT	diagnosis and treatment of cancers and immune disorders.
PS	
XX	Claim 1; Page 2700-2701; 3148PP; English.
XX	
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cyclostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC	and so may be used to detect and quantitate the presence of BLyS in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of BLyS. They may also be
CC	administered to treat diseases associated with aberrant BLyS expression
CC	and actively such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID)) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method of
CC	the invention
SQ	Sequence 243 AA;
XX	
Query Match	100.0%; Score 58; DB 5; Length 243;
Best Local Similarity	100.0%; Pred. No. 0.056;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 AAWDDSLSEFL 11
DB	222 AAWDDSLSEFL 232
RESULT 17	
ID	ADG96743 standard; protein; 243 AA.
XX	
AC	ADG96743;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Single chain antibody that immunospecifically binds BLyS SegID 1927.
XX	
KW	antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW	B cell proliferation; differentiation; scFv; myasthenia gravis;
KW	multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW	carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW	antiinflammatory; antiasthmatic; antiallergic; cyclostatic.
XX	
OS	unidentified.

CC preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

CC Sequence 243 AA;

Query Match 100.0%; Score 58; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 11
|||
DB 222 AAWDSLSEFL 232

RESULT 20
ADG34303
ID ADG34303 standard; protein; 244 AA.

AC ADG34303;

DT 26-FEB-2004 (first entry)

DE Neurokinin B antibody SEQ ID NO:26.

KM antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.

OS Synthetic.

PN WO2003102136-A2.

PD 11-DEC-2003.

PF 29-MAY-2003; 2003WO-US016802.

PR 30-MAY-2002; 2002US-0383802P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI, 2004-053456/05.

DR N-PSDB; ADG34284.

PT New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.

PS Claim 2; SEQ ID NO 26; 127bp; English.

CC The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

CC Sequence 244 AA;

Query Match 100.0%; Score 58; DB 8; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 11
|||
DB 223 AAWDSLSEFL 233

RESULT 21
ABP45915
ID ABP45915 standard; protein; 245 AA.

AC ABP45915;

XX 19-AUG-2002 (first entry)
DT Human Blys binding scFv SEQ ID 1926.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineutrotic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2699-2700; 3148bp; English.

CC This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antineutrotic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

CC Sequence 245 AA;

Query Match 100.0%; Score 58; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 11
|||
DB 224 AAWDSLSEFL 234

RESULT 22
ADG96742
ID ADG96742 standard; protein; 245 AA.

AC ADG96742;

DT 11-MAR-2004 (first entry)
XX Single chain antibody that immunospecifically binds Blys Segid 1926.
DE
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scfv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
XX 10-JUL-2003.
XX
PD 14-NOV-2002; 2002WO-US036496.
XX
PF 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
PT
XX
PS Example 1; SEQ ID NO 1926; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scfvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 58; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSSEFL 11
Db 224 AAMDLSSEFL 234
RESULT 23
ADG98057
ID ADG98057 standard; protein; 245 AA.
XX
AC ADG98057;
XX

DT 11-MAR-2004 (first entry)
XX TNF proliferation inducing protein ligand (APRIL) Segid 3241.
DE
XX
KW human; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic; APRIL; TNF;
KW ligand.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
XX 10-JUL-2003.
XX
PD 14-NOV-2002; 2002WO-US036496.
XX
PF 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
PT
XX
PS Claim 1; SEQ ID NO 3241; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scfvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is an APRIL protein, a TNF proliferation inducing
CC ligand that can form a fusion protein with a Blys protein of the
CC invention.
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 58; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSSEFL 11
Db 224 AAMDLSSEFL 234
RESULT 24
ADE83862
ID ADE83862 standard; protein; 245 AA.
XX
AC ADE83862;
XX

DT 29-JAN-2004 (first entry)
XX Chemokine beta-4 binding antibody F081C09 protein SEQ ID NO:21.
DE
XX antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
XX antiproliferative; dermatological; antiinflammatory; immunosuppressive;
XX antineoplastic; antirheumatic; cerebroprotective; cytostatic; anti-HIV;
XX vulnery; dermatitis; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; autoimmune encephalitis; cancer;
XX HIV infection; wound; inflammatory disorder; human; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX WO2003092597-A2.
XX
XX 13-NOV-2003.
XX
XX 30-APR-2003; 2003WO-US013414.
XX
XX 01-MAY-2002; 2002US-0376561P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2004-022614/02.
XX N-PSDB; ADE83845.
XX
XX New antibody that specifically binds to a chemokine beta-4 polypeptide,
XX useful for diagnosing, treating, preventing or ameliorating psoriasis,
XX rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
XX and wounds.
XX
XX Claim 1; SEQ ID NO 21; 181bp; English.
XX
XX The present invention describes an antibody (I) that specifically binds
XX to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
XX amino acid sequence at least 95% identical to a second amino acid
XX sequence comprising a VH complementarity determining region (CDR) or VL
XX CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
XX sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
XX (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
XX (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
XX cell comprising the vector of (3); (5) a cell line engineered to express
XX (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
XX that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
XX method for detecting aberrant expression of CK-B4 polypeptide; (9) a
XX assay of the level of CK-B4 polypeptide expression in a first biological
XX sample of an individual using at least one of (1), and comparing the
XX level of CK-B4 polypeptide assayed in the biological sample with a
XX standard level of CK-B4 polypeptide expression or level of CK-B4
XX polypeptide in a second, normal biological sample, where an increase or
XX decrease in the assayed level of CK-B4 polypeptide in the first
XX biological sample compared to the standard level is indicative of
XX aberrant expression; and (9) a method of treating, preventing or
XX ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
XX administering (1) to the animal. (I) has antiproliferative, dermatologic,
XX antiinflammatory, immunosuppressive, antineoplastic, antirheumatic,
XX cerebroprotective, cytostatic, anti-HIV and vulnery activities. The
XX methods and compositions of the present invention are useful for
XX diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
XX an autoimmune disease such as rheumatoid arthritis, systemic lupus
XX erythematosus and autoimmune encephalitis. They can also be used in
XX cancer, HIV infection, wounds and inflammatory disorders. The present
XX sequence is used in the exemplification of the present invention.
XX
XX Sequence 245 AA;

Query Match 100.0%; Score 58; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
DB 224 AAWDDSLSEFL 234
RESULT 25
ADG34308
ID ADG34308 standard; protein; 245 AA.
XX
XX ADG34308;
XX
XX 26-FEB-2004 (first entry)
XX
XX
XX Neurokinin B antibody SEQ ID NO:31.
XX
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
XX hypertension; pre-eclampsia; NKB.
XX
XX Synthetic.
XX
XX WO2003102136-A2.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US016802.
XX
XX 30-MAY-2002; 2002US-0383802P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2004-053456/05.
XX N-PSDB; ADG34289.
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 31; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
XX B. An antibody of the invention has hypotensive, and gynaecological
XX activity, and may have a use in gene therapy. The antibody is useful for
XX preparing a composition for treating or preventing hypertension or pre-
XX eclampsia. The present sequence is used in the exemplification of the
XX invention.
XX
XX Sequence 245 AA;
XX
XX Query Match 100.0%; Score 58; DB 8; Length 245;
XX Best Local Similarity 100.0%; Pred. No. 0.056;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAWDDSLSEFL 11
XX DB 224 AAWDDSLSEFL 234
XX
XX RESULT 26
XX ABP45902
XX ID ABP45902 standard; protein; 246 AA.
XX
XX ABP45902;
XX
XX 19-AUG-2002 (first entry)
XX
XX
XX Human Blys binding scFv SEQ ID 1913.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX
XX WO200202641-A1.
PN
XX
XX 10-JAN-2002.
PD
XX
XX 15-JUN-2001; 2001WO-US019110.
PF
XX
XX 16-JUN-2000; 2000US-0212210P.
PR
XX 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2683-2684; 3148pp; English.
PS
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosstatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX Sequence 246 AA;
SQ
Query Match 100.0%; Score 58; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSLEFL 11
Db 225 AAMDLSLEFL 235
RESULT 27
ABP45906
ID ABP45906 standard; protein; 246 AA.
XX
XX
XX ABP45906;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human Blys binding scFv SEQ ID 1917.
DE
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosstatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX
XX Homo sapiens.
OS
XX
XX WO200202641-A1.
PN
XX
XX 10-JAN-2002.
PD
XX
XX 15-JUN-2001; 2001WO-US019110.
PF
XX
XX 16-JUN-2000; 2000US-0212210P.
PR
XX 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2688-2689; 3148pp; English.
PS
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosstatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX Sequence 246 AA;
SQ
Query Match 100.0%; Score 58; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSLEFL 11
Db 225 AAMDLSLEFL 235
RESULT 28
ADG96733
ID ADG96733 standard; protein; 246 AA.
XX
XX
XX ADG96733;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Single chain antibody that immunospecifically binds Blys SeqID 1917.
DE
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
KW antiinflammatory; antiaesthetic; antiallergic; cytosstatic.
XX
XX Unidentified.
OS

XX PN WO2003055979-A2.
XX PN 10-JUL-2003.
XX PD 14-NOV-2002; 2002WO-US036496.
XX PF 16-NOV-2001; 2001US-0331469P.
XX PR 19-DEC-2001; 2001US-0340817P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX DR WPI; 2003-505530/47.
XX XX
XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX PT (Blys), useful for detecting and treating diseases or disorders e.g.
XX PT rheumatoid arthritis, asthma and leukemia.
XX XX
XX PS Example 1; SEQ ID NO 1917; 394bp; English.
XX XX
XX CC This invention relates to novel antibodies that immunospecifically bind
XX CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX CC chromosome 13q34 and encodes a protein that is a member of the tumour
XX CC necrosis factor superfamily and induces both in vivo and in vitro B cell
XX CC proliferation and differentiation. Specifically, it refers to single
XX CC chain antibody molecules (scFvs) derived, preferably, from the variable
XX CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX CC fragment thereof, of either human, murine, rat or monkey Blys. The
XX CC present invention refers to the use of such antibodies in various methods
XX CC for the detection, diagnosis and prognosis of diseases related to the
XX CC aberrant expression or inappropriate function of Blys or its receptor. As
XX CC such, these compositions are useful for identifying immune disorders
XX CC including myasthenia gravis and multiple sclerosis, inflammatory
XX CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX CC as AIDS and proliferative disorders including leukaemia, carcinoma and
XX CC lymphoma. Accordingly, they can be described as exhibiting various
XX CC activities such as antirheumatic, antiarthritic, neuroprotective,
XX CC antiinflammatory, antiallergic, antiaesthetic and cytostatic. This
XX CC polypeptide sequence is a single chain antibody that binds Blys of the
XX CC invention. NOTE: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 58; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. NO. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDDSLSEFL 11
Db 225 AAWDDSLSEFL 235
RESULT 29
ADG96729
ID ADE96729 standard; protein; 246 AA.
XX
XX AC ADE96729;
XX DT 11-MAR-2004 (first entry)
XX XX
XX DE Single chain antibody that immunospecifically binds Blys SeqID 1913.
XX XX
XX KM antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX KM B cell proliferation; differentiation; scFv; myasthenia gravis;
XX KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX KM carcinoma; lymphoma; antirheumatic; antiaesthetic; neuroprotective;
XX KM antiinflammatory; antiallergic; antiaesthetic; cytostatic.
XX XX
XX OS Unidentified.

XX XX WO2003055979-A2.
XX XX 10-JUL-2003.
XX PD 14-NOV-2002; 2002WO-US036496.
XX PF 16-NOV-2001; 2001US-0331469P.
XX PR 19-DEC-2001; 2001US-0340817P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX DR WPI; 2003-505530/47.
XX XX
XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX PT (Blys), useful for detecting and treating diseases or disorders e.g.
XX PT rheumatoid arthritis, asthma and leukemia.
XX XX
XX PS Example 1; SEQ ID NO 1913; 394bp; English.
XX XX
XX CC This invention relates to novel antibodies that immunospecifically bind
XX CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX CC chromosome 13q34 and encodes a protein that is a member of the tumour
XX CC necrosis factor superfamily and induces both in vivo and in vitro B cell
XX CC proliferation and differentiation. Specifically, it refers to single
XX CC chain antibody molecules (scFvs) derived, preferably, from the variable
XX CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX CC fragment thereof, of either human, murine, rat or monkey Blys. The
XX CC present invention refers to the use of such antibodies in various methods
XX CC for the detection, diagnosis and prognosis of diseases related to the
XX CC aberrant expression or inappropriate function of Blys or its receptor. As
XX CC such, these compositions are useful for identifying immune disorders
XX CC including myasthenia gravis and multiple sclerosis, inflammatory
XX CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX CC as AIDS and proliferative disorders including leukaemia, carcinoma and
XX CC lymphoma. Accordingly, they can be described as exhibiting various
XX CC activities such as antirheumatic, antiarthritic, neuroprotective,
XX CC antiinflammatory, antiallergic, antiaesthetic and cytostatic. This
XX CC polypeptide sequence is a single chain antibody that binds Blys of the
XX CC invention. NOTE: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 58; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. NO. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDDSLSEFL 11
Db 225 AAWDDSLSEFL 235
RESULT 30
ADE83872
ID ADE83872 standard; protein; 246 AA.
XX
XX AC ADE83872;
XX DT 29-JAN-2004 (first entry)
XX XX
XX DE Chemokine beta-4 binding antibody F002C08 protein SEQ ID NO:31.
XX XX
XX KM antibody; chemokine beta-4; CX-34; single chain Fvs; scFvs;
XX KM antiproliferative; dermatological; antiinflammatory; immunosuppressive;
XX KM antineuritic; antiaesthetic; neuroprotective; cytostatic; anti-HIV;
XX KM vulvovaginal; dermatitis; autoimmune disease; rheumatoid arthritis;
XX KM systemic lupus erythematosus; autoimmune encephalitis; cancer;
XX KM HIV infection; wound; inflammatory disorder; human; psoriasis.
XX XX

OS Synthetic.
OS Homo sapiens.
XX
PN WO2003092597-A2.
XX
XX 13-NOV-2003.
XX
PD 30-APR-2003; 2003WO-US013414.
XX
PF 01-MAY-2002; 2002US-0376561P.
XX
PR (HUMA-) HUMAN GENOME SCI INC.
XX
PA Rosen CA, Ruben SM;
XX
PI WPI: 2004-022614/02.
XX
DR N-P8DB; ADE83855.
XX
PT New antibody that specifically binds to a chemokine beta-4 polypeptide,
PT useful for diagnosing, treating, preventing or ameliorating psoriasis,
PT rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
PT and wounds.
XX
PS Claim 1; SEQ ID NO 31; 181bp; English.
XX
XX The present invention describes an antibody (I) that specifically binds
CC to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
CC amino acid sequence at least 95% identical to a second amino acid
CC sequence comprising a VH complementarity determining region (CDR) or VL
CC CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
CC sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
CC (1) a kit comprising (I); (2) an isolated nucleic acid molecule encoding
CC (I); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
CC cell comprising the vector of (3); (5) a cell line engineered to express
CC (I); (6) an antibody that binds the same epitope as (I); (7) an antibody
CC that competitively inhibits the binding (I) to a CK-B4 polypeptide; (8) a
CC method for detecting aberrant expression of CK-B4 polypeptide; (9) a
CC assay of the level of CK-B4 polypeptide expression in a first biological
CC sample of an individual using at least one of (I), and comparing the
CC level of CK-B4 polypeptide assayed in the biological sample with a
CC standard level of CK-B4 polypeptide expression or level of CK-B4
CC polypeptide in a second, normal biological sample, where an increase or
CC decrease in the assayed level of CK-B4 polypeptide in the first
CC biological sample compared to the standard level is indicative of
CC aberrant expression; and (9) a method of treating, preventing or
CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
CC administering (I) to the animal. (I) has antipsoriatic, dermatological,
CC antiinflammatory, immunosuppressive, antirheumatic, antiarthritic,
CC cerebroprotective, cytostatic, anti-HIV and vulnery activity. The
CC method and compositions of the present invention are useful for
CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
CC erythematosus and autoimmune encephalitis. They can also be used in
CC cancer, HIV infection, wounds and inflammatory disorders. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 246 AA;
Query Match 100.0%; Score 58; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDSLSEFL 11
Db 225 AAWDSLSEFL 235

RESULT 31
ID ABP45671 standard; protein; 247 AA.
XX
XX ABP45671;
XX

DT 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1682.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI: 2002-114799/15.
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2409-2410; 3148bp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDSLSEFL 11
Db 226 AAWDSLSEFL 236

RESULT 32
ID ABP45432 standard; protein; 247 AA.
XX
XX ABP45432;
XX
XX 19-AUG-2002 (first entry)
XX

XX DE Human Blys binding scFv SEQ ID 1443.
XX XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumor necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR WPI; 2002-114799/15.
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2124-2125; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumor necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX SQ Sequence 247 AA;
XX
OY Query Match 100.0%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 AAWDDSLSEFL 11
226 AAWDDSLSEFL 236

RESULT 33
ID ABP45923 standard; protein; 247 AA.
XX ABP45923;
XX AC
XX DT 19-AUG-2002 (first entry)
XX

DE DE Human Blys binding scFv SEQ ID 1934.
XX XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumor necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR WPI; 2002-114799/15.
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2708-2709; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumor necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX SQ Sequence 247 AA;
XX
OY Query Match 100.0%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 AAWDDSLSEFL 11
226 AAWDDSLSEFL 236

RESULT 34
ID ABP45917 standard; protein; 247 AA.
XX ABP45917;
XX AC
XX DT 19-AUG-2002 (first entry)
XX DE Human Blys binding scFv SEQ ID 1928.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX Homo sapiens.
XX OS
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240815P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR WPI; 2002-114799/15.
XX FT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2701-2702; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX SQ
XX Sequence 247 AA;
SQ
Query Match 100.0%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSSEFL 11
DB 226 AAMDLSSEFL 236
RESULT 35
ABP45696 standard; protein; 247 AA.
XX ABP45696;
XX AC
XX 19-AUG-2002 (first entry)
XX DT
XX Human Blys binding scFv SEQ ID 1707.
XX DE
XX KW

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX Homo sapiens.
XX OS
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240815P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR WPI; 2002-114799/15.
XX FT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2439-2440; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX SQ
XX Sequence 247 AA;
SQ
Query Match 100.0%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSSEFL 11
DB 226 AAMDLSSEFL 236
RESULT 36
ABP45888 standard; protein; 247 AA.
XX ABP45888;
XX AC
XX 19-AUG-2002 (first entry)
XX DT
XX Human Blys binding scFv SEQ ID 1899.
XX DE
XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US019110.
 XX PR 16-JUN-2000; 2000US-0212210P.
 XX PR 17-OCT-2000; 2000US-0240816P.
 XX PR 16-MAR-2001; 2001US-0276248P.
 XX PR 21-MAR-2001; 2001US-0277379P.
 XX PR 25-MAY-2001; 2001US-0293499P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX DR WPI; 2002-114799/15.
 XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 XX PT diagnosis and treatment of cancers and immune disorders.
 XX PS Claim 1; Page 2667-2668; 3148pp; English.
 XX SQ This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and actively such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX SQ Sequence 247 AA;
 XX
 XX Query March 100.0%; Score 58; DB 5; Length 247;
 XX Best Local Similarity 100.0%; Pred. No. 0.057;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAMDSEFL 11
 DB 226 AAMDSEFL 236
 XX
 XX RESULT 37
 XX ADG30413
 XX ID ADG30413 standard; protein; 247 AA.
 XX AC ADG30413;
 XX DT 26-FEB-2004 (first entry)
 XX DE Human GMBC609 scFv protein.
 XX GMAD; VH; CDR; complementarity determining region; VL; scFv;
 KW single chain antibody; antidiabetic; type II diabetes; human; GMBC609.

XX OS Homo sapiens.
 XX XX WO2003085093-A2.
 XX PD 16-OCT-2003.
 XX PF 28-MAR-2003; 2003WO-US009625.
 XX PR 01-APR-2002; 2002US-0368813P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Baker KP, Albert VR, Chowdhury P;
 XX DR WPI; 2003-804305/75.
 XX DR N-PSDB; ADG30510.
 XX PT New antibody that specifically binds to GMAD polypeptide, useful for
 XX PT diagnosing, monitoring, treating, preventing or ameliorating type II
 XX PT diabetes.
 XX PS Claim 2; SEQ ID NO 46; 410pp; English.
 XX SQ The invention relates to a novel antibody that specifically binds to a
 CC GMAD polypeptide comprising a first amino acid sequence that is at least
 CC 95% identical to a second amino acid sequence of a VH CDR
 CC (complementarity determining region) or VL CDR of an scFv (single chain
 CC antibody molecule). The antibody of the invention demonstrates
 CC antidiabetic activity and may be useful for diagnosing, monitoring,
 CC treating, preventing or ameliorating type II diabetes. The current
 CC sequence is that of the human scFv protein of the invention.
 XX SQ Sequence 247 AA;
 XX
 XX Query March 100.0%; Score 58; DB 7; Length 247;
 XX Best Local Similarity 100.0%; Pred. No. 0.057;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAMDSEFL 11
 DB 226 AAMDSEFL 236
 XX
 XX RESULT 38
 XX ADG30455
 XX ID ADG30455 standard; protein; 247 AA.
 XX AC ADG30455;
 XX DT 26-FEB-2004 (first entry)
 XX DE Human GMBC666 scFv protein.
 XX GMAD; VH; CDR; complementarity determining region; VL; scFv;
 KW single chain antibody; antidiabetic; type II diabetes; human; GMBC666.
 OS Homo sapiens.
 XX WO2003085093-A2.
 XX PD 16-OCT-2003.
 XX PF 28-MAR-2003; 2003WO-US009625.
 XX PR 01-APR-2002; 2002US-0368813P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Baker KP, Albert VR, Chowdhury P;
 XX DR WPI; 2003-804305/75.
 XX DR N-PSDB; ADG30552.

XX New antibody that specifically binds to GMD polypeptide, useful for
PT diagnosing, monitoring, treating, preventing or ameliorating type II
PT diabetes.
XX
PS Claim 2; SEQ ID NO 88; 410pp; English.
XX
CC The invention relates to a novel antibody that specifically binds to a
CC GMD polypeptide comprising a first amino acid sequence that is at least
CC 95% identical to a second amino acid sequence of a VH CDR of an scFv (single chain
CC complementarity determining region) or VL CDR of an scFv (single chain
CC antibody molecule). The antibody of the invention demonstrates
CC antidiabetic activity and may be useful for diagnosing, monitoring,
CC treating, preventing or ameliorating type II diabetes. The current
CC sequence is that of the human scFv protein of the invention.
XX
SQ Sequence 247 AA;
XX
Query Match 100.0%; Score 58; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AAMDLSSEFL 11
Db 226 AAMDLSSEFL 236
XX
RESULT 39
ADG96715
ID ADG96715 standard; protein; 247 AA.
XX
AC ADG96715;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SegID 1899.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
KW carcinoma; lymphoma; antineumatic; antiallergic; neuroprotective;
KW antineumatic; antiallergic; antiallergic; cystostatic.
XX
OS Unidentified.
XX
FN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PE 14-NOV-2002; 2002MO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
WP1; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1899; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or

CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineumatic, antiallergic, neuroprotective,
CC antineumatic, antiallergic, antiallergic and cystostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 247 AA;
XX
Query Match 100.0%; Score 58; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AAMDLSSEFL 11
Db 226 AAMDLSSEFL 236
XX
RESULT 40
ADG96498
ID ADG96498 standard; protein; 247 AA.
XX
AC ADG96498;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SegID 1682.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
KW carcinoma; lymphoma; antineumatic; antiallergic; neuroprotective;
KW antineumatic; antiallergic; antiallergic; cystostatic.
XX
OS Unidentified.
XX
FN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PE 14-NOV-2002; 2002MO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
WP1; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1682; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or

CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 247 AA;

Query Match 100.0%; Score 58; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
|||
Db 226 AAWDDSLSEFL 236

Search completed: March 31, 2005, 12:02:32
Job time : 86.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:44 ; Search time 21.4844 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAMDLSSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA: *
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4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	4	US-09-383-667-15
2	58	100.0	104	2	US-08-273-146-63
3	58	100.0	111	2	US-08-652-816A-15
4	46	79.3	11	2	US-08-350-260A-374
5	46	79.3	11	4	US-09-104-337A-374
6	44	75.9	11	2	US-08-350-260A-346
7	44	75.9	11	4	US-09-104-337A-346
8	43	74.1	9	2	US-08-665-202-60
9	43	74.1	9	4	US-09-315-574-60
10	43	74.1	10	2	US-08-350-260A-339
11	43	74.1	10	2	US-08-350-260A-497
12	43	74.1	10	4	US-09-104-337A-339
13	43	74.1	10	4	US-09-104-337A-497
14	43	74.1	11	2	US-08-350-260A-441
15	43	74.1	11	2	US-08-665-202-6
16	43	74.1	11	4	US-09-104-337A-441
17	43	74.1	11	4	US-09-315-574-6
18	43	74.1	98	1	US-08-211-202-111
19	43	74.1	98	4	US-08-665-202-38
20	43	74.1	98	4	US-09-315-574-38
21	43	74.1	109	3	US-09-240-274-59
22	43	74.1	110	3	US-09-240-274-60
23	43	74.1	111	2	US-08-665-202-35
24	43	74.1	111	2	US-08-665-202-43
25	43	74.1	111	4	US-09-315-574-36
26	43	74.1	111	4	US-09-315-574-43
27	43	74.1	112	2	US-08-665-202-39

28	43	74.1	112	4	US-09-315-574-39	Sequence 39, App1
29	43	74.1	113	1	US-08-211-202-112	Sequence 112, App
30	43	74.1	113	1	US-08-211-202-113	Sequence 113, App
31	43	74.1	113	1	US-08-211-202-114	Sequence 114, App
32	43	74.1	258	2	US-08-665-202-5	Sequence 5, App1
33	43	74.1	258	4	US-09-315-574-5	Sequence 5, App1
34	43	74.1	262	3	US-09-069-821-4	Sequence 4, App1
35	43	74.1	262	4	US-09-956-086-4	Sequence 4, App1
36	43	74.1	262	4	US-09-956-087-4	Sequence 4, App1
37	43	74.1	282	3	US-09-420-592A-7	Sequence 7, App1
38	43	74.1	282	4	US-09-985-442-7	Sequence 7, App1
39	43	74.1	282	4	US-09-983-580-7	Sequence 7, App1
40	41	70.7	111	2	US-08-665-202-40	Sequence 40, App1
41	41	70.7	111	4	US-09-315-574-40	Sequence 40, App1
42	40	69.0	10	2	US-08-350-260A-361	Sequence 361, App
43	40	69.0	10	2	US-08-350-260A-446	Sequence 446, App
44	40	69.0	10	2	US-08-350-260A-514	Sequence 514, App
45	40	69.0	10	4	US-09-104-337A-361	Sequence 361, App

ALIGNMENTS

```
RESULT 1
; US-09-383-667-15
; Sequence 15, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Baton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-15

Query Match      100.0%; Score 58; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAMDLSSEFL 11
DB      1 AAMDLSSEFL 11

RESULT 2
; US-08-273-146-63
; Sequence 63, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
```

TITLE OF INVENTION: The Isolation and Production of
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-146-63

Query Match 100.0%; Score 58; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
DB 83 AAWDDSLSEFL 93

RESULT 3
US-08-652-816A-15
Sequence 15, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCallerty, JG
TITLE OF INVENTION: Specific binding members, materials and
METHOD OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8

FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-15

Query Match 100.0%; Score 58; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
DB 90 AAWDDSLSEFL 100

RESULT 4
US-08-350-260A-374
Sequence 374, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Niselim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
METHOD OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-374

Query Match          79.3%; Score 46; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.05;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDLSLSEFL 11
Db 1 AAWDLSLSEFL 11

RESULT 5
US-09-104-337A-374
Sequence 374, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESS: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-104-337A-374

Query Match          79.3%; Score 46; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.05;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDLSLSEFL 11
Db 1 AAWDLSLSEFL 11

RESULT 6
US-08-350-260A-346
Sequence 346, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESS: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-346

Query Match 75.9%; Score 44; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAMDDSLSEPL 11
Db 1 AAMDDSLAWFV 11

RESULT 7
US-09-104-337A-346
Sequence 346, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nisim, Abuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-09-104-337A-346

Query Match 75.9%; Score 44; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAMDDSLSEPL 11
Db 1 AAMDDSLAWFV 11

RESULT 8
US-08-665-202-60
Sequence 60, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-60

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSIS 8
Db 1 AAWDSIS 8

RESULT 9
US-09-315-574-60
Sequence 60, Application US/09315574
Patent No. 6512897
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schler, Robert
TITLE OF INVENTION: NO. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-315-574-60

Query Match 74.1%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSIS 8
Db 1 AAWDSIS 8

RESULT 10
US-08-350-260A-339
Sequence 339, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissem, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-339

Query Match
Best Local Similarity 74.1%; Score 43; DB 2; Length 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 11
US-08-350-260A-497
Sequence 497, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01114
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-497

Query Match
Best Local Similarity 74.1%; Score 43; DB 2; Length 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 12
US-09-104-337A-339
Sequence 339, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Andrew L. Bartnicki
STREET: Marshall, Gerstein & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 339:
US-09-104-337A-339

Query Match 74.1%; Score 43; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 13
US-09-104-337A-497
Sequence 497, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 497:
US-09-104-337A-497

Query Match 74.1%; Score 43; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 14
US-08-350-260A-441
Sequence 441, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-441

Query Match 74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 15
US-08-665-202-6
Sequence 6, Application US/08665202
Patent No. 597322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 5973222e1 High Affinity Human Antibodies to
Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-665-202-6

Query Match 74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 16

US-09-104-337A-441
Sequence 441, Application US/09104337A
Patent No. 6492160

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul

Griffiths, Andrew David

Williams, Samuel Cameron

Waterhouse, Peter

Nissim, Ahuva

Johnson, Kevin Stuart

Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific
binding pairs

NUMBER OF SEQUENCES: 600

CORRESPONDENCE ADDRESS:

ADDRESSEE: Audrey L. Bartnicki

STREET: Marshall, Gerstein & Borun

6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A

FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: GB 9110549.4

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

APPLICATION NUMBER: US 08/150,002

FILING DATE: 31-MAR-1994

APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.

REGISTRATION NUMBER: 40,499

REFERENCE/DOCKET NUMBER: 28111/32372A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 441:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 441:

US-09-104-337A-441

Query Match 74.1%; Score 43; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 17
US-09-315-574-6
Sequence 6, Application US/09315574
Patent No. 6512097


```

; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Huse P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-6

Query Match 74.1%; Score 43; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 18
US-08-211-202-111
; Sequence 111, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matreus
; APPLICANT: BAIRER, Michael
; APPLICANT: JESPERSEN, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Botum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
```

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-111

Query Match 74.1%; Score 43; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 90 AAWDSLS 97

RESULT 19
US-08-665-202-38
; Sequence 38, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; ADDRESSEE: Two Embarcadero Center, Eighth Floor
; STREET: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-38

Query Match 74.1%; Score 43; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8
Db 90 AAWDSLS 97

RESULT 20
US-09-315-574-38
Sequence 38, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
NUMBER OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hane P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-38

Query Match 74.1%; Score 43; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8
Db 90 AAWDSLS 97

RESULT 21
US-09-240-274-59
Sequence 59, Application US/09240274
Patent No. 625455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain M02
US-09-240-274-59

Query Match 74.1%; Score 43; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8
Db 89 AAWDSLS 96

RESULT 22
US-09-240-274-60
Sequence 60, Application US/09240274
Patent No. 625455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 60
 LENGTH: 110
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: anti-Rh(D) chain M03
 US-09-240-274-60

Query Match 74.1%; Score 43; DB 3; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
 |||||
 Db 89 AAMDLS 96

RESULT 23
 US-08-665-202-36
 Sequence 36, Application US/08665202
 Patent No. 5977322
 GENERAL INFORMATION:
 APPLICANT: Marks, James D.
 APPLICANT: Schier, Robert
 TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,202
 FILING DATE: 13-JUN-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061410
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-665-202-36

Query Match 74.1%; Score 43; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAMDLS 8
 |||||
 Db 90 AAMDLS 97

RESULT 24
 US-08-665-202-43
 Sequence 43, Application US/08665202
 Patent No. 5977322
 GENERAL INFORMATION:
 APPLICANT: Marks, James D.
 APPLICANT: Schier, Robert
 TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,202
 FILING DATE: 13-JUN-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061410
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-665-202-43

Query Match 74.1%; Score 43; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
 |||||
 Db 90 AAMDLS 97

RESULT 25
 US-09-315-574-36
 Sequence 36, Application US/09315574
 Patent No. 6512097
 GENERAL INFORMATION:
 APPLICANT: Marks, James D.
 APPLICANT: Schier, Robert
 TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco

```
STATE: California.
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-36

Query Match      74.1%; Score 43; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDSLS 8
      |||||
Db      90 AAWDSLS 97

RESULT 26
US-09-315-574-43
; Sequence 43, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 36:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-43

Query Match      74.1%; Score 43; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDSLS 8
      |||||
Db      90 AAWDSLS 97

RESULT 27
US-08-665-202-39
; Sequence 39, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-39

Query Match 74.1%; Score 43; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
|||||
Db 90 AAMDLS 97

RESULT 28
US-09-315-574-39
Sequence 39, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315.574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-39

Query Match 74.1%; Score 43; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLS 8

Db 90 AAMDLS 97
|||||

RESULT 29
US-08-211-202-112
Sequence 112, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matreus
APPLICANT: BAIRER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-112

Query Match 74.1%; Score 43; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 90 AAMDLS 97
QY 1 AAMDLS 8
|||||

RESULT 30
US-08-211-202-113
; Sequence 113, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
; APPLICANT: BAIRER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-113

Query Match 74.1%; Score 43; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSDL 8
Db 90 AAMDSDL 97

RESULT 31
US-08-211-202-114
; Sequence 114, Application US/08211202
; Patent No. 5565332

; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
; APPLICANT: BAIRER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-114

Query Match 74.1%; Score 43; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSDL 8
Db 90 AAMDSDL 97

RESULT 32
US-08-665-202-5
; Sequence 5, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-202-5

Query Match 74.1%; Score 43; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
Db 234 AAMDLS 241

RESULT 33
US-09-315-574-5
Sequence 5, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-315-574-5

Query Match 74.1%; Score 43; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
Db 234 AAMDLS 241

RESULT 34
US-09-069-821-4
Sequence 4, Application US/09069821
Patent No. 6323322
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
APPLICANT: WANG, MAOLIAN
APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821
FILING DATE: 30-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-069-821-4

Query Match 74.1%; Score 43; DB 3; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 35
US-09-956-086-4
Sequence 4, Application US/09956086
Patent No. 6743896
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LHSYNG S.
COUNTRY: USA
ZIP: 20005
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. 6743896 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-086-4

Query Match 74.1%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 36
US-09-956-087-4
Sequence 4, Application US/09956087
Patent No. 6743908
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LHSYNG S.
COUNTRY: USA
ZIP: 20005
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-087-4

Query Match 74.1%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 37

US-09-420-592A-7
; Sequence 7, Application US/09420592A
; Patent No. 6333396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-420-592A-7

Query Match 74.1%; Score 43; DB 3; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 38

US-09-985-442-7
; Sequence 7, Application US/09985442
; Patent No. 6692942
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6692942el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-985-442-7

Query Match 74.1%; Score 43; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8

Db 90 AAMDLS 97

RESULT 39

US-09-983-580-7
; Sequence 7, Application US/09983580
; Patent No. 6764853
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6764853el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-983-580-7

Query Match 74.1%; Score 43; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 40

US-08-665-202-40
; Sequence 40, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marka, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom


```
RESULT 2
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match          100.0%; Score 58; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 AAMDLSSEFL 11
      |||||
Db      222 AAMDLSSEFL 232

RESULT 3
US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match          100.0%; Score 58; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 AAMDLSSEFL 11
      |||||
Db      222 AAMDLSSEFL 232
```

```
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 AAMDLSSEFL 11
      |||||
Db      224 AAMDLSSEFL 234

RESULT 4
US-10-293-418-1926
; Sequence 1926, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926

Query Match          100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 AAMDLSSEFL 11
      |||||
Db      224 AAMDLSSEFL 234

RESULT 5
US-10-293-418-3241
; Sequence 3241, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
```

;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 3241
;; LENGTH: 245
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1241

Query Match 100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
Db 225 AAMDLSSEFL 234

RESULT 6
US-09-880-748-1913
;; Sequence 1913, Application US/09880748
;; Publication No. US20030059937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1913

Query Match 100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
Db 225 AAMDLSSEFL 235

RESULT 7
US-09-880-748-1917
;; Sequence 1917, Application US/09880748
;; Publication No. US20030059937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21

;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1917
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1917

Query Match 100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
Db 225 AAMDLSSEFL 235

RESULT 8
US-10-293-418-1913
;; Sequence 1913, Application US/10293418
;; Publication No. US2003022396A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523p2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1913

Query Match 100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
Db 225 AAMDLSSEFL 235

RESULT 9
US-10-293-418-1917
;; Sequence 1917, Application US/10293418
;; Publication No. US2003022396A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523p2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16

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; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1917
```

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Query Match          100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AAWDSLSEFL 11
        |||||
Db      226 AAWDSLSEFL 235
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RESULT 10
US-09-880-748-1443
; Sequence 1443, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1443
```

```

Query Match          100.0%; Score 58; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 AAWDSLSEFL 11
        |||||
Db      226 AAWDSLSEFL 236
```

```

RESULT 11
US-09-880-748-1682
; Sequence 1682, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1682
```

```

Query Match          100.0%; Score 58; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 AAWDSLSEFL 11
        |||||
Db      226 AAWDSLSEFL 236
```

```

RESULT 12
US-09-880-748-1707
; Sequence 1707, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1707
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1707
```

```

Query Match          100.0%; Score 58; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 AAWDSLSEFL 11
        |||||
Db      226 AAWDSLSEFL 236
```

```

RESULT 13
US-09-880-748-1899
; Sequence 1899, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
```

```

? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
? FILE REFERENCE: p5523
? CURRENT APPLICATION NUMBER: US/09/880,748
? CURRENT FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-15
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 3239
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1899
? LENGTH: 247
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-09-880-748-1899

```

Query Match	100.0%;	Score 58;	DB 10;	Length 247;
Best Local Similarity	100.0%;	Pred. No. 0.037;		
Matches 11;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	AAWDDSLSEPL	11	
Db	226	AAWDDSLSEPL	236	

```

RESULT 14
US-09-880-748-1928
; Sequence 1928, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-880-748-1928

```

Query Match	100.0%;	Score 58;	DB 10;	Length 247;
Best Local Similarity	100.0%;	Pred. No. 0.037;		
Matches	11;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0
Q7	1	AAWDDSLSEFL	11	
Db	226	AAWDDSLSEFL	236	

RESULT 15
US-09-880-748-1934
; Sequence 1934, Application US/09880748
; Publication No. US20030059937A1

```

? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly
? FILE REFERENCE: p523
? CURRENT APPLICATION NUMBER: US/09/880,748
? CURRENT FILING DATE: 2001-06-15
? -PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-15
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 3239
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1934
? LENGTH: 247
? TYPE: PRT
? ORGANISM: Homo sapiens
? JS-09-880-748-1934

```

	Best Query Match	100.0%;	Score 58;	DB 10;	Length 247;
	Best Local Similarity	100.0%;	Pred. No. 0.037;		
	Matches 11; Conservative	0;	Mismatches	0;	Gaps 0;
QY	1 AAMDSTSEFL	11			
bB	226 AAMDSTSEFL	236			

```

RESULT 16
US-10-293-418-1443
; Sequence 1443, Application US/10293418
; Publication No. US2003022396CA1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIORITY APPLICATION NUMBER: 60/331,469
PRIORITY FILING DATE: 2001-11-16
PRIORITY APPLICATION NUMBER: 60/340,817
PRIORITY FILING DATE: 2001-12-19
PRIORITY APPLICATION NUMBER: 09/880,748
PRIORITY FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/293,499
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: 60/277,379
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/276,248
PRIORITY FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: 60/240,816
PRIORITY FILING DATE: 2000-10-17
PRIORITY APPLICATION NUMBER: 60/212,210
PRIORITY FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1443
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1443

```

```

Query Match 100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDSDISEFL 11
        |||||
Db       226 AAWDSDISEFL 236

```

```
RESULT 17
US-10-293-418-1682
; Sequence 1682, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1682

Query Match      100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDSLSEFL 11
Db      226 AAWDSLSEFL 236

RESULT 18
US-10-293-418-1707
; Sequence 1707, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1707
; LENGTH: 247
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1707

Query Match      100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDSLSEFL 11
Db      226 AAWDSLSEFL 236

RESULT 19
US-10-293-418-1899
; Sequence 1899, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1899

Query Match      100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDSLSEFL 11
Db      226 AAWDSLSEFL 236

RESULT 20
US-10-293-418-1928
; Sequence 1928, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
```



```

; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1928

```

```

Query Match          100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AAWDSEFL 11
        |||||
Db      226 AAWDSEFL 236

```

```

RESULT 21
US-10-293-418-1934
; Sequence 1934, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1934

```

```

Query Match          100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AAWDSEFL 11
        |||||
Db      226 AAWDSEFL 236

```

```

RESULT 22
US-09-880-748-1419
; Sequence 1419, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

```

```

; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1419
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1419

```

```

Query Match          100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AAWDSEFL 11
        |||||
Db      228 AAWDSEFL 238

```

```

RESULT 23
US-09-880-748-1618
; Sequence 1618, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1618

```

```

Query Match          100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AAWDSEFL 11
        |||||
Db      228 AAWDSEFL 238

```

```

RESULT 24
US-09-880-748-2049
; Sequence 2049, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

```

```
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PE523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2049
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2049
```

```
Query Match      100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDLSSEFL 11
        |||||
Db      228 AAWDLSSEFL 238
```

RESULT 25

```
US-09-880-748-2065
; Sequence 2065, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PE523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2065
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2065
```

```
Query Match      100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDLSSEFL 11
        |||||
Db      228 AAWDLSSEFL 238
```

RESULT 26

```
US-10-293-418-1419
; Sequence 1419, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PE523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1419
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1419
```

```
Query Match      100.0%; Score 58; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDLSSEFL 11
        |||||
Db      228 AAWDLSSEFL 238
```

RESULT 27

```
US-10-293-418-1618
; Sequence 1618, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PE523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1618
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1618
```

```
Query Match      100.0%; Score 58; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AAMDLSSEFL 11
 |||||
 Db 228 AAMDLSSEFL 238

RESULT 28

US-10-293-418-2049
 ; Sequence 2049, Application US/10293418
 ; Publication No. US20030223996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 2049
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-2049

Query Match 100.0%; Score 58; DB 15; Length 249;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
 |||||
 Db 228 AAMDLSSEFL 238

RESULT 29

US-10-293-418-2065
 ; Sequence 2065, Application US/10293418
 ; Publication No. US20030223996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 2065
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-2065

Query Match 100.0%; Score 58; DB 15; Length 249;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
 |||||
 Db 228 AAMDLSSEFL 238

RESULT 30

US-09-880-748-1309
 ; Sequence 1309, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1309
 ; LENGTH: 251
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-748-1309

Query Match 100.0%; Score 58; DB 10; Length 251;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
 |||||
 Db 230 AAMDLSSEFL 240

RESULT 31

US-09-880-748-1671
 ; Sequence 1671, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499

;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 1671
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1671

Query Match 100.0%; Score 58; DB 10; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSISEFL 11
|||
Db 230 AAWDSISEFL 240

RESULT 32
US-09-880-748-1809
; Sequence 1809, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1809
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1809

Query Match 100.0%; Score 58; DB 10; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSISEFL 11
|||
Db 230 AAWDSISEFL 240

RESULT 33
US-10-293-418-1309
; Sequence 1309, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1309
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1309

Query Match 100.0%; Score 58; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSISEFL 11
|||
Db 230 AAWDSISEFL 240

RESULT 34
US-10-293-418-1671
; Sequence 1671, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1671
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1671

Query Match 100.0%; Score 58; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSISEFL 11
|||
Db 230 AAWDSISEFL 240

RESULT 35
US-10-293-418-1809
; Sequence 1809, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

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FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1809
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1809

Query Match
Best Local Similarity 100.0%; Score 58; DB 15; Length 251;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
DB 230 AAMDLSSEFL 240

RESULT 36
US-09-880-748-1698
Sequence 1698, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499,
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1698
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1698

Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 252;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
DB 231 AAMDLSSEFL 241

RESULT 37
```

```
US-10-293-418-1698
Sequence 1698, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1698
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1698

Query Match
Best Local Similarity 100.0%; Score 58; DB 15; Length 252;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
DB 231 AAMDLSSEFL 241

RESULT 38
US-09-880-748-929
Sequence 929, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 929
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-929

Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 253;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAWDLSSEFL 11
 |||||
 Db 232 AAWDLSSEFL 242

RESULT 39
 US-09-880-748-935
 ; Sequence 935, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 935
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-935

Query Match 100.0%; Score 58; DB 10; Length 253;
 Best Local Similarity 100.0%; Pred.No. 0.038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDLSSEFL 11
 |||||
 Db 232 AAWDLSSEFL 242

RESULT 40
 US-09-880-748-939
 ; Sequence 939, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 939
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-939

Query Match 100.0%; Score 58; DB 10; Length 253;
 Best Local Similarity 100.0%; Pred.No. 0.038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDLSSEFL 11
 |||||
 Db 232 AAWDLSSEFL 242

Search completed: March 31, 2005, 12:46:10
 UOB time : 61.5312 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 15.6406 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-15

Perfect score: 58

Sequence: 1 AAWDSLSSEFL 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	74.1	98	2	S36048
2	43	74.1	129	2	S78058
3	43	74.1	235	2	S25750
4	41	70.7	112	1	L1HUMM
5	40	69.0	95	2	S49571
6	40	69.0	98	2	S36047
7	40	69.0	98	2	S36046
8	40	69.0	109	1	L1HUMA
9	40	69.0	117	2	S23627
10	40	69.0	149	2	S23626
11	40	69.0	233	2	S25752
12	40	69.0	234	2	S25757
13	40	69.0	235	2	S25754
14	40	69.0	355	2	S87394
15	40	69.0	497	2	G95983
16	40	69.0	502	1	B54802
17	40	69.0	4367	1	B54802
18	39	67.2	110	2	S57428
19	39	67.2	112	2	D44151
20	39	67.2	130	2	S78057
21	39	67.2	397	1	OKBOB2
22	39	67.2	1995	2	T08166
23	39	67.2	4344	1	A53489
24	38	65.5	210	2	G84751
25	38	65.5	329	2	T18622
26	38	65.5	423	2	S41389
27	38	65.5	443	2	T30619
28	38	65.5	842	2	B55853
29	38	65.5	885	1	WMBY3L

30	37.5	64.7	166	2	C83366	hypothetical prote
31	37	63.8	259	2	T40104	conserved hypothet
32	37	63.8	371	2	AH0147	outer membrane pro
33	37	63.8	395	2	T40102	conserved hypothet
34	37	63.8	476	2	H84228	thiamin biosynthes
35	37	63.8	644	2	F84698	probable thiamin b
36	37	63.8	655	2	A70931	probable PPE prote
37	37	63.8	857	2	B69798	hypothetical prote
38	37	63.8	1485	2	S23756	CFTR protein - Afr
39	36	62.1	184	1	IVHOA1	interferon alpha-1
40	36	62.1	184	1	IVHOA2	interferon alpha-1
41	36	62.1	184	1	IVHOA3	interferon alpha-1
42	36	62.1	184	1	IVHOA4	interferon alpha-1
43	36	62.1	227	2	F81855	insertion element
44	36	62.1	280	2	C98208	probable sugar tra
45	36	62.1	280	2	AF3078	hypothetical prote

ALIGNMENTS

RESULT 1

S36048 Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

C/Accession: S36048; S36049

R:Williams, S.C.

Submitted to the EMBL Data Library, April 1993

A/Reference number: S36046

A/Accession: S36048

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 <NT>

A/Cross-references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 98;

Best Local Similarity 100.0%; Pred.No. 1.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8

Db 90 AAWDSLS 97

RESULT 2

S78058 Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78058; S23723

R:Harindranath, N.

Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78058

A/Molecule type: mRNA

A/Residues: 1-129 <HAR>

A/Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121

R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Bursaturo, S.E.; Wilder, R.L.; Nockin

Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and i

patient.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23723

A/Molecule type: mRNA

A/Residues: 19-129 <HAR>

A/Cross-references: EMBL:X54446

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>

F:19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:33-109/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSTLS 8
|||||
Db 108 AAWDSTLS 115

RESULT 3

S25750

Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25750
R/Contributor: G.; Klobbeck, H.G.
R/Title: V(lambda) 21, 1513-1522, 1991
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25750
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-235 <COM>
A/Cross-references: EMBL:X57815; NID:g33729; PIDN:CAA0552.1; PID:g33730
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSTLS 8
|||||
Db 109 AAWDSTLS 116

RESULT 4

LIHUM

Ig lambda chain V-I region (Mem) - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C/Accession: A25479
R/Mihaesco, E.; Roy, J.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.
R/Title: The amino acid sequence of a lambda light chain presenting abnormal physicochem
A/Reference number: A25479; MUID:85257662; PMID:2410269
A/Accession: A25479
A/Molecule type: protein
A/Residues: 1-112 <MIH>
A/Cross-references: UNIPROT:P06887
A/Note: residues 33-36 and some of the sequenced peptides were positioned by homology
C/Comment: The C region of this chain has the Mgr+ and Kern+ markers.
C/Genetics:
A/Gene: GDB:IGLV@
A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F:15-92/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyroglutamic acid (Gln) #status experimental
F:22-90/Disulfide bonds: #status predicted

Query Match 70.7%; Score 41; DB 1; Length 112;
Best Local Similarity 63.6%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAWDSTLSEFL 11

|||||
Db 91 AAWDSTLGGYV 101

RESULT 5

S49571

Ig lambda chain precursor V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C/Accession: S49571
R/Giachino, C.; Padovan, B.; Lanzavecchia, A.
A/Description: k+1+ dual receptor B cells are present in the human peripheral repertoire
A/Reference number: S49571
A/Accession: S49571
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-95 <GIA>
A/Cross-references: EMBL:Z46625; NID:g575259; PIDN:CAA6595.1; PID:g575260
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 69.0%; Score 40; DB 2; Length 95;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSTLS 8
|||||
Db 76 AAWDSTLT 83

RESULT 6

S36047

Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36047
R/Williams, S.C.
A/Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36047
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <WIL>
A/Cross-references: EMBL:Z22188; NID:g312291; PIDN:CAA60198.1; PID:g312292
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSTLS 8
|||||
Db 90 AAWDSTLN 97

RESULT 7

S36046

Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S36046
R/Williams, S.C.
A/Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36046
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <WIL>
A/Cross-references: EMBL:Z22187; NID:g312312; PIDN:CAA60197.1; PID:g312313
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8
Db 90 AAMDLSLN 97

RESULT 8

Ig lambda chain V-I region (Wah) - human

C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Jul-2004

C:Accession: A01967

R:Takehash, Y.; Takehash, N.; Tetaert, D.; Putnam, F.W.

A:Title: Complete covalent structure of a human immunoglobulin D: sequence of the lambda

A:Reference number: A01967; PMID:8322161; PMID:6407018

A:Accession: A01967

A:Molecule type: protein

A:Residues: 1-109 <TAK>

A:Cross-references: UNIPROT:P04208

C:Gene: GDB:IGLV@

A:Cross-references: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-91/Domain: immunoglobulin homology <IMM>

F:98-109/Region: V segment

F:22-89/Disulfide bonds: #status predicted

Query Match 69.0%; Score 40; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSL 10
Db 90 AAMDLSLW 99

RESULT 9

Ig lambda chain precursor - human

C:Species: Homo sapiens (man)
C>Date: 13-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S23627

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deflos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A:Reference number: S23627; PMID:92156804; PMID:1740665

A:Accession: S23627

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <OLB>

A:Cross-references: EMBL:X59707; NID:G34426; PIDN:CAA42228.1; PID:G34427

C:Gene: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 117;
Best Local Similarity 87.5%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8

Db 109 AAMDLSLN 116

RESULT 10

Ig lambda chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S23626

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deflos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A:Reference number: S23623; PMID:92156804; PMID:1740665

A:Accession: S23626

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 <OLB>

A:Cross-references: EMBL:X59706; NID:G34204; PIDN:CAA42227.1; PID:G34205

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 149;
Best Local Similarity 87.5%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8
Db 109 AAMDLSLN 116

RESULT 11

S25752

Ig lambda chain - human

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25752

R:Combrato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin

A:Reference number: S16439; PMID:91257162; PMID:1904362

A:Accession: S25752

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-233 <COM>

A:Cross-references: EMBL:X57817; NID:G33733; PIDN:CAA40954.1; PID:G33734

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 233;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8
Db 107 AAMDLSLN 114

RESULT 12

S25757

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25757

R:Combrato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin

A:Reference number: S16439; PMID:91257162; PMID:1904362

A:Accession: S25757

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-234 <COM>
A:Cross-references: EMBL:X57822; NID:g33743; PIDD:CAA40956.1; PID:g33744
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:149-217/Domain: immunoglobulin homology <IMM>
Query Match 69.0%; Score 40; DB 2; Length 234;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAMDSTLS 8
Db 108 AAMDSTLS 115
RESULT 13
IG lambda chain - human (fragment)
S25754
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25754
R:Combiato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25754
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57819; NID:g33737; PIDD:CAA40956.1; PID:g33738
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>
Query Match 69.0%; Score 40; DB 2; Length 235;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAMDSTLS 8
Db 108 AAMDSTLS 115
RESULT 14
concealed hypothetical protein CC1169 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: E87394
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <STO>
A:Cross-references: UNIPROT:Q9A925; GB:AE005673; NID:g13422491; PIDD:AAK23153.1; GSPDB:C
C:Genetic8;
A:Gene: CC1169
Query Match 69.0%; Score 40; DB 2; Length 355;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAMDSTLS 8
Db 138 SAMDSTLS 145
RESULT 15

G95983
Probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95983
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrester, J.; Chain, P.; Vorholter, F.J.; Herman
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95983
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <KUR>
A:Cross-references: UNIPROT:O86033; GB:A5591985; PIDD:CA949535.1; PID:g15141022; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; LaLaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: g1pk; SMD21009
A:Genome: plasmid
C:Superfamily: xylinokinase
C:Keywords: phosphotransferase
Query Match 69.0%; Score 40; DB 2; Length 497;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 AAMDSTSEFL 11
Db 197 AAMDSTSEFL 206
RESULT 16
S49113
hypothetical protein 2 - Microcystis aeruginosa
C:Species: Microcystis aeruginosa
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49113
R:Juerchott, K.; Boerner, T.
submitted to the EMBL Data Library, November 1993
A:Description: Sequence of the cyanobacterial plasmid pMA1 from Microcystis aeruginosa H
A:Reference number: S49112
A:Accession: S49113
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <JNB>
A:Cross-references: UNIPROT:Q48904; EMBL:Z28337; NID:g509352; PIDD:CAA82191.1; PID:g5093
C:Superfamily: Microcystis aeruginosa hypothetical protein 2
Query Match 69.0%; Score 40; DB 2; Length 502;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 2 AAMDSTSEFL 11
Db 434 SWEDELAFL 443
RESULT 17
B54802
dynein heavy chain, cytosolic - Neurospora crassa
N:Contains: dynein ATPase (BC 3.6.4.2)
C:Species: Neurospora crassa
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B54802
R:Pilmann, M.; Minke, P.F.; Tinsley, J.H.; Bruno, K.S.

J. Cell Biol. 127, 139-149, 1994
 A:Title: Cytoplasmic dynein and actin-related protein Arp1 are required for normal nucleocytoplasmic transport
 A:Reference number: A54802; MUID:95014704; PMID:7929559
 A:Accession: B54802
 A:Molecule type: DNA
 A:Residues: 1-4367 <PLA>
 A:Cross-references: UNIPROT:P45443; GB:LJ1504; NID:9473489; PDB:AAA64908.1; PID:9473490
 C:Genetics:
 A:Introns: 104/1; 4205/3
 C:Superfamily: dynein heavy chain, cytosolic
 C:Keywords: ATP; heterotetramer; hydrolyase; microtubule binding; nucleotide binding; P-1
 F:1943-1950/Region: nucleotide-binding motif A (P-loop)
 F:2240-2247/Region: nucleotide-binding motif A (P-loop)
 F:2605-2612/Region: nucleotide-binding motif A (P-loop)
 F:2947-2954/Region: nucleotide-binding motif A (P-loop)
 F:1949/Binding site: ATP (Lys) #status predicted
 F:2246/Binding site: ATP (Lys) #status predicted
 F:2611/Binding site: ATP (Lys) #status predicted
 F:2953/Binding site: ATP (Lys) #status predicted

Query Match 69.0%; Score 40; DB 1; Length 4367;
 Best Local Similarity 66.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAMDLSHF 10
 |||||
 |||||
 Db 455 AAMDLSHF 463

RESULT 18
 S57428
 Ig light chain V-J region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S57428
 R:Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
 submitted to the EMBL Data Library, June 1995
 A:Description: Analysis of anti-GM1 ganglioside IGM antibodies cloned from motor neurone
 A:Reference number: S57408
 A:Accession: S57428
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-110 <PAR>
 A:Cross-references: EMBL:X87890; NID:9871271; PDB:CAA61141.1; PID:9871272
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 7
 |||||
 |||||
 Db 90 AAMDLS 96

RESULT 19
 D44151
 Ig lambda chain V region (BO-12) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
 C:Accession: D44151
 R:Zebedes, S.L.; Barbas III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pye
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
 A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
 A:Reference number: A44151; MUID:92228746; PMID:1373487
 A:Accession: D44151
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-112 <ZEB>
 A>Note: nucleotide translation is not given
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
 F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 7
 |||||
 |||||
 Db 89 AAMDLS 95

RESULT 20
 S78057
 Ig lambda chain precursor V-J region (clone mAb 61VL) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
 C:Accession: S78057; S23722
 R:Harindranath, N.
 submitted to the EMBL Data Library, August 1990
 A:Reference number: S78051
 A:Accession: S78057
 A:Molecule type: mRNA
 A:Residues: 1-130 <HAR>
 A:Cross-references: EMBL:X54438; NID:937920; PDB:CAA38307.1; PID:937921
 R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burnstero, S.E.; Wilder, R.L.; Nockins
 Int. Immunol. 3, 865-875, 1991
 A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
 patient.
 A:Reference number: S23716; MUID:92031262; PMID:1718404
 A:Accession: S23722
 A:Molecule type: mRNA
 A:Residues: 20-130 <HAR>
 A:Cross-references: EMBL:X54438
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
 F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 130;
 Best Local Similarity 87.5%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
 |||||
 |||||
 Db 109 AAMDLS 116

RESULT 21
 OKB082
 protein kinase (EC 2.7.1.37), CAMP-dependent, beta-2 catalytic chain - bovine
 C:Comment: Bos primigenius taurus (cattle)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A23716
 R:Wiemann, S.; Kinzel, V.; Peyerin, W.
 J. Biol. Chem. 266, 5140-5146, 1991
 A:Title: Isoform Cbeta2, an unusual form of the bovine catalytic subunit of CAMP-depend
 A:Reference number: A23716; MUID:91161607; PMID:2002051
 A:Accession: A23716
 A:Molecule type: mRNA
 A:Residues: 1-397 <WIE>
 A:Cross-references: UNIPROT:P24256; GB:M60482; NID:9162786; PDB:AAA30424.1; PID:9162787
 C:Comment: The inactive enzyme contains two regulatory chains and two catalytic chains.
 C:Two types found in mammalian tissue are distinguished by having either type I or type
 C:Comment: Both alpha and beta catalytic chains are found in many tissues, with the alpha
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: alternative splicing; ATP; CAMP binding; heterotetramer; magnesium; phospho
 F:2-397/Product: protein kinase, CAMP-dependent, beta-2 catalytic chain #status predicte
 F:88-344/Domain: protein kinase homology <KIN>
 F:96-104/Region: protein kinase ATP-binding motif
 F:101,102,166,174,217,230/Binding site: Mg-ATP (Phe, Gly, Glu, Glu, Glu, Thr) #status pr
 F:119,138,213,215/Active site: Lys, Glu, Asp, Lys #status predicted

F:218,231/Binding site: magnesium (Asn, Asp) #status predicted
F:244/Binding site: phosphate (Thr) (covalent) #status predicted
F:38/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 67.2%; Score 39; DB 1; Length 397;
Best Local Similarity 63.6%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||:|
DB 56 ALMDRSMKEFL 66

RESULT 22

T08166
Probable membrane protein 1995 - Chlamydomonas reinhardtii chloroplast
C:Species: chloroplast Chlamydomonas reinhardtii
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08166; A24829
R:Boudreau, E.; Tumele, M.; Goldschmidt-Clermont, M.; Rochaix, J.D.; Sivan, S.; Michaelis
Mol. Gen. Genet. 253, 649-653, 1997
A:Title: A large unidentified open reading frame (ORF1995) in Chlamydomonas reinhardtii
A:Reference number: Z16392; MUID:97218038; PMID:9065699
A:Accession: T08166

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1995 <BOU>
A:Cross-references: UNIPROT:P36495; EMBL:X92726; NID:g1054719; PIDN:CAA63385.1; PID:g105
R:Moessner, J.P.; Gillham, N.W.; Boynton, J.E.
Gene 44, 17-28, 1986

A:Title: The sequence of the chloroplast atpB gene and its flanking regions in Chlamydomon
A:Reference number: A24829; MUID:87031585; PMID:2876928
A:Accession: A24829

A:Molecule type: DNA
A:Residues: 1935-1995 <MOB>
A:Cross-references: GB:M13704; NID:g33666; PIDN:AAA84144.1; PID:g895614
A>Note: the authors translated the codon GAA for residue 1957 as Gly
C:Genetics:

A:Genome: chloroplast
C:Keywords: chloroplast; membrane protein

Query Match 67.2%; Score 39; DB 2; Length 1995;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||:|
DB 1581 AGWDESLKKEV 1591

RESULT 23

A53489
dynein heavy chain, cytosolic - Emeritella nidulans
N:Contains: dynein ATPase (RC 3.6.4.2)
C:Species: Emeritella nidulans, Aspergillus nidulans
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A53489

R:Xiang, X.; Beckwith, S.M.; Morris, N.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2100-2104, 1994
A:Title: Cytosolic dynein is involved in nuclear migration in Aspergillus nidulans.
A:Reference number: A53489; MUID:94181539; PMID:8134356
A:Accession: A53489

A:Molecule type: DNA
A:Residues: 1-4344 <XIA>
A:Cross-references: UNIPROT:P45444; GB:U03904; NID:g451538; PIDN:AAA18338.1; PID:g451539
C:Superfamily: dynein heavy chain, cytosolic

C:Keywords: ATP; heterotrimer; hydrolase; microtubule binding; nucleotide binding; P-1
F:1933-1940/Region: nucleotide-binding motif A (P-loop)
F:2228-2235/Region: nucleotide-binding motif A (P-loop)
F:2592-2599/Region: nucleotide-binding motif A (P-loop)
F:2932-2939/Region: nucleotide-binding motif A (P-loop)
F:1939/Binding site: ATP (Lys) #status predicted
F:2234/Binding site: ATP (Lys) #status predicted

F:2598/Binding site: ATP (Lys) #status predicted
F:2938/Binding site: ATP (Lys) #status predicted

Query Match 67.2%; Score 39; DB 1; Length 4344;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDSLSSEFL 10
|||:|
DB 446 WDDNLKEFL 453

RESULT 24

G84751
hypothetical protein At2g34050 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84751
R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.
euss, D.; Mernan, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617157
A:Accession: G84751

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-210 <STO>

A:Cross-references: UNIPROT:O22958; GB:AE002093; NID:g2342725; PIDN:AA67623.1; GSPDB:GN
C:Genetics:

A:Gene: At2g34050
A:Map position: 2

Query Match 65.5%; Score 38; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDSLSSEFL 11
|||:|
DB 99 WDDVLSKFL 107

RESULT 25

T18622
hypothetical protein AH6.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18622

R:Berks, M.

submitted to the EMBL Data Library, January 1995

A:Reference number: Z18998

A:Accession: T18622

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-329 <WTL>

A:Cross-references: UNIPROT:Q09205; EMBL:Z48009; PIDN:CAA8086.1; GSPDB:GN00020; CESP:AH
A:Experimental source: clone AH6

C:Genetics:

A:Gene: CESP:AH6.7

A:Map position: 2

A:introns: 217/2; 279/3

C:Superfamily: Caenorhabditis elegans hypothetical protein AH6.4

Query Match 65.5%; Score 38; DB 2; Length 329;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDSLSSEFL 10
|||:|
DB 164 WDDPLSEFL 171

RESULT 26

S41289
hypothetical protein ORF-S - Chlamydomonas reinhardtii
C/Species: Chlamydomonas reinhardtii
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S41289
R/Sivan, S.; Michaels, A.
submitted to the EMBL Data Library, December 1993
A/Reference number: S41289
A/Accession: S41289
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-423 <SV>
A/Cross-references: UNIPROT:P36495; EMBL:X76934; NID:G440398; PID:G440399
C/Keywords: chloroplast

Query Match 65.5%; Score 38; DB 2; Length 423;
Best Local Similarity 54.5%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
| | | | |
DB 9 AGWDESLKRFV 19

RESULT 27
T30619
probable serine/threonine-specific protein kinase 17L - Molluscum contagiosum virus 1
N/Alternate names: MCO17L
C/Species: Molluscum contagiosum virus 1
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 27-Oct-2003
C/Accession: T30619
R/Senkevich, T.G.; Bugert, J.J.; Stalder, J.R.; Koonin, E.V.; Darai, G.; Mose, B.
Science 273, 813-816, 1996
A/Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A/Reference number: 220876; MUID:96325459; PMID:8670425
A/Accession: T30619
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-443 <SEN>
A/Cross-references: EMBL:U60315; NID:G1491943; PIDN:AA05145.1; PID:G1491960
C/Genetics: MCO17L
A/Note: MCO17L
C/Superfamily: Ser/Thr protein kinase, poxviridae type
C/Keywords: serine/threonine-specific protein kinase

Query Match 65.5%; Score 38; DB 2; Length 443;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
| | | | |
DB 390 AAMSKALSEFL 400

RESULT 28
B55853
outer membrane usher protein aggc precursor - Escherichia coli
C/Species: Escherichia coli
C/Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C/Accession: B55853
R/Savarino, S.J.; Fox, P.; Yikang, D.; Nataro, J.P.
J. Bacteriol. 176, 4949-4957, 1994
A/Title: Identification and characterization of a gene cluster mediating enteroaggregati
A/Reference number: A55853; MUID:94327462; PMID:7914189
A/Accession: B55853
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-842 <SAV>
A/Cross-references: UNIPROT:P46005; GB:U12894; NID:G531396; PIDN:AAA57452.1; PID:G531396
C/Genetics: aggc
A/Gene: aggc
C/Superfamily: outer membrane usher protein fliM
C/Keywords: membrane protein

Query Match 65.5%; Score 38; DB 2; Length 842;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 11
| | | | |
DB 161 WDDGISLRF 169

RESULT 29
NM8YJL
ribonucleoside-diphosphate reductase (EC 1.17.4.1) 3 large chain - Yeast (Saccharomyces
N/Alternate names: protein YIL066c; ribonucleotide reductase regulatory chain 3
C/Species: Saccharomyces cerevisiae
C/Date: 30-Sep-1991 #sequence_revision 19-Jul-1996 #text_change 21-Jul-2000
C/Accession: S48413; S12066; B35845; A35930
R/Smith, V.
submitted to the EMBL Data Library, September 1994
A/Reference number: S48407
A/Accession: S48413
A/Molecule type: DNA
A/Residues: 1-885 <SMI>
A/Cross-references: EMBL:Z38060; NID:G557796; PIDN:CA86157.1; PID:G557803; GSPDB:GN0000
R/Yagle, K.; McIntee, K.
Mol. Cell. Biol. 10, 5553-5557, 1990
A/Title: The DNA damage-inducible gene DIN1 of Saccharomyces cerevisiae encodes a regula
A/Reference number: A35930; MUID:90377250; PMID:2204819
A/Accession: S12066
A/Molecule type: DNA
A/Residues: 17-142; 'TRY', 147-227, 'L', 229-262, 'VLS', 267-302, 'TRVTRD', 315, 'V', 317, 'S', 319
A/Cross-references: EMBL:M58012; NID:G171398; PIDN:AAA34569.1; PID:G171399
R/Elledge, S.J.; Davis, R.W.
Genes Dev. 4, 740-751, 1990
A/Title: Two genes differentially regulated in the cell cycle and by DNA-damaging agents
A/Reference number: A35845; MUID:90337312; PMID:2199320
A/Accession: B35845
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 17-36, 'VL', 39-52, 'F', 54-73, 'T', 75-84, 'H', 86-98, 'T', 100-117, 'TGR', 668-691, 'L'
C/Genetics: SGD:RMN3; DIN1, MIPS:YIL066c
A/Gene: SGD:RMN3; DIN1, MIPS:YIL066c
A/Cross-references: SGD:S0001328; MIPS:YIL066c
A/Map position: 9L
C/Superfamily: herpesvirus ribonucleoside-diphosphate reductase large chain
C/Keywords: deoxyribonucleotide biosynthesis; heterotetramer; oxidoreductase; redox-acti
F/234-459,880-883/Distalide bonds: redox-active #status predicted
F/442,446/Active site: Asn, Glu #status predicted
F/444/Active site: Cys (cysteine thiol radical intermediate) #status predicted

Query Match 65.5%; Score 38; DB 1; Length 885;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 11
| | | | |
DB 671 WDDSKQYFL 679

RESULT 30
C83366
hypothetical protein PA2226 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C83366
R/Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kaab, A.; Lardig, K.; Lam,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:1094043
A/Accession: C83366
A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-166 <STO>
A:Cross-references: UNIPROT:Q911P3; GB:AE004649; GB:AE004091; NID:g9948246; PIDN:AAG0561
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2226

Query Match 64.7%; Score 37.5; DB 2; Length 166;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 0; Indels 5; Gaps 1;

Qy 1 AAMD-----DSLSFL 11
||| |
Db 107 AAMDASVAMDNISFLV 122

RESULT 31
T40104 conserved hypothetical protein SPBC2D10.01c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40104
R:Wood, V.; Rajandream, M.A.; Barrett, B.G.; Taylor, K.; Harris, D.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21906
A:Accession: T40104
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-259 <MOO>
A:Cross-references: UNIPROT:Q9UUM3; EMBL:AL031788; PIDN:CAA21159.1; GSPDB:GN00067; SPDB:
C:Genetics:
A:Experimental source: strain 972h-, cosmid C2D10
A:Gene: SPDB:SPBC2D10.01c
A:Map position: 2

Query Match 63.8%; Score 37; DB 2; Length 259;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WDSLSFL 11
||| |
Db 9 WPSLSKFL 17

RESULT 32
AH0147 outer membrane protein C2 ompC2 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0147
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:1156360
A:Accession: AH0147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-371 <KUR>
A:Cross-references: UNIPROT:Q8ZGS6; GB:AL590842; PIDN:CAC90043.1; PID:g15979264; GSPDB:G
C:Genetics:
A:Gene: ompC2
C:Superfamily: outer membrane protein phoB

Query Match 63.8%; Score 37; DB 2; Length 371;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEF 10
||| |
Db 124 AAWTDLPEF 133

RESULT 33
T40102 conserved hypothetical protein SPBC2A9.11c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40102
R:Barrett, B.G.; Rajandream, M.A.; Lyne, M.; Skelton, J.; Churcher, C.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21905
A:Accession: T40102
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <BAR>
A:Cross-references: UNIPROT:Q9UUM3; EMBL:AL049495; PIDN:CAB39853.1; GSPDB:GN00066; SPDB:
A:Experimental source: strain 972h-, cosmid C2A9_3p
C:Genetics:
A:Gene: SPDB:SPBC2A9.11c
A:Map position: 1
A:Insertions: 216/3; 260/1

Query Match 63.8%; Score 37; DB 2; Length 395;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WDSLSFL 11
||| |
Db 9 WPSLSKFL 17

RESULT 34
H84228 chitin biosynthesis protein [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84228
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithner, B.; Keller, K.; Cruz, R.; Danon, M.D.; Hough, D.W.; Maddock, D.G.; Jablon
Jung, K.H.; Alam, M.; Prells, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:2050483; PMID:11016950
A:Accession: H84228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <STO>
A:Cross-references: UNIPROT:Q9HRG2; GB:AE004437; NID:g10580294; PIDN:AAG19196.1; GSPDB:G
C:Genetics:
A:Gene: chitC
C:Superfamily: chitin biosynthesis protein chitC

Query Match 63.8%; Score 37; DB 2; Length 476;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WDSLSL 9
||| |
Db 363 WDDLSLSE 369

RESULT 35
F84698 probable thiamin biosynthesis protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84698
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84698
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-644 <SNO>
A:Cross-references: UNIPROT:O82392; GB:AE002093; NID:g3582335; PIDN:AAC35232.1; GSPDB:GN
C:Genetics:
A:Gene: At2g29630
A:Map position: 2
C:Superfamily: thiamin biosynthesis protein thic

Query Match 63.8% Score 37; DB 2; Length 644;
Best Local Similarity 75.0% Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWDLSSE 9
Db 524 AWDALSK 531

RESULT 36

A70931
probable ppe protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: A70931

R:Conor, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Rajandream, M.A.; Rogers, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Nature 393, 537-544, 1998

A:Authors: Sgarbes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70931

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-655 <COL>
A:Cross-references: UNIPROT:O53949; GB:AL022021; GB:AL123456; NID:g350669; PIDN:CAA1772

A:Experimental source: strain H37RV

C:Genetics:
A:Gene: ppe

Query Match 63.8% Score 37; DB 2; Length 655;
Best Local Similarity 77.8% Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAWDSLSE 9
Db 31 AAWDDLASE 39

RESULT 37

B69798
hypothetical protein yecA - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: B69798

R:Kunst, F.; Ogatawa, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Gallizzi, A.; Gallier
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lartinois,
A:Authors: Lander, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauei
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeder, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tempstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: B69798

Query Match 63.8% Score 37; DB 2; Length 644;
Best Local Similarity 75.0% Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-857 <KUN>
A:Cross-references: UNIPROT:O31530; GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12528.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yecA
C:Superfamily: Bacillus subtilis hypothetical protein yecA

Query Match 63.8% Score 37; DB 2; Length 857;
Best Local Similarity 75.0% Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WDDLSSEF 10
Db 733 WDDLSSEF 740

RESULT 38

S23756
CFTR protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 05-Mar-1994 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C:Accession: S23756

R:Tucker, S.J.; Tannahill, D.; Higgins, C.F.
Hum. Mol. Genet. 1, 77-82, 1992

A>Title: Identification and developmental expression of the Xenopus laevis cystic fibrosis

A:Reference number: S23756; MUID:93244789; PMID:1284470

A:Accession: S23756

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1485 <TUC>

A:Cross-references: UNIPROT:P26363; EMBL:X65256; NID:g64622; PIDN:CAA6348.1; PID:g64623

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein

F:442-623/Domain: ATP-binding cassette homology <ABC1>
F:459-466/Region: nucleotide-binding motif A (P-loop)
F:1230-1422/Domain: ATP-binding cassette homology <ABC2>
F:1247-1254/Region: nucleotide-binding motif A (P-loop)

Query Match 63.8% Score 37; DB 2; Length 1485;
Best Local Similarity 50.0% Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAWDSLSEF 10
Db 400 ASWDEGIEF 409

RESULT 39

LYHOA1
interferon alpha-I-1 precursor - horse

N:Alternate names: EqlFN-alpha-I-1; type I interferon

C:Species: Equus caballus (domestic horse)

C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C:Accession: A24912

R:Himler, A.; Hauptmann, R.; Adolf, G.R.; Svelly, P.
DNA 5, 345-356, 1986

A>Title: Molecular cloning and expression in Escherichia coli of equine type I interferon

A:Reference number: A90956; MUID:87053170; PMID:3022999

A:Accession: A24912
A:Molecule type: DNA
A:Residues: 1-184 <HIM>
A:Cross-references: UNIPROT:P05003; GB:M14540; NID:g164226; PIDN:AAA0953.1; PID:g164227

C:Superfamily: interferon alpha
C:Keywords: antiviral
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-184/Product: interferon alpha-I-1 #status predicted <MAT>
F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 62.1% Score 36; DB 1; Length 184;
Best Local Similarity 63.6% Pred. No. 45;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAWDSLSEFL 11
 |||:|:|
 Db 98 AAWDSLIDLKL 108

RESULT 40

IVHOA2
 Interferon alpha-1-2 precursor - horse
 N/Alternate names: EqlFN-alpha-1-2; type I interferon
 C/Species: Equus caballus (domestic horse)
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C/Accession: B24912
 R/Himmler, A.; Hauptmann, R.; Adolf, G.R.; Sweetly, P.
 DNA 5, 345-356, 1986
 A/Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
 A/Reference number: A90956; MUID:87053170; PMID:3022999
 A/Accession: B24912
 A/Molecule type: DNA
 A/Residues: 1-184 <HIM>
 A/Cross-references: UNIPROT:P05004; GB:M14541; NID:G164218; PIDN:AAA10950.1; PID:G164221
 C/Superfamily: Interferon alpha
 C/Keywords: antiviral
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-184/Product: interferon alpha-1-2 #status predicted <MAT>
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 62.1% Score 36; DB 1; Length 184;
 Best Local Similarity 63.6% Pred. No. 45;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAWDSLSEFL 11
 |||:|:|
 Db 98 AAWDSLIDLKL 108

Search completed: March 31, 2005, 12:11:17
 Job time : 15.6406 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 73.0469 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAMDLSSEFL 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	44	75.9	108 2	Q96SB0 homo sapien
2	43	74.1	236 2	Q8NEJ1
3	43	74.1	628 2	O6CIT9
4	41	70.7	112 1	LVYH.HUMAN
5	41	70.7	237 2	Q6DHW4
6	40	69.0	109 1	LVYF.HUMAN
7	40	69.0	355 2	Q9A925
8	40	69.0	376 1	CEA2.RAT
9	40	69.0	381 1	CEA2.HUMAN
10	40	69.0	381 1	CEA2.MOUSE
11	40	69.0	497 1	GLPK.RHIME
12	40	69.0	502 2	Q48904
13	40	69.0	1714 1	YP93.CAEEL
14	40	69.0	4367 1	DYHC.NEUCR
15	39	67.2	182 2	O8TGV3
16	39	67.2	236 2	O6GMV7
17	39	67.2	397 1	KAPI.BOVIN
18	39	67.2	398 2	O723M1
19	39	67.2	578 2	O8W0B5
20	39	67.2	751 2	O6C0Z1
21	39	67.2	894 2	O7AB13
22	39	67.2	969 2	O7RY83
23	39	67.2	1466 2	O98TR8
24	39	67.2	1995 2	YCX7.CHLRE
25	39	67.2	4344 1	DYHC.EMENTI
26	38	65.5	170 2	O7JYB0
27	38	65.5	215 2	O67NP3
28	38	65.5	244 2	O31358
29	38	65.5	252 2	O631V6
30	38	65.5	252 2	O72Y69
31	38	65.5	252 2	O815W5

32	38	65.5	252 2	O81X10	O81X10 bacillus an
33	38	65.5	252 2	O6HBPI	O6hbpi bacillus th
34	38	65.5	299 2	O74E50	O74e50 geobacter s
35	38	65.5	302 1	DAPA.XANAC	O8p1ns xanthomonas
36	38	65.5	329 1	SRA3.CAEEL	O09205 caenorhabdi
37	38	65.5	348 2	O9F6D9	O9f6d9 streptomyce
38	38	65.5	395 2	O6R8A6	O6r8a6 sodalis glo
39	38	65.5	443 2	O76S23	O76s23 molluscum c
40	38	65.5	443 2	O83155	O83155 molluscum c
41	38	65.5	496 2	O9B091	O9b091 mycobacteri
42	38	65.5	514 2	O7WZ48	O7wz48 nonomuraea
43	38	65.5	605 1	P8B1.CANAL	O9wuf6 candida alb
44	38	65.5	842 1	AGGC.ECOLI	P46005 escherichia
45	38	65.5	869 1	RIR3_YEAST	P21672 saccharomyc

ALIGNMENTS

RESULT 1					
ID	Q96SB0	PRELIMINARY;	PRT;	108 AA.	
AC	Q96SB0				
DT	01-DEC-2001 (TREMblrel. 19, Created)				
DT	01-DEC-2001 (TREMblrel. 19, Last sequence update)				
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)				
DE	Anti-streptococcal/anti-mycosin immunoglobulin lambda light chain variable region (Fragment).				
DE	variable region (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98375893; PubMed=9712075;				
RA	Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;				
RT	"Molecular analysis of polyclonal monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin antibody V region genes."				
RL	J. Immunol. 161:2020-2031(1998).				
DR	EMBL; U96394; AAB8783.1; -.				
DR	PDB; 1KU4; Model; L=1-108.				
DR	InterPro; IPR007110; IG-1-like.				
DR	InterPro; IPR003596; IG_V.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
FT	NON_TER				
FT	SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;				
Query Match					
Beet Local Similarity 72.7%; Pred. NO. 3.1;					
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY	1 AAMDLSSEFL 11				
DB	90 AAMDRLSGFM 100				
RESULT 2					
ID	Q8NEJ1	PRELIMINARY;	PRT;	236 AA.	
AC	Q8NEJ1				
DT	01-OCT-2002 (TREMblrel. 22, Created)				
DT	01-OCT-2002 (TREMblrel. 22, Last sequence update)				
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RT	TISSUE=Lung;				

```

RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klusner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stjepic M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krywaniak M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RC SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; -
DR HSSP; P01703; 7PAB.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003806; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sect; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 74.1%; Score 43; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSDL 8
Db 109 AAMDSDL 116

RESULT 3
ID Q6CLT9 PRELIMINARY; PRT; 628 AA.
AC Q6CLT9;
DT 25-OCT-2004 (TRENBLrel. 28. Created)
DT 25-OCT-2004 (TRENBLrel. 28. Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28. Last annotation update)
DE Similar to sp|Q9HFC6 Yarrowia lipolytica Calnexin.
GN ORFNames=KLA0F004629;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
CX NCBI_TaxID=2845590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durand P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Franquet L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Baryme S., Blanchin S., Beckerich J.M., Beyne E., Bleksten C.,
RA Boissiere A., Boyer J., Cattolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreay F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,

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RA Nicaud J.M., Nikolski M., Oztes S., Ozler-Kalgeropoulos O.,
RA Pellens S., Potter S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Texela F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
[2]
RC SEQUENCE FROM N.A.
RP STRAIN=NRRL Y-1140;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382126; CAG97807.1; -
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calret/calnex.
DR InterPro; IPR008985; CnA-like_lcc-gl.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN 1; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
SQ SEQUENCE 628 AA; 70981 MW; B0D8A6D1A6464FE CRC64;

Query Match 74.1%; Score 43; DB 2; Length 628;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 WDSLSEFL 11
Db 309 WDSLSEFL 317

RESULT 4
LVTH HUMAN STANDARD; PRT; 112 AA.
ID LVTH HUMAN;
AC P06887;
DT 01-JAN-1988 (Rel. 06. Created)
DT 01-JAN-1988 (Rel. 06. Last sequence update)
DT 05-JUL-2004 (Rel. 44. Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=65257662; PubMed=2410269;
RA Minaesaco E., Roy J.P., Congy N., Peran-Rivat L., Minaesaco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features."
RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
CC were positioned by homology.
CC -1- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
CC markers.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region;
KM Monoclonal antibody; Pyridone carboxylic acid.
FT MOD_RES 1 106 Ig-like.
FT DISULFID 22 90 Pyroliidone carboxylic acid.
FT NON_TER 112 112 By similarity.

```

SO SEQUENCE 112 AA; 11789 MW; 748124F079CFBEB4 CRC64;
 Query Match 70.7%; Score 41; DB 1; Length 112;
 Best Local Similarity 63.6%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 11
 |||||
 :
 Db 91 AAMDLSLGV 101

RESULT 5
 Q6DHW4 PRELIMINARY; PRT; 237 AA.
 AC Q6DHW4;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millay S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC075843; AAH75843.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1ike.
 DR InterPro; IPR003597; IG-Cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-secl.1.
 DR Pfam; PF00047; IG.2.
 DR SMART; SM00409; IG.2.
 DR SMART; SM00406; IGV.1.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS00835; IG_LIKE.2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
 KW Hypothetical protein.
 SQ SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;

Query Match 70.7%; Score 41; DB 2; Length 237;
 Best Local Similarity 67.5%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8

Db 109 AAMDLSMS 116
 |||||
 :
 ID LVIF_HUMAN STANDARD; PRT; 109 AA.
 AC P04208;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda chain V-I region WH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=8322161; PubMed=6407018;
 RA Takahashi Y., Takahashi N., Teraert D., Putnam F.W.;
 RT "Complete covalent structure of a human immunoglobulin D: sequence of
 RT the lambda light chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
 RL PIR; A01967; LIGHWA.
 DR HSP; P01703; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-1ike.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG.1.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS00835; IG_LIKE.1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 97
 FT DOMAIN 2 109
 FT DISULFID 22 89
 FT NON TER 109 109
 FT BY similarity.
 SQ SEQUENCE 109 AA; 11725 MW; B17785F6ADP9BAC CRC64;

Query Match 69.0%; Score 40; DB 1; Length 109;
 Best Local Similarity 80.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 10
 |||||
 :
 Db 90 AAMDLSLWVF 99

RESULT 7
 Q9A925 PRELIMINARY; PRT; 355 AA.
 ID Q9A925;
 AC Q9A925;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein CC1169.
 GN OrderedLocustNames=CC1169;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Deboy R.T., Nelson W.C., Newton A.S., Stephens C., Phadt D.H.,
 RA Kolony J.F., Smit J., Craven M.B., Knouri H.M., Shetty J.,
 RA Berry K.J., Uetback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
 RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,

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RA  Fraser C.M.;
RT  "Complete genome sequence of Caulobacter crescentus.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
DR  EMBL; AE005795; AK23153.1; -.
DR  PIR; E87394; E87394.
DR  TIGR; CC1169; -.
DR  InterPro; IPR011251; Luciferase-like.
DR  Pfam; PF00296; Bac_Luciferase; 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 355 AA; 38552 MW; 3C4AEF42825E5567 CRC64;

Query Match          69.0%; Score 40; DB 2; Length 355;
Best Local Similarity 87.5%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY  1 AAMDLS 8
DB  138 SAMDLS 145

RESULT 8
CE2_RAT  STANDARD; PRT; 376 AA.
ID  CE2_RAT
AC  Q9UK15;
DT  25-OCT-2004 (Rel. 45, Created)
DT  25-OCT-2004 (Rel. 45, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Centaurin alpha 2.
GN  Name=Cent2;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A., INTERACTION WITH PTDS(4,5)P2, PTDS(3,4,5)P3
RP  AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
RP  ARG-275.
RC  TISSUE=Adipocyte;
RX  MEDLINE=22012451; PubMed=12018390;
RA  Whitley P., Glibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
RA  Prestwich G.D., Holman G.D.;
RT  "Identification of centaurin-alpha2: a phosphatidylinositol-binding
RT  protein present in fat, heart and skeletal muscle.";
RL  Eur. J. Cell Biol. 81:222-230(2002).

CC  -1- FUNCTION: GTPase-activating protein for the ADP ribosylation
CC  factor family (Potential).
CC  -1- SUBUNIT: Binds phosphatidylinositol 4,5-bisphosphate,
CC  phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3) and inositol
CC  1,3,4,5-tetrakisphosphate (InsP4). Binding of phosphatidylinositol
CC  3,5-bisphosphate and phosphatidylinositol 3,4-bisphosphate occurs
CC  at a much lower affinity. Possesses a stoichiometry of two binding
CC  sites for InsP4 with identical affinity (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
CC  the plasma membrane. Excluded from the nucleus (By similarity).
CC  -1- TISSUE SPECIFICITY: Expressed in many tissues, with highest levels
CC  in fat, heart and skeletal muscle. Also detected in kidney, liver
CC  and lung.
CC  -1- SIMILARITY: Contains 1 Arf-GAP domain.
CC  -1- SIMILARITY: Contains 2 PH domains.
CC  -----
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CC  entities requires a license agreement (see http://www.ebi.ac.uk/announcements
CC  or send an email to license@ebi.ac.uk).
CC  -----
DR  EMBL; AJ238993; CAB88403.1; -.
DR  RGD; 708487; LOC56826.
DR  InterPro; IPR001164; hrp_1ike.
DR  InterPro; IPR001849; PH.
DR  InterPro; IPR011036; PH_related.

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DR  Pfam; PF01412; ArfGAP; 1.
DR  Pfam; PF00169; PH; 2.
DR  PRINTS; PR00405; REVINTRACTING.
DR  SMART; SM00105; ArfGAP; 1.
DR  SMART; SM00233; PH; 2.
DR  PROSITE; PS50115; ARFGAP; 1.
DR  PROSITE; PS50003; PH_DOMAIN; 2.
KW  GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
FT  DOMAIN 9 130 Arf-GAP.
FT  ZN_FING 25 48 C4-type.
FT  DOMAIN 131 232 PH 1.
FT  DOMAIN 254 360 PH 2.
FT  MUTAGEN 151 151 R->C: Almost complete loss of InsP4
FT  MUTAGEN 275 275 binding.
FT  MUTAGEN 275 275 R->C: No loss of InsP4 binding. Almost
FT  complete loss of InsP4 binding; when
FT  associated with C-151.
SQ  SEQUENCE 376 AA; 43524 MW; E357392F38F0166 CRC64;

Query Match          69.0%; Score 40; DB 1; Length 376;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY  3 WDSLSRFL 11
DB  69 WDSNVEFPM 77

RESULT 9
CE2_HUMAN  STANDARD; PRT; 381 AA.
ID  CE2_HUMAN
AC  Q9NPF8; Q8N406; Q96SD5;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Centaurin alpha 2.
GN  Name=CENT2;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RX  MEDLINE=22012451; PubMed=12018390;
RA  Whitley P., Glibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
RA  Prestwich G.D., Holman G.D.;
RT  "Identification of centaurin-alpha2: a phosphatidylinositol-binding
RT  protein present in fat, heart and skeletal muscle.";
RL  Eur. J. Cell Biol. 81:222-230(2002).

CC  [2]
CC  SEQUENCE FROM N.A. (ISOFORM 1).
CC  MEDLINE=20304757; PubMed=10843809; DOI=10.1006/geno.2000.6179;
CC  Jenne D.E., Tinschert S., Stegmann E., Reimann H., Nurnberg P.,
CC  Horn D., Naumann I., Buske A., Thiel G.;
CC  "A common set of at least 11 functional genes is lost in the majority
CC  of NFI patients with gross deletions.";
CC  Genomics 66:93-97(2000).
CC  [3]
CC  SEQUENCE FROM N.A. (ISOFORM 1).
CC  Bertsch U., Illies C., Mayr G.M.;
CC  Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
CC  [4]
CC  SEQUENCE FROM N.A. (ISOFORM 2).
CC  TISSUE=Leukocyte;
CC  MEDLINE=22388257; PubMed=12477937; DOI=10.1073/pnas.242603899;
CC  Strauberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
CC  Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
CC  Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.R.,
CC  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
CC  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC  Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC  Brownstein M.J., Uedin T.B., Tothiyk S., Carninci P., Prange C.J.,
CC  Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN INTERACTION WITH PTDS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE
 RP SPECIFICITY, AND SUBCELLULAR LOCATION.
 RX PubMed=14690521;
 RA Hanck T., Stricker R., Sedehzade F., Reiser G.,
 RT "Identification of gene structure and subcellular localization of
 RT human centaurin alpha 2, and p42IP4, a family of two highly
 RT homologous, Ins 1,3,4,5-P4-/Ptdins 3,4,5-P3-binding, adapter
 RT proteins.";
 RT J. Neurochem. 88:326-336(2004).
 RL J. Neurochem. 88:326-336(2004).
 CC -1- FUNCTION: GTPase-activating protein for the ADP ribosylation
 CC factor family (Potential).
 CC -1- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdinsP3)
 CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
 CC stoichiometry of two binding sites for InsP4 with identical
 CC affinity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
 CC the plasma membrane. Excluded from the nucleus.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9NPP8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9NPP8-2; Sequence=VSP_011180;
 CC Note=May be due to a competing acceptor splice site. No
 CC experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney,
 CC skeletal muscle and adrenal gland. Weakly expressed in thyroid,
 CC liver, heart, lung, small intestine, peritoneal blood leukocytes.
 CC Not detected in spinal cord, brain, stomach, trachea, colon, lymph
 CC node and bone marrow.
 CC -1- SIMILARITY: Contains 1 Arf-GAP domain.
 CC -1- SIMILARITY: Contains 2 PH domains.
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 CC -----
 DR EMBL; AJ238994; CAB88383.1; -;
 DR EMBL; AJ272195; CAB77266.1; -;
 DR EMBL; AJ242783; CAC40651.1; -;
 DR EMBL; BC033758; AAC33758.1; -;
 DR GeneW; HGNC:16487; CEN1A2.
 DR H-InvDB; HIX0013699; -;
 DR MIM; 608635; -;
 DR InterPro; IPR001164; hrip_1like.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011036; PH_related.
 DR Pfam; PF01412; ArfGAP; 1.
 DR Pfam; PF00169; PH; 2.
 DR PRINTS; PR00405; REVINTRACTNG.
 DR SMART; SM00105; ArfGAP; 1.
 DR SMART; SM00233; PH; 2.
 DR PROSITE; PS50115; ARRGAP; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 2.
 KW Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc;
 KW Zinc-finger.

FT DOMAIN 9 131 Arf-GAP.
 FT ZN FING 25 48 C4-type.
 FT DOMAIN 132 233 PH 1.
 FT DOMAIN 255 361 PH 2.
 FT VASAPLIC 269 269 Missing (in isoform 2).
 FT FT 12 /FTId=VSP_011180.
 FT CONFLICT 12 L -> P (in Ref. 3).
 SQ SEQUENCE 381 AA; 44348 MM; 4FAE208072A92C01 CRC64;
 Query Match 69.0%; Score 40; DB 1; Length 381;
 Best Local Similarity 66.7%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 WDDSLSEFL 11
 Db 69 WDDSLSEFL 77
 RESULT 10
 CE22_MOUSE STANDARD; PRT; 381 AA.
 AC OBR2V5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Centaurin alpha 2.
 GN Name=Cent2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL J. Neurochem. 88:326-336(2004).
 CC -1- FUNCTION: GTPase-activating protein for the ADP ribosylation
 CC factor family (Potential).
 CC -1- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdinsP3)
 CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
 CC stoichiometry of two binding sites for InsP4 with identical
 CC affinity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
 CC the plasma membrane. Excluded from the nucleus (By similarity).
 CC -1- SIMILARITY: Contains 1 Arf-GAP domain.
 CC -1- SIMILARITY: Contains 2 PH domains.
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CC -----
DR EMBL: BC027165; AA027165.1; -.
DR MGD; MGI:2663075; Centa2.
DR InterPro; IPR001164; hRIP_1like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR Pfam; PF01412; ArfGAP; 1.
DR Pfam; PF00169; PH; 2.
DR PRINTS; PR00405; REVINTACTING.
DR SMART; SM00105; ArfGAP; 1.
DR SMART; SM00233; PH; 2.
DR PROSITE; PS00115; ARFGAP; 1.
DR PROSITE; PS00003; PH DOMAIN; 2.
KW GTPase activation; Metal-binding; Repeat; zinc; zinc-finger.
FT DOMAIN 9 132
FT 2N_FING 25 48
FT 2N_FING 132 233
FT DOMAIN 255 361
FT 2N_FING 255 361
FT PH 2.
SQ SEQUENCE 381 AA; 43989 MW; 2E504CEFOACD84D5 CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 1; Length 381;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WDDSLSEFL 11
DB 69 WDDSLSEFL 77

RESULT 11
GLPK_RHIME STANDARD; PRT; 497 AA.
ID 086033;
AC 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
DE (Glycerokinase) (GK).
GN Name=glpk; OrderedLocustNames=RB1135; ORFNames=SMB21009;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteriia; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
RA Golding B., Pehler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti."
RT Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
RN [2]
RP SEQUENCE OF 1-59 FROM N.A.
RC STRAIN=SU47 / 1021;
RX MEDLINE=99121023; PubMed=9922248;
RA Aneja P., Charles T.C.;
RT "Poly-3-hydroxybutyrate degradation in Rhizobium (Sinorhizobium)
RT meliloti: isolation and characterization of a gene encoding 3-
RT hydroxybutyrate dehydrogenase."
RT J. Bacteriol. 181:849-857(1999).
CC -1- FUNCTION: Key enzyme in the regulation of glycerol uptake and
CC metabolism.
CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol 3-
CC phosphate.
CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
CC -1- SIMILARITY: Belongs to the fucokinase / glucokinase /
CC glycerokinase / xylokinase family.
CC -----
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CC -----
DR EMBL: AL591985; CAC49535.1; -.
DR EMBL; AF080548; AAD12735.1; -.
DR PIR; G95983; G95983.
DR HSSP; P08859; 1GLC.
DR HAMAP; MF_00186; -.
DR InterPro; IPR000577; PGKY kin.
DR InterPro; IPR005929; Glycerol_kin.
DR Pfam; PF02782; PGKY_C; 1.
DR Pfam; PF00370; PGKY_N; 1.
DR TIGRFAMs; TIGR01311; glycerol_kin; 1.
DR PROSITE; PS00933; PGKY_KINASES_1; FALSE_NEG.
DR PROSITE; PS00445; PGKY_KINASES_2; 1.
KW ATP-binding; Complete proteome; Glycerol metabolism; Kinase; Plasmid;
KW Transferase.
FT NP_BIND 153 165
FT SEQUENCE 497 AA; 54419 MW; 42D342835ACC287 CRC64;
SQ SEQUENCE 497 AA; 54419 MW; 42D342835ACC287 CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 1; Length 497;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 AMDSLSEFL 11
DB 197 AMDDELTEVL 206

RESULT 12
Q48904 PRELIMINARY; PRT; 502 AA.
ID Q48904;
AC Q48904;
DT 01-NOV-1996 (TRENDEL. 01, Created)
DT 01-NOV-1996 (TRENDEL. 01, Last sequence update)
DT 01-MAR-2004 (TRENDEL. 26, Last annotation update)
DE ORP2.
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HUB 5-2-4;
RA Juerchott K., Boerner T.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z28337; CA882191.1; -.
DR PIR; S49113; S49113.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007936; VIRE.
DR Pfam; PF05272; VIRE; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 502 AA; 58859 MW; 98E61D5C214520B6 CRC64;

Query Match
Best Local Similarity 60.0%; Score 40; DB 2; Length 502;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 AMDSLSEFL 11
DB 434 SWEDSLSEFL 443

RESULT 13
YP93 CAEEL STANDARD; PRT; 1714 AA.
ID YP93 CAEEL;
AC Q09475;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative helicase C28H6.3 (EC 3.6.1.-).

```

GN ORFNames=C28H8.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Chabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: Belongs to the helicase family. SKI2 subfamily.
 CC -----
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 CC -----
 CC EMBL, U20861; AAA62291.2; -.
 DR WormBase; WBGene00016194; C28H8.3.
 DR WormPep; C28H8.3; CE29195.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD, 1.
 DR Pfam; PF00271; Helicase_C, 1.
 DR SMART; SM00487; DEADC, 1.
 DR SMART; SM00487; HELIC; 1.
 DR TIGFAMS; TIGR01870; cas TM1810; 2.
 KW ATP-binding; Helicase; Hydrolase; Hypothetical protein;
 KW Nuclear protein.
 FT NP_BIND 607 614 ATP (Potential).
 FT NP_BIND 806 813 ATP (Potential).
 FT SITE 913 916 DEVD box.
 SQ SEQUENCE 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;

 Query Match 69.0%; Score 40; DB 1; Length 1714;
 Best Local Similarity 88.9%; Pred. No. 3.4e-02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 AAMDLSSE 9
 DB 5 AAMDSDSE 13

RESULT 14
 ID_DYHC_NEUCR STANDARD; PRT; 4367 AA.
 AC P45443; Q7RVH1;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Dynein heavy chain, cytosolic (DYHC).
 GN Name=ro-1; ORFNames=NCU06976.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=95014704; PubMed=7929559; DOI=10.1083/jcb.127.1.139;
 RA Plamann M., Minko P.F., Tinley J.H., Bruno K.S.;
 RA "Cytoplasmic dynein and actin-related protein Arp1 are required for

RT normal nuclear distribution in filamentous fungi.",
 RL J. Cell Biol. 127:139-149(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX PubMed=12712197; DOI=10.1038/nature01554;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Renhan B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endtz M.,
 RA Qui D., Tanke P., Bell-Pedersen D., Nelson M.A.,
 RA Werner-Washburne M., Selitrenikoff C.P., Kinney J.A., Braun E.L.,
 RA Zelter A., Schulte U., Kotne G.O., Jedd G., Mewes H.-W., Staben C.,
 RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
 RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamyskas M.,
 RA Mancuel E., Bielke C., Rudd S., Friseman D., Kravtsova S.,
 RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
 RA Macino G., Catchside D., Li M., Pratt R.J., Omani S.A.,
 RA Desouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
 RA Yarden O., Plamann M., Siller S., Dunlap J., Radford A., Aramayo R.,
 RA Narey D.O., Alex L.A., Mannhaupt G., Eboile D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
 RA "The genome sequence of the filamentous fungus Neurospora crassa.",
 RL Nature 422:859-868(2003).
 CC -1- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
 CC retrograde motility of vesicles and organelles along microtubules.
 CC Dynein has ATPase activity; the force-producing power stroke is
 CC thought to occur on release of ADP. Required to maintain uniform
 CC nuclear distribution in hyphae.
 CC -1- SUBUNIT: Consists of at least two heavy chains and a number of
 CC intermediate and light chains.
 CC -1- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
 CC (which binds cargo and interacts with other dynein components),
 CC and the head or motor domain. The motor contains six tandemly-
 CC linked AAA domains in the head, which form a ring. A stalk-like
 CC structure (formed by two of the coiled coil domains) protrudes
 CC between AAA 4 and AAA 5 and terminates in a microtubule-binding
 CC site. A seventh domain may also contribute to this ring; it is not
 CC clear whether the N-terminus or the C-terminus forms this extra
 CC domain. There are four well-conserved and two non-conserved ATPase
 CC sites, one per AAA domain. Probably only one of these (within AAA
 CC 1) actually hydrolyzes ATP, the others may serve a regulatory
 CC function.
 CC -1- SIMILARITY: Belongs to the dynein heavy chain family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, L31504; AAA64908.1; -.
 DR EMBL; AABX01000204; EAA33380.1; -.
 DR PIR; B54802; B54802.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR004273; Dynein_heavy.
 DR Pfam; PF03028; Dynein_heavy, 1.
 DR SMART; SM00382; AAA, 3.
 KW ATP-binding; Coiled coil; Dynein; Microtubule; Motor protein; Repeat.
 FT DOMAIN 1 1904 Stem (By similarity).
 FT DOMAIN 1905 2130 AAA 1 (By similarity).
 FT DOMAIN 2202 2460 AAA 2 (By similarity).
 FT DOMAIN 2566 2815 AAA 3 (By similarity).
 FT DOMAIN 2909 3179 AAA 4 (By similarity).
 FT DOMAIN 3193 3481 Stalk (By similarity).
 FT DOMAIN 3565 3794 AAA 5 (By similarity).
 FT DOMAIN 4003 4215 AAA 6 (By similarity).
 FT DOMAIN 676 693 Coiled coil (Potential).
 FT DOMAIN 1176 1215 Coiled coil (Potential).
 FT DOMAIN 1357 1351 Coiled coil (Potential).
 FT DOMAIN 1557 1574 Coiled coil (Potential).


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FT DOMAIN 1637 1668 Coiled coil (Potential).
FT DOMAIN 2195 2228 Coiled coil (Potential).
FT DOMAIN 3193 3236 Coiled coil (Potential).
FT DOMAIN 3423 3481 Coiled coil (Potential).
FT DOMAIN 3778 3809 Coiled coil (Potential).
FT NP_BIND 1943 1950 ATP (Potential).
FT NP_BIND 2240 2247 ATP (Potential).
FT NP_BIND 2605 2612 ATP (Potential).
FT NP_BIND 2947 2954 ATP (Potential).
SQ SEQUENCE 4367 AA; 495568 MW; 1E10F3E2D170D6DF CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 1; Length 4367;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AAMDLSLEP 10
Db 455 AMDESIKEF 463

RESULT 15
O87GV3 PRELIMINARY; PRT; 182 AA.
AC O87GV3;
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Hypothetical protein VPA1212.
GN OrderedLocusNames=VPA1212;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
CC NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Matino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nishima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yagunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
KM EMBL; AP005088; BAC62555.1; -
SQ SEQUENCE 182 AA; 2133 MW; 2559BEC89FD78332 CRC64;

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 182;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAMDLSLEP 10
Db 27 SSMDDNLTOF 36

RESULT 16
O6GMV7 PRELIMINARY; PRT; 236 AA.
AC O6GMV7;
DT 05-JUN-2004 (TRENBLREL. 27, Created)
DT 05-JUN-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUN-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheetz C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heltón E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DE EMBL; BC073795; AAR73795.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-bet; I.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 24950 MW; 3B0477247847E930 CRC64;

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 236;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAMDLSL 7
Db 109 AAMDLSL 115

RESULT 17
KAPI_BOVIN STANDARD; PRT; 397 AA.
ID KAPI_BOVIN
AC P24256;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE CAMP-dependent protein kinase, beta-2-catalytic subunit (EC 2.7.1.37)
DE (PKA C-beta-2).
GN Name=PRKCB2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=91161607; PubMed=2002051;
RA Wiemann S., Kinzel V., Pyerin W.;
RT "Isoform C beta 2, an unusual form of the bovine catalytic subunit of
RT CAMP-dependent protein kinase.";
RL J. Biol. Chem. 266:5140-5146(1991).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

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CC -1- ENZYME REGULATION: Activated by cAMP.
CC -1- SUBUNIT: A number of inactive tetrameric holoenzymes are produced
CC by the combination of homo- or heterodimers of the different
CC regulatory subunits associated with two catalytic subunits. cAMP
CC causes the dissociation of the inactive holoenzyme into a dimer of
CC regulatory subunits bound to four cAMP and two free monomeric
CC catalytic subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=N-terminal differences in alternatively spliced products
CC could be involved in regulation such as alternative targeting;
CC Name=2; Synonyms=Beta-2;
CC IsoId=P24256-1; Sequence=Displayed;
CC Name=1; Synonyms=Beta-1;
CC IsoId=P05131-1; Sequence=External;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Mainly expressed in heart and brain tissue.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. cAMP
CC subfamily.
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DR EMBL, M60482; AAA30424.1; -.
DR PIR, A23716; OKBOB2.
DR HSSP, P36887; ICTP.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000961; Kinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_kin_AS.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR Pfam: PF00433; Kinase C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART, SM00133; S_TK_X; 1.
DR SMART, SM00220; S_TK; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; ATP-binding; cAMP; Multigene family;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 90 344 Protein kinase.
FT NP_BIND 96 104 ATP (By similarity).
FT BINDING 119 119 ATP (By similarity).
FT ACT_SITE 213 213 Proton acceptor (By similarity).
FT MOD_RES 244 244 Phosphothreonine (By similarity).
FT MOD_RES 385 385 Phosphoserine (By similarity).
SQ SEQUENCE 397 AA; 46108 MW; 7F87EF50C32FE29 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 397;
Best Local Similarity 63.6%; Pred. No. 1.le+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AAMDLSSEFL 11
Db .56 ALMDRSMEFL 66

RESULT 18
OZ3M1 PRELIMINARY; PRT; 398 AA.
AC OZ3M1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp66H10244 (Hypothetical protein
DE DKFZp66K18247).
GN Name=DKFZp66H10244; Synonyms=DKFZp66K18247;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RG The German cDNA Consortium;
RA Mamut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC EMBL, BX537705; CAD97818.1; -.
CC EMBL, BX641026; CAB46017.1; -.
DR HSSP, P36887; ICTP.
DR GO, GO:0005524; F:ATP binding; IEA.
DR GO, GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO, GO:0016740; F:transferase activity; IEA.
DR GO, GO:0004686; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_kin_AS.
DR Pfam, PF00069; Kinase; 1.
DR ProDom, PD000001; Prot_kinase; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 398 AA; 46236 MW; 49EFAF3E426468FC CRC64;

Query Match 67.2%; Score 39; DB 2; Length 398;
Best Local Similarity 63.6%; Pred. No. 1.le+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AAMDLSSEFL 11
Db 57 ALMDRSMEFL 67

RESULT 19
O8W0B5 PRELIMINARY; PRT; 578 AA.
AC O8W0B5;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative cytochrome P-450LXX1A1 (CYP71A1) family.
GN Name=P0452P10.8;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijiishi S., Honda M., Ichikawa Y., Iiduma A., Iijima M., Ikeda M.,
RA Ikano M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono J.,
RA Machita K., Maehara T., Mizuno H., Mizuyayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,

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RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
 RA Shirokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yokawa K.,
 RA Zhong H., Iwana H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yan M., Jiang J., Gojobori T.,
 RT "The genome sequence and structure of rice chromosome 1,"
 CC Nature 420:312-316(2002).
 DR EMBL: AP003434; BAB78671.1; -.
 DR HSSP: P77901; IH5Z.
 DR Gramene; Q8W0B5; -.
 DR GO: GO:0004497; F:monooxygenase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR Pfam: PF00067; p450; 1.
 DR PRINTS: PR00463; EP4501.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 KW Heme; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 578 AA; 62437 MW; 11FEF3A4D3D1FB5 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 578;
 Best Local Similarity 63.6%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAMDLSSEFL 11
 DB 466 AAMGDSAEFV 476

RESULT 20
 OC021 PRELIMINARY; PRT; 751 AA.
 ID 06C021
 AC 06C021
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Similarity.
 GN ORFNames=YAL10F20614g;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=284591;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla B.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissarie A., Boyer J., Catolico L., Comandollet F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellens S., Portier S., Richard G.F., Straub M.E., Suleau A.,
 RA Swennens D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR382132; CAC78480.1; -.
 DR InterPro: IPR001623; DnaJ_N.
 DR Pfam: PF00226; DnaJ_1.
 DR SMART: SM00271; DnaJ_1.
 DR PROSITE: PS50076; DnaJ_2; 1.
 SQ SEQUENCE 751 AA; 85290 MW; 0A9E620ECB01102E CRC64;

Query Match 67.2%; Score 39; DB 2; Length 751;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WDDSLSEF 10
 DB 87 WDDSLSEF 94

RESULT 21
 OC7AB13 PRELIMINARY; PRT; 894 AA.
 ID 07AB13
 AC 07AB13
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE 2-oxoglutarate dehydrogenase, E1 component (EC 1.2.4.2).
 GN Name=SucA; OrderedLocustNames=GSU2449;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCA / ATCC 51573;
 RC PubMed=14671304; DOI=10.1126/science.1088727;
 RA Melhe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouir H.M., Feldblyum T.V., Uitterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments";
 RL Science 302:1967-1969(2003).
 DR EMBL: AE017180; AAR35822.1; -.
 DR TIGR: GSU2449; -.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0004491; F:oxoglutarate dehydrogenase (succinyl-transf. .); IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR001017; Dehydrogenase_E1.
 DR InterPro: IPR005475; Transketolase_CR.
 DR Pfam: PF00676; E1_dh; 1.
 DR Pfam: PF02779; Transket_pyr; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 894 AA; 99395 MW; C33888A0C8EFOA66 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 894;
 Best Local Similarity 77.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAMDLSSEF 10
 DB 620 AAMDLSSEF 628

RESULT 22
 OC7RY83 PRELIMINARY; PRT; 969 AA.
 ID 07RY83
 AC 07RY83
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU00022.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN-OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitchugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engle R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Innakiev P., Pedersen D., Nelson M., Mashburne M.,
RA Seitzemunkoft C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal K., Kanyasselli M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kyrstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.C., Glass L., Ordach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Navvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL: AABX01000729; EAA27773.1; -
SQ SEQUENCE 969 AA; 10665 MW; 869181A24C9DB1D CRC64;

Query Match 67.2%; Score 39; DB 2; Length 969;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WDDSLSEFL 11
Db 667 WDDALSEWV 675

RESULT 23
ID Q98TR8 PRELIMINARY; PRT; 1466 AA.
AC Q98TR8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Cyclic fibrosis transmembrane conductance regulator.
GN Name=CFTR;
OS Bufo bufo (European toad).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Bufonidae; Bufo.
CX NCBI_TaxId=8384;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Belly skin;
RA Amstrup J., Hvid Larsen E.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC EMBL: AY026761; AAK07685.1; -.
DR HSP; 000555; ICKX.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity; coupled to transmembrane m. .; IEA.
DR GO: GO:0005254; F:chloride channel activity; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR001527; ABC membrane 1.
DR InterPro: IPR001439; ABC TM transp.
DR InterPro: IPR005291; CMF_cl_channel.
DR InterPro: IPR009147; CyfIb_channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR PRINTS: PRO1851; CYSP1BRGTLR.
DR ProDom: PD000006; ABC_transporter; 2.
DR SMART: SM00382; AAA; 3.
DR TIGRFAMs: TIGR00953; 3a01202; 1.
DR TIGRFAMs: TIGR01271; CTR_protein; 1.
DR PROSITE: PS50929; ABC_TM1F; 2.

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DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1466 AA; 16596 MW; EB692EC3C611C169 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 1466;
Best Local Similarity 54.5%; Pred. No. 4.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
Db 395 ASWDGFEFL 405

RESULT 24
ID YCX7_CHLRE STANDARD; PRT; 1995 AA.
AC P36495; Q37303;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 232.2 kDa protein (ORF1995) (ORF-8) (ORFA).
OS Chlamydomonas reinhardtii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
CX NCBI_TaxId=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97218038; PubMed=9065699; DOI=10.1007/s004380050368;
RA Boudreau E., Turmel M., Goldschmidt-Clermont M., Rochaix J.-D.,
RA Sivan S., Michaels A., Leu S.;
RT "A large open reading frame (orf1995) in the chloroplast DNA of
RT Chlamydomonas reinhardtii encodes an essential protein.";
RL Mol. Genet. 253:649-653(1997).
RN [2]
RP SEQUENCE OF 1573-1995 FROM N.A.
RC STRAIN=cw15;
RA Sivan S., Michaels A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1897-1995 FROM N.A.
RX MEDLINE=87031585; PubMed=2876928; DOI=10.1016/0378-1119(86)90038-7;
RA Woessner J.P., Gilham N.W., Boynton J.E.;
RT "The sequence of the chloroplast atpB gene and its flanking regions in
RT Chlamydomonas reinhardtii.";
RL Gene 44:17-28(1986).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=94207185; PubMed=8155879;
RA Boudreau E., Otis C., Turmel M.;
RT "Conserved gene clusters in the highly rearranged chloroplast genomes
RT of Chlamydomonas moewusii and Chlamydomonas reinhardtii.";
RL Plant Mol. Biol. 24:585-602(1994).
RN [5]
RP COMPLETE PLASTID GENOME.
RX MEDLINE=22305394; PubMed=12417694;
RA Maul J.E., Lilly J.W., Cui L., dePamphilis C.W., Miller W.,
RA Harris E.H., Stern D.B.;
RT "The Chlamydomonas reinhardtii plastid chromosome: islands of genes in
RT a sea of repeats.";
RL Plant Cell 14:2659-2679(2002).
CC -1- FUNCTION: Essential for cell growth. May be involved in binding
CC chloroplast DNA to either the chloroplast envelope or the
CC thylakoid membrane.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: To C.vulgaris ORF919.
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DR EMBL; X92726; CAA63385.1; -

DR EMBL; X76934; CAA54257.1; -

DR EMBL; M13704; AAA84144.1; ALT_INIT.

DR EMBL; BK00554; DAA00959.1; -

DR PIR; S41289; S41289.

DR PIR; 108166; 108166.

DR InterPro; IPR008934; AcPase_VanParase.

DR InterPro; IPR001123; Lyase_

KW Chloroplast; Thylakoid; Transmembrane.

FT TRANSMEM 31 51 Potential.

FT TRANSMEM 53 73 Potential.

FT TRANSMEM 106 126 Potential.

FT TRANSMEM 157 177 Potential.

FT TRANSMEM 212 232 Potential.

FT TRANSMEM 254 274 Potential.

FT TRANSMEM 307 327 Potential.

FT CONFLICT 1588 1588 K -> R (in Ref. 2).

FT SEQUENCE 1995 AA; 232194 MW; 55A3F167EAF5FC8A CRC64;

Query Match 67.2%; Score 39; DB 1; Length 1995;
Best Local Similarity 54.5%; Pred. No. 6, 2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 11
Db 1581 AGWDESLKFKV 1591

RESULT 25
DTHC_EMENTI STANDARD; PRT; 4344 AA.

AC P45444;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN Name=NDHA;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94181539; PubMed=8134356;
RA Xiang X., Beckwith S.M., Morris R.N.;
RT "Cytoplasmic dynein is involved in nuclear migration in Aspergillus
nidulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2100-2104(1994).
CC -1- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
retrograde motility of vesicles and organelles along microtubular
Dynein has ATPase activity; the force-producing power stroke is
thought to occur on release of ADP. Required to maintain uniform
nuclear distribution in hyphae.
CC -1- SUBUNIT: Consists of at least two heavy chains and a number of
intermediate and light chains.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
(which binds cargo and interacts with other dynein components),
and the head or motor domain. The motor contains six tandemly-
linked AAA domains in the head, which form a ring. A stalk-like
structure (formed by two of the coiled coil domains) protrudes
between AAA 4 and AAA 5 and terminates in a microtubule-binding
site. A seventh domain may also contribute to this ring; it is not
clear whether the N-terminus or the C-terminus forms this extra
domain. There are four well-conserved and two non-conserved ATPase
sites, one per AAA domain. Probably only one of these (within AAA
1) actually hydrolyzes ATP, the others may serve a regulatory
function.
CC -1- SIMILARITY: Belongs to the dynein heavy chain family.

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CC -----

DR EMBL; U03904; AAA18338.1; -

DR PIR; A53489; A53489.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR004273; Dynein_heavy.

DR Pfam; PF03028; Dynein_heavy; 1.

DR SMART; SM00382; AAA; 3.

KW ATP-binding; Coiled coil; Dynein; Microtubule; Motor protein; Repeat.

FT DOMAIN 1 1894 AAA 1 (By similarity).

FT DOMAIN 1895 2120 AAA 2 (By similarity).

FT DOMAIN 2190 2448 AAA 3 (By similarity).

FT DOMAIN 2553 2800 AAA 4 (By similarity).

FT DOMAIN 2894 3163 AAA 5 (By similarity).

FT DOMAIN 3179 3463 Stalk (By similarity).

FT DOMAIN 3549 3780 AAA 6 (By similarity).

FT DOMAIN 3994 4206 AAA 6 (By similarity).

FT DOMAIN 667 687 Coiled coil (Potential).

FT DOMAIN 913 933 Coiled coil (Potential).

FT DOMAIN 1321 1341 Coiled coil (Potential).

FT DOMAIN 1548 1564 Coiled coil (Potential).

FT DOMAIN 1627 1656 Coiled coil (Potential).

FT DOMAIN 3179 3270 Coiled coil (Potential).

FT DOMAIN 3407 3463 Coiled coil (Potential).

FT DOMAIN 3700 3798 Coiled coil (Potential).

FT NP_BIND 1933 1940 ATP (Potential).

FT NP_BIND 2223 2230 ATP (Potential).

FT NP_BIND 2592 2599 ATP (Potential).

FT NP_BIND 2932 2939 ATP (Potential).

FT SEQUENCE 4344 AA; 492470 MW; 302A586C4F8BD019 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 4344;
Best Local Similarity 75.0%; Pred. No. 1, 4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WDDSLSEFL 10
Db 446 WDDNLKEF 453

RESULT 26
Q73YE0 PRELIMINARY; PRT; 170 AA.

AC Q73YE0;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=MAP2016;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang O., Amonsin A., Alt D., Kapur V.;
RL Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017234; AAS04333.1; -
KW Complete proteome.
SQ SEQUENCE 170 AA; 19523 MW; 3A0C9E48C606E3B2 CRC64;

Query Match 65.5%; Score 38; DB 2; Length 170;
Best Local Similarity 77.8%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAMDLSLSEFL 10

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Db      20  AAMDVLSTF 28

RESULT 27
Q67NP3  PRELIMINARY; PRT; 215 AA.
ID Q67NP3
AC Q67NP3;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=STH1715;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCB1_TaxId=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14863;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsui T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum."
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006840; BAD40700.1; -.
DR InterPro; IPR003817; PS_Decarboxylase.
DR InterPro; IPR004428; PS_Decarb_rel.
DR Pfam; PF02666; PS_Decarboxylase; 1.
DR TIGRFAMs; TIGR00164; PS_decarb_rel; 1.
KW Hypothetical protein.
SQ SEQUENCE 215 AA; 23743 MW; C502881B596D8E9 CRC64;

Query Match      65.5%; Score 38; DB 2; Length 215;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAMDLSLSE 9
DB 122 AAMDPTVGE 130

RESULT 28
Q31358  PRELIMINARY; PRT; 244 AA.
ID Q31358
AC Q31358;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Major histocompatibility class II protein.
GN Name=mhc2deb; Synonyms=MHC Brre-DEB;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCB1_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95130065; PubMed=7829056;
RA Sultman H., Mayer W.E., Figueroa F., O'Huigin C., Klein J.;
RT "Organization of Mhc class II B genes in the zebrafish (Brachydanio
RT rerio)."
RN Genomics 23:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC Submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.
RA EMBL; U08874; AA87895.1; -.
DR HSSP; Q31135; 1ES0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045012; P:MHC class II receptor activity; IEA.
DR GO; GO:0018884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0018886; P:antigen processing, exogenous antigen via M..; IEA.
DR GO; GO:0006955; P:immune response; IEA.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR Prodom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 244 AA; 28014 MW; 6A84C5AD721CEB8F8 CRC64;

Query Match      65.5%; Score 38; DB 2; Length 244;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAMDLSLSE 9
DB 201 AAMDSSLSE 208

RESULT 29
Q631V6  PRELIMINARY; PRT; 252 AA.
ID Q631V6
AC Q631V6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Probable transcriptional regulator.
GN ORFNames=BTZK4740;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCB1_TaxId=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (Jul-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU15537.1; -.
SQ SEQUENCE 252 AA; 29184 MW; 208B07DEB90A1DB2 CRC64;

Query Match      65.5%; Score 38; DB 2; Length 252;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAMDLSLSEFL 11
DB 129 SAMNDTLEVL 139

RESULT 30
Q72Y69  PRELIMINARY; PRT; 252 AA.
ID Q72Y69
AC Q72Y69;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedlocusNames=BCE5152;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCB1_TaxId=222523;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oksford O.A., Helgason B., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Anguino J.S.V., Kolonay J.F.,
RA Nelson W.C., Koileov A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1."
RL Nucleic Acids Res. 32:977-988(2004).

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DR EMBL: AB017280; AAS44053.1; -.
DR TIGR: BCE5152; -.
DR InterPro: IPR002831; TrmB_Trans_reg.
DR InterPro: IPR009058; Wng_hlx_DNA_bnd.
DR InterPro: IPR011571; Wng_hlx_trn_reg.
DR Pfam: PF01978; TrmB; 1.
DR ProDom: PD006327; Wng_hlx_trn_reg; 1.
KW Complete proteome.
SQ
SEQUENCE 252 AA; 29139 MW; DDCFBEDA0CA40DED CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 11
Db 129 SAMMDTLEFL 139

RESULT 31
Qy 0815W5 PRELIMINARY; PRT; 252 AA.
AC 0815W5;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transcriptional regulator.
GN OrderedLocustNames=BC5010;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01562;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapatarel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
RA Overbeek R., Kyridides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL: AE017014; AAP11882.1; -.
DR InterPro: IPR002831; TrmB_Trans_reg.
DR InterPro: IPR009058; Wng_hlx_DNA_bnd.
DR InterPro: IPR011571; Wng_hlx_trn_reg.
DR Pfam: PF01978; TrmB; 1.
DR ProDom: PD006327; Wng_hlx_trn_reg; 1.
KW Complete proteome.
SQ
SEQUENCE 252 AA; 29164 MW; 3C0334F2B14A5C8C CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 11
Db 129 SAMMDTLEFL 139

RESULT 32
Qy 081X10 PRELIMINARY; PRT; 252 AA.
AC 081X10; Q6HRB3; Q6KNO;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BA5257; BAA54883; GBA5257;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Ames / Isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01566;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettein H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rillestone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Binkac L.M., Gwin M.L.,
RA Deboy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / Isolate 0581;
RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Fedorova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Stearns;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE017040; AAP28922.1; -.
DR EMBL: AE017034; AAP24368.1; -.
DR EMBL: AE017225; AAP57175.1; -.
DR TIGR: BA5257; -.
DR TIGR: GBA5257; -.
DR InterPro: IPR002831; TrmB_Trans_reg.
DR InterPro: IPR009058; Wng_hlx_DNA_bnd.
DR InterPro: IPR011571; Wng_hlx_trn_reg.
DR Pfam: PF01978; TrmB; 1.
DR ProDom: PD006327; Wng_hlx_trn_reg; 1.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 252 AA; 29185 MW; 282127D6704FD5C CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 11
Db 129 SAMMDTLEFL 139

RESULT 33
Qy 06HBPI PRELIMINARY; PRT; 252 AA.
ID 06HBPI;
AC 06HBPI;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Probable transcriptional regulator.
GN OrderedLocustNames=BR9727_4725;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL "Complete genome sequence of Bacillus thuringiensis 97-27."

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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT62564.1; -.
DR InterPro; IPR002831; Trmb_trans_reg.
DR InterPro; IPR009058; Wng_hlx_DNA_bnd.
DR InterPro; IPR011571; Wng_hlx_trns_reg.
DR Pfam; PF01978; Trmb; 1.
DR ProDom; PD006327; Wng_hlx_tran_reg; 1.
KW Complete proteome.
SQ SEQUENCE 252 AA; 29185 MW; 282127D06704F5DC CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 11
Db 129 SAMDTLLEFL 139

RESULT 34
074E50 PRELIMINARY; PRT; 299 AA.
AC 074E50;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE TPR domain protein.
OS OrderedLocustNames=GSU1114;
OC Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolony J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weltsman J.E., Lovley H.M., Feldlyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Frazer C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34440.1; -.
DR TIGR; GSU114; -.
DR InterPro; IPR008940; Prenyl_trans.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR_1; 4.
DR SMART; SM00028; TPR; 5.
DR PROSITE; PS50005; TPR; 5.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Repeat; TPR repeat.
SQ SEQUENCE 299 AA; 33461 MW; AB663B1549C7342E CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 299;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 10
Db 164 WDDAISQF 171

RESULT 35
DAPA_XANAC STANDARD; PRT; 302 AA.
AC 06PLN5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 41, Last annotation update)

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DE Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDDS).
GN Name=dapa; OrderedLocustNames=XAC1760;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Queglio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cammaran F., Cardozo J., Chamargo F., Ciapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rosel N.M.,
RA Martins E.C., Melandris J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitejima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463 (2002).
CC -1- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate =
CC dihydrodipicolinate + 2 H(2)O.
CC -1- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
CC semialdehyde; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the DHDS family.
CC -----
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CC -----
DR EMBL; AE011807; AAM3624.1; -.
DR HSSP; P05640; IDHP.
DR HAMAP; MF_00418; -, 1.
DR InterPro; IPR005263; DAPA_synth.
DR InterPro; IPR002220; DHDS.
DR Pfam; PF00701; DHDS; 1.
DR PRINTS; PR00146; DHPICSNTHASE.
DR ProDom; PD001859; DHDS; 1.
DR TIGRFAMs; TIGR00674; dapa; 1.
DR PROSITE; PS00665; DHDS_1; 1.
DR PROSITE; PS00666; DHDS_2; 1.
KW Complete proteome; Diaminopimelate biosynthesis; Lyase;
KW Lysine biosynthesis.
FT ACT_SITE 162
SQ SEQUENCE 302 AA; 31018 MW; 884C08BD13DC299 CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 1; Length 302;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 10
Db 231 AAWDARLSEFL 240

RESULT 36
SRA3_CAEEL STANDARD; PRT; 329 AA.
ID SRA3_CAEEL
AC 009205;

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DN Serpinine receptor class alpha 3 (Sra-3 protein).
GN Name=sra-3; ORFNames=AH6.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
KW (1)
RN SEQUENCE FROM N.A.
RC STRAIN=Briscot N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the C.elegans receptor-like protein sra
family.
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CC EMBL, 248009; CAA88086.1; -.
CC PIR, T18622; T18622.
CC WormBase, WBGene00005029; sra-3.
CC WormPeP, AH6.7; CE01461.
CC InterPro, IPR000344; Sra_chemrecept.
CC Pfam, PF02117; Sra; 1.
CC PRINTS, PR00697; TMPTREINSRA.
KW Multigene family; Transmembrane.
FT TRANSMEM 25 45 Potential.
FT TRANSMEM 104 124 Potential.
FT TRANSMEM 144 164 Potential.
FT TRANSMEM 187 207 Potential.
FT TRANSMEM 238 258 Potential.
FT TRANSMEM 273 293 Potential.
SQ SEQUENCE 329 AA; 38548 MW; 5AC3FB73B996287 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 329;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDDSLSEF 10
DB 164 WDDPLSEY 171

RESULT 37
Q9F6D9 PRELIMINARY; PRT; 348 AA.
AC Q9F6D9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Acyl transferase.
GN Name=znuC;
OS Streptomyces sp. R1128.
OC Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=140437;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN=R1128;
RX MEDLINE=20517899; PubMed=10931852; DOI=10.1074/jbc.M006766200;
RA Marti T., Hu Z., Pohl N.L., Shah A.N., Khoeta C.,
"Cloning, nucleotide sequence, and heterologous expression of the

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RT biosynthetic gene cluster for R1128, a non-steroidal estrogen receptor
antagonist. Insights into an unusual priming mechanism.";
RL J. Biol. Chem. 275:33443-33448(2000).
DR EMBL, AF293442; AAC30190.1; -.
DR GO, GO:0016740; F:transferase activity; IEA.
DR GO, GO:0008152; P:metabolism; IEA.
DR InterPro, IPR01227; AC_transferase.
DR Pfam, PF00698; Acyl_transf_1; 1.
KW Transferase.
SQ SEQUENCE 348 AA; 36543 MW; D83E2D0C855A660 CRC64;

Query Match 65.5%; Score 38; DB 2; Length 348;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWDLSLSE 9
DB 322 AWDPLAE 329

RESULT 38
Q6R8A6 PRELIMINARY; PRT; 395 AA.
ID Q6R8A6;
AC Q6R8A6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Prgh.
GN Name=prgh;
OS Sodalis glossinidius.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_Taxid=63612;
RN (1)
RN SEQUENCE FROM N.A.
RA Dale C., Jones T., Pontes M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY508229; AAS6870.1; -.
SQ SEQUENCE 395 AA; 43940 MW; 3D2FA4BA8CA6696 CRC64;

Query Match 65.5%; Score 38; DB 2; Length 395;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAMDLSLEF 10
DB 119 AAMDITLNF 128

RESULT 39
Q76S23 PRELIMINARY; PRT; 443 AA.
ID Q76S23;
AC Q76S23;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE MC017L (B-M,N,L,7 protein).
GN Name=MC017L; Synonyms=B-M,N,L,7;
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_Taxid=10280;
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE=96325459; PubMed=8670425;
RA Senkevitch T.G., Bugert J.D., Sisler J.R., Koonin E.V., Darai G.,
Moss B.;
"Genome sequence of a human tumorigenic poxvirus: prediction of
RT specific host response-evasion genes.";
RL Science 273:813-816(1996).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97093414; PubMed=8938976;

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RA Martin-Gallardo A., Moratilla M., Funes J.M., Agromayor M., Nunez A.,
 RA Varas A.J., Collado M., Valencia A., Lopez-Estebaranz J.L.,
 RA Estebaranz M.;
 RT "Sequence analysis of a Molluscum contagiosum virus DNA region which
 RT includes the gene encoding protein kinase 2 and other genes with
 RT unique organization.";
 RL Virus Genes 13:19-29(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159;
 RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
 RA Lopez-Estebaranz J.L., Estebaranz M., Martin-Gallardo A.,
 RT "A random DNA sequencing, computer-based approach for the generation
 RT of a gene map of molluscum contagiosum virus.";
 RL Virus Genes 14:73-80(1997).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL, U60315; AAC55145.1; -.
 DR EMBL, U86894; AAB57937.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR008790; Pox_ser_thr_kin.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001854; Ribosomal_L29.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF05445; Pox_ser_thr_kin; 1.
 DR PIRSF; PIRSF015695; STPK_F10L; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00579; RIBOSOMAL_L29; UNKNOWN 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 443 AA; 52077 MW; 6EE91137BA113CEA CRC64;

Query Match 65.5%; Score 38; DB 2; Length 443;
 Best Local Similarity 63.6%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 AAMDLSLEFL 11
 Db 390 AAMSKALGEFL 400

RESULT 40
 083155 PRELIMINARY; PRT; 443 AA.
 AC 083155; O12529; O12603; O12818; O12884;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Protein kinase 2 homolog (CK2 protein).
 GN Name=LIL; Synonyms=CK2;
 OS Molluscum contagiosum virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10279;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Martin-Gallardo A., Moratilla M., Funes J.M., Agromayor M., Nunez A.,
 RA Varas A.J., Collado M., Valencia A., Lopez-Estebaranz J.L.,
 RA Estebaranz M.;
 RT "Sequence analysis of a Molluscum contagiosum virus DNA region which
 RT includes the gene encoding protein kinase 2 and other genes with
 RT unique organization.";
 RL Virus Genes 0:0-0(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCV 1;
 RX MEDLINE=97152522; PubMed=9000105;
 RA Douglas N.J., Blake N.W., Cream J.J., Soteriou B.A., Zhang H.Y.,
 RA Theodoridou A., Archard L.C.;
 RT "Similarity in genome organization between Molluscum contagiosum virus

RT (MCV) and vaccinia virus (VV): identification of MCV homologues of the
 RT VV genes for protein kinase 2, structural protein VP8, RNA polymerase
 RT 35 kDa subunit and beta-hydroxysteroid dehydrogenase.";
 RL J. Gen. Virol. 77:3113-3120(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCV 1;
 RA Douglas N., Blake N., Archard L.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL, U52849; AAB97934.1; -.
 DR EMBL, U32423; AAB9658.1; -.
 DR PIR; T30619; T30619.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR008790; Pox_ser_thr_kin.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001854; Ribosomal_L29.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF05445; Pox_ser_thr_kin; 1.
 DR PIRSF; PIRSF015695; STPK_F10L; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00579; RIBOSOMAL_L29; UNKNOWN 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 443 AA; 52077 MW; 6EE91137BA113CEA CRC64;

Query Match 65.5%; Score 38; DB 2; Length 443;
 Best Local Similarity 63.6%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 AAMDLSLEFL 11
 Db 390 AAMSKALGEFL 400

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 Job time : 75.2135 secs

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